SEQUENCE LISTING

<110> Pompejus, Markus
Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor
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    135                 140                 145

ggt ggt cag cag cag cgt ctg tgc atc gct cgc gcg atc gcg gtt gag   595
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cca gaa atc ctc ctc atg gac gag cct tgc tcc gcg ctt gac cca atc   643
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gat cag acc gcg ttc tac tcc ctg gag gcg acc ggt agg cca ggt cgt   787
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230                 235                 240                 245

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         35                  40                  45

Ile Asn Arg Met His Glu Val Thr Pro Gly Ala Tyr Val Lys Gly Glu
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Ile Leu Leu Asp Gly Glu Asn Ile Tyr Gly Ser Lys Ile Asp Pro Val
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Ala Val Arg Asn Thr Ile Gly Met Val Phe Gln Lys Ala Asn Pro Phe
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Arg Gly Ala Asn Leu Trp Glu Glu Val Lys Asp Arg Leu Asp Lys Pro
    130                 135                 140

Gly Gly Gly Leu Ser Gly Gly Gln Gln Gln Arg Leu Cys Ile Ala Arg
145                 150                 155                 160

Ala Ile Ala Val Glu Pro Glu Ile Leu Leu Met Asp Glu Pro Cys Ser
                165                 170                 175

Ala Leu Asp Pro Ile Ser Thr Leu Ala Val Glu Asp Leu Ile His Glu
            180                 185                 190

Leu Lys Glu Glu Phe Thr Ile Val Ile Val Thr His Asn Met Gln Gln
        195                 200                 205

Ala Ala Arg Val Ser Asp Gln Thr Ala Phe Tyr Ser Leu Glu Ala Thr
    210                 215                 220

Gly Arg Pro Gly Arg Leu Val Glu Ile Gly Pro Thr Lys Lys Ile Phe
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09/16/2003 15:39:39

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                                              Met Thr Asn Asn Val
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gtt act ccg cgc atg gat gag cct tta aag aag agc tca gcc ttc acc 163
Val Thr Pro Arg Met Asp Glu Pro Leu Lys Lys Ser Ser Ala Phe Thr
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gac atc tcc tcc agc cgt aag acc acc aac acc gca gca acc gtc atc 211
Asp Ile Ser Ser Ser Arg Lys Thr Thr Asn Thr Ala Ala Thr Val Ile
            25                  30                  35

att tat ggt gcg atg ctc atc gca gct gtg cca ctg gtt tgg gtg ctg 259

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Ile Tyr Gly Ala Met Leu Ile Ala Ala Val Pro Leu Val Trp Val Leu
          40                  45                  50

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     55                  60                  65

tgg tcc acc tcc cag gct ggc gtc atg ctg atg ctg cca ggc ggc ggt   355
Trp Ser Thr Ser Gln Ala Gly Val Met Leu Met Leu Pro Gly Gly Gly
 70                  75                  80                  85

gca gct cac ccc atg atc ggt acc ttc atg cag gcg gta gtc acc tcg   403
Ala Ala His Ala Met Ile Gly Thr Phe Met Gln Ala Val Val Thr Ser
                 90                  95                 100

gtg att tcc att cca atc ggt atc ttc acc gca atc tac ttg gtg gaa   451
Val Ile Ser Ile Pro Ile Gly Ile Phe Thr Ala Ile Tyr Leu Val Glu
            105                 110                 115

tac tcc aac ggt aac cgt ctc gga cgc ttg acc acc ttc atg gtt gac   499
Tyr Ser Asn Gly Asn Arg Leu Gly Arg Leu Thr Thr Phe Met Val Asp
        120                 125                 130

atc ctc acc ggt gtt cct tcc atc gtt gcg gca ctg ttc gtg tac tcc   547
Ile Leu Thr Gly Val Pro Ser Ile Val Ala Ala Leu Phe Val Tyr Ser
    135                 140                 145

ttg tgg atc gtg ctc ttc ggc ttc gac cgc tcc ggc ttc gca gtg tcc   595
Leu Trp Ile Val Leu Phe Gly Phe Asp Arg Ser Gly Phe Ala Val Ser
150                 155                 160                 165

ctg tca ctg gtg att ttg atg gtt cca gtg atc atc cga aac acc gaa   643
Leu Ser Leu Val Ile Leu Met Val Pro Val Ile Ile Arg Asn Thr Glu
                170                 175                 180

gaa atg ctc cgc gtt gtt cct cag gat ctg cgt gaa gcg tcc tac gca   691
Glu Met Leu Arg Val Val Pro Gln Asp Leu Arg Glu Ala Ser Tyr Ala
            185                 190                 195

ctg ggc gtg cca aag tgg aag acc atc gca aag atc gtt ctc cca acc   739
Leu Gly Val Pro Lys Trp Lys Thr Ile Ala Lys Ile Val Leu Pro Thr
        200                 205                 210

gca ctg tcc ggt atc gtc acc ggc gtc atg ctc gca gtc gct cgt gtc   787
Ala Leu Ser Gly Ile Val Thr Gly Val Met Leu Ala Val Ala Arg Val
    215                 220                 225

atg ggt gag tcc gca cca gtt ctg gtc ttg gtt ggt tcc tcc cag gcc   835
Met Gly Glu Ser Ala Pro Val Leu Val Leu Val Gly Ser Ser Gln Ala
230                 235                 240                 245

atc aac tgg aac cca ttc ggc ggt ccg cag gct tcc ctt cca ctg atg   883
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atg ctt gat atg tac aag gcc ggc acc gca cca gca acg ctg gac aag   931
Met Leu Asp Met Tyr Lys Ala Gly Thr Ala Pro Ala Thr Leu Asp Lys
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ctg tgg ggc gca gcc ctc acc ctg gtg ctc atc atc gct gtc ctg aac   979
Leu Trp Gly Ala Ala Leu Thr Leu Val Leu Ile Ile Ala Val Leu Asn
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        280                 285                 290

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         35                  40                  45

Leu Val Trp Val Leu Trp Thr Val Ile Ser Arg Gly Ile Ala Pro Ile
     50                  55                  60

Leu Thr Ala Asp Trp Trp Ser Thr Ser Gln Ala Gly Val Met Leu Met
 65                  70                  75                  80

Leu Pro Gly Gly Gly Ala Ala His Ala Met Ile Gly Thr Phe Met Gln
                 85                  90                  95

Ala Val Val Thr Ser Val Ile Ser Ile Pro Ile Gly Ile Phe Thr Ala
            100                 105                 110

Ile Tyr Leu Val Glu Tyr Ser Asn Gly Asn Arg Leu Gly Arg Leu Thr
        115                 120                 125

Thr Phe Met Val Asp Ile Leu Thr Gly Val Pro Ser Ile Val Ala Ala
    130                 135                 140

Leu Phe Val Tyr Ser Leu Trp Ile Val Leu Phe Gly Phe Asp Arg Ser
145                 150                 155                 160

Gly Phe Ala Val Ser Leu Ser Leu Val Ile Leu Met Val Pro Val Ile
                165                 170                 175

Ile Arg Asn Thr Glu Glu Met Leu Arg Val Val Pro Gln Asp Leu Arg
            180                 185                 190

Glu Ala Ser Tyr Ala Leu Gly Val Pro Lys Trp Lys Thr Ile Ala Lys
        195                 200                 205

Ile Val Leu Pro Thr Ala Leu Ser Gly Ile Val Thr Gly Val Met Leu
    210                 215                 220

Ala Val Ala Arg Val Met Gly Glu Ser Ala Pro Val Leu Val Leu Val
225                 230                 235                 240

Gly Ser Ser Gln Ala Ile Asn Trp Asn Pro Phe Gly Gly Pro Gln Ala
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245 250 255

Ser Leu Pro Leu Met Met Leu Asp Met Tyr Lys Ala Gly Thr Ala Pro
260 265 270

Ala Thr Leu Asp Lys Leu Trp Gly Ala Ala Leu Thr Leu Val Leu Ile
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Val Lys Gln
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Met Ala Thr Asn Glu
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tca gtc tcg gag aag caa cgc ctg gat gca acc agg gtg cag gca cat 163
Ser Val Ser Glu Lys Gln Arg Leu Asp Ala Thr Arg Val Gln Ala His
10 15 20

cct gta gca gtt aat gcg aac tcc tct cag acc aag cct tca aag aag 211
Pro Val Ala Val Asn Ala Asn Ser Ser Gln Thr Lys Pro Ser Lys Lys
25 30 35

att gtc gcc gaa ggt ggc gga agc gtt aag cgt ccc ggc gat cgc atc 259
Ile Val Ala Glu Gly Gly Gly Ser Val Lys Arg Pro Gly Asp Arg Ile
40 45 50

ttc gaa gtc cta tcc acc gct tct gca gca atc att act gcg ata atc 307
Phe Glu Val Leu Ser Thr Ala Ser Ala Ala Ile Ile Thr Ala Ile Ile
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Arg Asn Ala Glu Gly Ile Gly Gly Phe Phe Thr Tyr Ser Gly Ala Trp
90 95 100

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Asn Thr Thr Asp Ile Asp Ala Met Tyr Phe Gly Ile Pro Asn Leu Leu
105 110 115

gct gca aca ctt ctc atc tct gtc atc gca ctg atc atc gcc atg ccg 499

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Ala Ala Thr Leu Leu Ile Ser Val Ile Ala Leu Ile Ile Ala Met Pro
        120                 125                 130

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    135                 140                 145

ctg gtt aag cca ctt ggc tac atg gtg gac atg ctg gct gct gtg cct   595
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150                 155                 160                 165

tcc atc gtc tac ggc ctt tgg ggc tgg cag gtg ctc gga cca gct ctg   643
Ser Ile Val Tyr Gly Leu Trp Gly Trp Gln Val Leu Gly Pro Ala Leu
                170                 175                 180

tcc ggt ttc tac acc tgg att gaa agc tgg ggc gga agc ttc ttc ctc   691
Ser Gly Phe Tyr Thr Trp Ile Glu Ser Trp Gly Gly Ser Phe Phe Leu
            185                 190                 195

ttc gct act tac caa aac tca cct tct ttt gct acc ggc cgt aac atg   739
Phe Ala Thr Tyr Gln Asn Ser Pro Ser Phe Ala Thr Gly Arg Asn Met
        200                 205                 210

ctc acc ggt ggc atc gtg ctc gca gtg atg atc ctt cct gtt atc gaa   787
Leu Thr Gly Gly Ile Val Leu Ala Val Met Ile Leu Pro Val Ile Glu
    215                 220                 225

gca acc gca cgt gaa gtt ttc ata cag act cca aag ggc cac att gaa   835
Ala Thr Ala Arg Glu Val Phe Ile Gln Thr Pro Lys Gly His Ile Glu
230                 235                 240                 245

tct gct ctt gca ctt ggc gca acc cgc tgg gaa gtc gtt cgt ttg acg   883
Ser Ala Leu Ala Leu Gly Ala Thr Arg Trp Glu Val Val Arg Leu Thr
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Val Leu Pro Phe Gly Met Ser Gly Tyr Val Ser Gly Ala Met Leu Gly
            265                 270                 275

ctc ggc cgc gca ctg ggt gag acc atg gcg cta tac atg gtt gtt tct   979
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        280                 285                 290

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Pro Ser Ser Ala Phe Arg Phe Ser Leu Phe Asp Gly Gly Thr Thr Phe
    295                 300                 305

gca acg gcc atc gcc aat gcc gct cca gaa ttc aac gac aac acc cgc  1075
Ala Thr Ala Ile Ala Asn Ala Ala Pro Glu Phe Asn Asp Asn Thr Arg
310                 315                 320                 325

gca ggc gcg tac atc tcc gcc ggc ctc gtg ctg ttc gcc ctt acc ttc  1123
Ala Gly Ala Tyr Ile Ser Ala Gly Leu Val Leu Phe Ala Leu Thr Phe
                330                 335                 340

atc gtc aac gct ggc gct cgc gcc atg gtt aac cgc gga aag           1165
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Lys Pro Ser Lys Lys Ile Val Ala Glu Gly Gly Gly Ser Val Lys Arg
        35                  40                  45

Pro Gly Asp Arg Ile Phe Glu Val Leu Ser Thr Ala Ser Ala Ala Ile
    50                  55                  60

Ile Thr Ala Ile Ile Ile Ala Ile Ala Ala Phe Leu Ile Trp Arg Ala
65                  70                  75                  80

Val Pro Ala Leu Met Arg Asn Ala Glu Gly Ile Gly Gly Phe Phe Thr
                85                  90                  95

Tyr Ser Gly Ala Trp Asn Thr Thr Asp Ile Asp Ala Met Tyr Phe Gly
            100                 105                 110

Ile Pro Asn Leu Leu Ala Ala Thr Leu Leu Ile Ser Val Ile Ala Leu
        115                 120                 125

Ile Ile Ala Met Pro Ile Ala Leu Gly Ile Ala Ile Phe Leu Ser Asn
    130                 135                 140

Tyr Ser Pro Lys Arg Leu Val Lys Pro Leu Gly Tyr Met Val Asp Met
145                 150                 155                 160

Leu Ala Ala Val Pro Ser Ile Val Tyr Gly Leu Trp Gly Trp Gln Val
                165                 170                 175

Leu Gly Pro Ala Leu Ser Gly Phe Tyr Thr Trp Ile Glu Ser Trp Gly
            180                 185                 190

Gly Ser Phe Phe Leu Phe Ala Thr Tyr Gln Asn Ser Pro Ser Phe Ala
        195                 200                 205

Thr Gly Arg Asn Met Leu Thr Gly Gly Ile Val Leu Ala Val Met Ile
    210                 215                 220

Leu Pro Val Ile Glu Ala Thr Ala Arg Glu Val Phe Ile Gln Thr Pro
225                 230                 235                 240

Lys Gly His Ile Glu Ser Ala Leu Ala Leu Gly Ala Thr Arg Trp Glu
                245                 250                 255

Val Val Arg Leu Thr Val Leu Pro Phe Gly Met Ser Gly Tyr Val Ser
            260                 265                 270

Gly Ala Met Leu Gly Leu Gly Arg Ala Leu Gly Glu Thr Met Ala Leu
        275                 280                 285
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Tyr Met Val Val Ser Pro Ser Ser Ala Phe Arg Phe Ser Leu Phe Asp
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Gly Gly Thr Thr Phe Ala Thr Ala Ile Ala Asn Ala Ala Pro Glu Phe
305                 310                 315                 320

Asn Asp Asn Thr Arg Ala Gly Ala Tyr Ile Ser Ala Gly Leu Val Leu
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Phe Ala Leu Thr Phe Ile Val Asn Ala Gly Ala Arg Ala Met Val Asn
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                                              1               5

gat gcc ctc ctg cgc act tct ttg gca tcg gca gaa agc gct tta ggc   163
Asp Ala Leu Leu Arg Thr Ser Leu Ala Ser Ala Glu Ser Ala Leu Gly
                 10                  15                  20

aat gca gaa aag ctt gaa gag ctt cgt act gga tgc gag tct caa gcc   211
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             25                  30                  35

gtc gaa ctt ttg gcg ctt gaa act cct gta gcc cgt gat ctt cgc cag   259
Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala Arg Asp Leu Arg Gln
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Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile Thr Arg Met Gly Ala
     55                  60                  65

ctg gca atg cac gtg gct aat tcc gtg cgc cgc cgt tac ccc gat ccg   355
Leu Ala Met His Val Ala Asn Ser Val Arg Arg Arg Tyr Pro Asp Pro
 70                  75                  80                  85

gtg atc ccg gag gac atg cgt ggc tat ttc aag gag atg gcc cgc ctc   403
Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys Glu Met Ala Arg Leu
                 90                  95                 100

gca gct gac atg aca gat cat att cgt cag atc ctc att gat cct gaa   451
Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile Leu Ile Asp Pro Glu
            105                 110                 115
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cca gat ctt gcc cta gag atg gct aaa agc gat gac gcg gtg gat gat   499
Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp Asp Ala Val Asp Asp
        120                 125                 130

ctg cat cag cac atc atg cgt att ctc acg ctg cgt cct tgg cct cac   547
Leu His Gln His Ile Met Arg Ile Leu Thr Leu Arg Pro Trp Pro His
    135                 140                 145

gac acc aag agc gcg gtt gat ttg acg ctg ctt tcc cgc ttc tac gag   595
Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu Ser Arg Phe Tyr Glu
150                 155                 160                 165

cgt tac gcc gat cac acg gta aac gtg gcc gcc cgt atc att tac ctg   643
Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala Arg Ile Ile Tyr Leu
                170                 175                 180

tcc acc ggg ctg cac ccg gag gag tac atg gaa aag cgc gag caa caa   691
Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu Lys Arg Glu Gln Gln
            185                 190                 195

agg gcc gat gcc gac atg gag aag cgc tgg gcc gag ctg gag cgg cag   739
Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala Glu Leu Glu Arg Gln
        200                 205                 210

ttc cgc acc agc gag taaaaagctg cttctcgacg cta                    777
Phe Arg Thr Ser Glu
    215
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            20                  25                  30

Cys Glu Ser Gln Ala Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala
        35                  40                  45

Arg Asp Leu Arg Gln Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile
    50                  55                  60

Thr Arg Met Gly Ala Leu Ala Met His Val Ala Asn Ser Val Arg Arg
65                  70                  75                  80

Arg Tyr Pro Asp Pro Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys
                85                  90                  95

Glu Met Ala Arg Leu Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile
            100                 105                 110

Leu Ile Asp Pro Glu Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp
        115                 120                 125

Asp Ala Val Asp Asp Leu His Gln His Ile Met Arg Ile Leu Thr Leu
    130                 135                 140
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Arg Pro Trp Pro His Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu
145                 150                 155                 160

Ser Arg Phe Tyr Glu Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala
                165                 170                 175

Arg Ile Ile Tyr Leu Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu
            180                 185                 190

Lys Arg Glu Gln Gln Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala
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Glu Leu Glu Arg Gln Phe Arg Thr Ser Glu
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                                              Met Val Asn Ser Glu
                                                1               5

caa gcg ctt cat cag cat gat cct gca cca atc ctt cag ttg gat aaa   163
Gln Ala Leu His Gln His Asp Pro Ala Pro Ile Leu Gln Leu Asp Lys
                10                  15                  20

gtc tcc aag tcg ttt ggc cca gtc aac gtc att aat caa gtg agc atc   211
Val Ser Lys Ser Phe Gly Pro Val Asn Val Ile Asn Gln Val Ser Ile
            25                  30                  35

gat gtt cgc cct ggc agg gtg ctt gcg ctg ttg ggt gaa aat ggt gcg   259
Asp Val Arg Pro Gly Arg Val Leu Ala Leu Leu Gly Glu Asn Gly Ala
        40                  45                  50

ggt aaa tct acg ctg atc aag atg atg tcg ggt gtg tat cag cct gat   307
Gly Lys Ser Thr Leu Ile Lys Met Met Ser Gly Val Tyr Gln Pro Asp
    55                  60                  65

ggc ggg cag att ttg gtg gat gga aag ccc acg act ttg cct gat acg   355
Gly Gly Gln Ile Leu Val Asp Gly Lys Pro Thr Thr Leu Pro Asp Thr
70                  75                  80                  85

aaa act gct gag tct ttt ggc atc gct acg att cac cag gaa ttg aat   403
Lys Thr Ala Glu Ser Phe Gly Ile Ala Thr Ile His Gln Glu Leu Asn
                90                  95                  100

ctg gtg ccc acg atg acg gtg gcg gaa aac gtc atg ctg ggc cgc act   451
Leu Val Pro Thr Met Thr Val Ala Glu Asn Val Met Leu Gly Arg Thr
            105                 110                 115
```

```
cct cgg aag tgg ggt ttg gtc aat ttc aaa cat ttg cgc agg cag gca   499
Pro Arg Lys Trp Gly Leu Val Asn Phe Lys His Leu Arg Arg Gln Ala
        120                 125                 130

cag gcg gcg ctg gat ctc atc ggc gtg gat gtg gat ctg aat gct cag   547
Gln Ala Ala Leu Asp Leu Ile Gly Val Asp Val Asp Leu Asn Ala Gln
    135                 140                 145

gtg ggt tct tta gga atc gct agg cag cag atg gtg gag atc gcc aag   595
Val Gly Ser Leu Gly Ile Ala Arg Gln Gln Met Val Glu Ile Ala Lys
150                 155                 160                 165

gcg ttg tcc atg aat gcg cgg ata ttg att ttg gat gag ccc act gca   643
Ala Leu Ser Met Asn Ala Arg Ile Leu Ile Leu Asp Glu Pro Thr Ala
                170                 175                 180

gcg ttg act ggt cgt gaa att gat cag tta ttc aaa gtg gtg gat cag   691
Ala Leu Thr Gly Arg Glu Ile Asp Gln Leu Phe Lys Val Val Asp Gln
            185                 190                 195

ctg aaa gaa aaa ggc gtg gcc atg gtg ttt att tcg cac cac ttg gat   739
Leu Lys Glu Lys Gly Val Ala Met Val Phe Ile Ser His His Leu Asp
        200                 205                 210

gag atc gcg cgc atc ggc gat acc gtc tct gtg ctg cgt gat ggc cag   787
Glu Ile Ala Arg Ile Gly Asp Thr Val Ser Val Leu Arg Asp Gly Gln
    215                 220                 225

ttc atc gcg gag ctg cca gcg gat act gat gaa gat gag ctg gtg cgg   835
Phe Ile Ala Glu Leu Pro Ala Asp Thr Asp Glu Asp Glu Leu Val Arg
230                 235                 240                 245

ctg atg gtg ggt cgt agc att gaa aac cag tat ccg cgt agt gcg cca   883
Leu Met Val Gly Arg Ser Ile Glu Asn Gln Tyr Pro Arg Ser Ala Pro
                250                 255                 260

gag atc ggg cag cca ctg ttg gag gtg aaa aac ctc aac gcg gag ggc   931
Glu Ile Gly Gln Pro Leu Leu Glu Val Lys Asn Leu Asn Ala Glu Gly
            265                 270                 275

cgg ttc acg gat att tcc ttg act gtt cgc gct ggt gaa gtc gta ggc   979
Arg Phe Thr Asp Ile Ser Leu Thr Val Arg Ala Gly Glu Val Val Gly
        280                 285                 290

ctt gcc ggt ctt gtg ggt gct ggt cgc acg gaa gtg gtt cgc tcg att   1027
Leu Ala Gly Leu Val Gly Ala Gly Arg Thr Glu Val Val Arg Ser Ile
    295                 300                 305

gct ggc gtg gac aaa gtt gat tcc ggt gag gtg atc gtt gct ggc aag   1075
Ala Gly Val Asp Lys Val Asp Ser Gly Glu Val Ile Val Ala Gly Lys
310                 315                 320                 325

aaa ttg cgc ggc ggc gat att tcc gag gct att aaa aac ggc atc ggg   1123
Lys Leu Arg Gly Gly Asp Ile Ser Glu Ala Ile Lys Asn Gly Ile Gly
                330                 335                 340

cac att ccg gaa gat cga aaa gcc cag ggc ctg gtg ctg ggg tcg tct   1171
His Ile Pro Glu Asp Arg Lys Ala Gln Gly Leu Val Leu Gly Ser Ser
            345                 350                 355
```

Date Recue/Date Received 2020-05-15

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gtg gag gac aac ctg gga ttg gcg act ttg gcg tcg aca gcc cgc gca   1219
Val Glu Asp Asn Leu Gly Leu Ala Thr Leu Ala Ser Thr Ala Arg Ala
        360                 365                 370

ggt ttg gtc gat cga tca gga cag cac aaa cga gcc gcc gag gtc gcg   1267
Gly Leu Val Asp Arg Ser Gly Gln His Lys Arg Ala Ala Glu Val Ala
    375                 380                 385

gaa aaa ctc cgc atc cgg atg gca agc ctc aaa caa ccg att agc gat   1315
Glu Lys Leu Arg Ile Arg Met Ala Ser Leu Lys Gln Pro Ile Ser Asp
390                 395                 400                 405

tta tcg ggc ggc aat cag caa aag gcc gtg ttc ggc cgc tgg gtg ctt   1363
Leu Ser Gly Gly Asn Gln Gln Lys Ala Val Phe Gly Arg Trp Val Leu
                410                 415                 420

gcc ggg tca aac gtg ctg ctt ctc gac gaa ccg acc cgt ggc gtt gac   1411
Ala Gly Ser Asn Val Leu Leu Leu Asp Glu Pro Thr Arg Gly Val Asp
            425                 430                 435

gtc ggc gcg aag gtg gaa att tac aac atc att aat gag atg acg gaa   1459
Val Gly Ala Lys Val Glu Ile Tyr Asn Ile Ile Asn Glu Met Thr Glu
        440                 445                 450

aaa ggt ggc gct gtg ctc atg gtg tca tcg gag ctt ccc gaa gtc ttg   1507
Lys Gly Gly Ala Val Leu Met Val Ser Ser Glu Leu Pro Glu Val Leu
    455                 460                 465

ggc atg gct gat cgc att ttg gtc atg tct ggt gga cgc atc gca ggc   1555
Gly Met Ala Asp Arg Ile Leu Val Met Ser Gly Gly Arg Ile Ala Gly
470                 475                 480                 485

gaa ctg cca gcg aag gga aca acc cag gac gat gtc atg gct cta gct   1603
Glu Leu Pro Ala Lys Gly Thr Thr Gln Asp Asp Val Met Ala Leu Ala
                490                 495                 500

gtt tcc cag gtg gat gat tcc atc acc gag gaa gct gct gca gaa atc   1651
Val Ser Gln Val Asp Asp Ser Ile Thr Glu Glu Ala Ala Ala Glu Ile
            505                 510                 515

gaa aac aca aag gag gac cgt tgagcaccgc cgtagtttca cag            1695
Glu Asn Thr Lys Glu Asp Arg
        520
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<210> 10
<211> 524
<212> PRT
<213> Corynebacterium glutamicum

<400> 10

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Met Val Asn Ser Glu Gln Ala Leu His Gln His Asp Pro Ala Pro Ile
  1               5                  10                  15

Leu Gln Leu Asp Lys Val Ser Lys Ser Phe Gly Pro Val Asn Val Ile
             20                  25                  30

Asn Gln Val Ser Ile Asp Val Arg Pro Gly Arg Val Leu Ala Leu Leu
         35                  40                  45

Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Ile Lys Met Met Ser Gly
```

Substitute Page (Rule 26)

```
     50                  55                  60

Val Tyr Gln Pro Asp Gly Gly Gln Ile Leu Val Asp Gly Lys Pro Thr
 65                  70                  75                  80

Thr Leu Pro Asp Thr Lys Thr Ala Glu Ser Phe Gly Ile Ala Thr Ile
                 85                  90                  95

His Gln Glu Leu Asn Leu Val Pro Thr Met Thr Val Ala Glu Asn Val
            100                 105                 110

Met Leu Gly Arg Thr Pro Arg Lys Trp Gly Leu Val Asn Phe Lys His
        115                 120                 125

Leu Arg Arg Gln Ala Gln Ala Ala Leu Asp Leu Ile Gly Val Asp Val
    130                 135                 140

Asp Leu Asn Ala Gln Val Gly Ser Leu Gly Ile Ala Arg Gln Gln Met
145                 150                 155                 160

Val Glu Ile Ala Lys Ala Leu Ser Met Asn Ala Arg Ile Leu Ile Leu
                165                 170                 175

Asp Glu Pro Thr Ala Ala Leu Thr Gly Arg Glu Ile Asp Gln Leu Phe
            180                 185                 190

Lys Val Val Asp Gln Leu Lys Glu Lys Gly Val Ala Met Val Phe Ile
        195                 200                 205

Ser His His Leu Asp Glu Ile Ala Arg Ile Gly Asp Thr Val Ser Val
    210                 215                 220

Leu Arg Asp Gly Gln Phe Ile Ala Glu Leu Pro Ala Asp Thr Asp Glu
225                 230                 235                 240

Asp Glu Leu Val Arg Leu Met Val Gly Arg Ser Ile Glu Asn Gln Tyr
                245                 250                 255

Pro Arg Ser Ala Pro Glu Ile Gly Gln Pro Leu Leu Glu Val Lys Asn
            260                 265                 270

Leu Asn Ala Glu Gly Arg Phe Thr Asp Ile Ser Leu Thr Val Arg Ala
        275                 280                 285

Gly Glu Val Val Gly Leu Ala Gly Leu Val Gly Ala Gly Arg Thr Glu
    290                 295                 300

Val Val Arg Ser Ile Ala Gly Val Asp Lys Val Asp Ser Gly Glu Val
305                 310                 315                 320

Ile Val Ala Gly Lys Lys Leu Arg Gly Gly Asp Ile Ser Glu Ala Ile
                325                 330                 335

Lys Asn Gly Ile Gly His Ile Pro Glu Asp Arg Lys Ala Gln Gly Leu
            340                 345                 350

Val Leu Gly Ser Ser Val Glu Asp Asn Leu Gly Leu Ala Thr Leu Ala
        355                 360                 365

Ser Thr Ala Arg Ala Gly Leu Val Asp Arg Ser Gly Gln His Lys Arg
    370                 375                 380
```

```
Ala Ala Glu Val Ala Glu Lys Leu Arg Ile Arg Met Ala Ser Leu Lys
385                 390                 395                 400

Gln Pro Ile Ser Asp Leu Ser Gly Gly Asn Gln Gln Lys Ala Val Phe
                405                 410                 415

Gly Arg Trp Val Leu Ala Gly Ser Asn Val Leu Leu Leu Asp Glu Pro
            420                 425                 430

Thr Arg Gly Val Asp Val Gly Ala Lys Val Glu Ile Tyr Asn Ile Ile
        435                 440                 445

Asn Glu Met Thr Glu Lys Gly Gly Ala Val Leu Met Val Ser Ser Glu
    450                 455                 460

Leu Pro Glu Val Leu Gly Met Ala Asp Arg Ile Leu Val Met Ser Gly
465                 470                 475                 480

Gly Arg Ile Ala Gly Glu Leu Pro Ala Lys Gly Thr Thr Gln Asp Asp
                485                 490                 495

Val Met Ala Leu Ala Val Ser Gln Val Asp Asp Ser Ile Thr Glu Glu
            500                 505                 510

Ala Ala Ala Glu Ile Glu Asn Thr Lys Glu Asp Arg
        515                 520
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US20050153423A1

<210> 11
<211> 882
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(859)
<223> RXA02438

<400> 11

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caggttggaa ccctgactgg ttcatgttct tcctcggcgg caccctactt ctggctgttt 60

tgctcaatca ccgattcgag cgtttcaaca aggagcgatc atg aca gac ctc att   115
                                               Met Thr Asp Leu Ile
                                                 1               5

caa ctc cgc gaa gta tcc aaa aaa tac ggt gct ttc cag gcc ctc aac   163
Gln Leu Arg Glu Val Ser Lys Lys Tyr Gly Ala Phe Gln Ala Leu Asn
                10                  15                  20

gac atc aat ttg aac gtc cgc gca ggc gaa gtc acc tgt gtt ctg ggt   211
Asp Ile Asn Leu Asn Val Arg Ala Gly Glu Val Thr Cys Val Leu Gly
            25                  30                  35

gac aac ggc gcc gga aaa tcc acc ctc atc aag att ctc tcc ggc ctg   259
Asp Asn Gly Ala Gly Lys Ser Thr Leu Ile Lys Ile Leu Ser Gly Leu
        40                  45                  50

cat ccc gcc acc tcc ggc gaa gta atc gtg gcc ggc gat gta gtg aat   307
His Pro Ala Thr Ser Gly Glu Val Ile Val Ala Gly Asp Val Val Asn
    55                  60                  65
```

```
ttt gga tcc ccc cgc gac gcc ctc gac gcc gga atc gcc acc gtc tac   355
Phe Gly Ser Pro Arg Asp Ala Leu Asp Ala Gly Ile Ala Thr Val Tyr
 70                  75                  80                  85

caa gac cta gca gtg gtc ggg cag atg agt gtg tgg cgc aac ttc ttc   403
Gln Asp Leu Ala Val Val Gly Gln Met Ser Val Trp Arg Asn Phe Phe
                90                  95                 100

ctc ggc cag gaa ctc acc ggc cga ttt ggc gtt ctg aaa caa gaa gaa   451
Leu Gly Gln Glu Leu Thr Gly Arg Phe Gly Val Leu Lys Gln Glu Glu
            105                 110                 115

atg cgc cgc atc acc gac gaa caa ctc cgc gaa atg ggc atc gaa ctc   499
Met Arg Arg Ile Thr Asp Glu Gln Leu Arg Glu Met Gly Ile Glu Leu
        120                 125                 130

cgc gat gtc gac gtc cct gtg gcc tcc ctt tca ggt ggt caa cgc caa   547
Arg Asp Val Asp Val Pro Val Ala Ser Leu Ser Gly Gly Gln Arg Gln
    135                 140                 145

gtt gtc gcc atc gcc cgc gcc atc tac ttc ggc gcg cgc gtc ctc att   595
Val Val Ala Ile Ala Arg Ala Ile Tyr Phe Gly Ala Arg Val Leu Ile
150                 155                 160                 165

ttg gac gag ccc acc gca gcg ctg ggc gtg aaa caa tct ggc atg gtg   643
Leu Asp Glu Pro Thr Ala Ala Leu Gly Val Lys Gln Ser Gly Met Val
                170                 175                 180

ctg cgc ttt att gcc gca gca cgc gac cgg ggg atc ggc gtc att ttc   691
Leu Arg Phe Ile Ala Ala Ala Arg Asp Arg Gly Ile Gly Val Ile Phe
            185                 190                 195

atc acg cac aac ccc cac cac gcc tac ctt gtc ggt gat cac ttc atc   739
Ile Thr His Asn Pro His His Ala Tyr Leu Val Gly Asp His Phe Ile
        200                 205                 210

ctg ctc aac tta ggc aag cag gtc atg gac aaa tcc cgc gca gaa gtc   787
Leu Leu Asn Leu Gly Lys Gln Val Met Asp Lys Ser Arg Ala Glu Val
    215                 220                 225

gag ctg gaa gaa ctc acc ctc gcc atg tcc ggc ggc ggc gag ctc gac   835
Glu Leu Glu Glu Leu Thr Leu Ala Met Ser Gly Gly Gly Glu Leu Asp
230                 235                 240                 245

tca ctc agc cac gaa ttg aag cgt taacctactt cttcttttcg ctc         882
Ser Leu Ser His Glu Leu Lys Arg
                250
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<210> 12
<211> 253
<212> PRT
<213> Corynebacterium glutamicum

<400> 12

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Met Thr Asp Leu Ile Gln Leu Arg Glu Val Ser Lys Lys Tyr Gly Ala
  1               5                  10                  15

Phe Gln Ala Leu Asn Asp Ile Asn Leu Asn Val Arg Ala Gly Glu Val
            20                  25                  30
```

Thr Cys Val Leu Gly Asp Asn Gly Ala Gly Lys Ser Thr Leu Ile Lys
35 40 45

Ile Leu Ser Gly Leu His Pro Ala Thr Ser Gly Glu Val Ile Val Ala
50 55 60

Gly Asp Val Val Asn Phe Gly Ser Pro Arg Asp Ala Leu Asp Ala Gly
65 70 75 80

Ile Ala Thr Val Tyr Gln Asp Leu Ala Val Val Gly Gln Met Ser Val
85 90 95

Trp Arg Asn Phe Phe Leu Gly Gln Glu Leu Thr Gly Arg Phe Gly Val
100 105 110

Leu Lys Gln Glu Glu Met Arg Arg Ile Thr Asp Glu Gln Leu Arg Glu
115 120 125

Met Gly Ile Glu Leu Arg Asp Val Asp Val Pro Val Ala Ser Leu Ser
130 135 140

Gly Gly Gln Arg Gln Val Val Ala Ile Ala Arg Ala Ile Tyr Phe Gly
145 150 155 160

Ala Arg Val Leu Ile Leu Asp Glu Pro Thr Ala Ala Leu Gly Val Lys
165 170 175

Gln Ser Gly Met Val Leu Arg Phe Ile Ala Ala Ala Arg Asp Arg Gly
180 185 190

Ile Gly Val Ile Phe Ile Thr His Asn Pro His His Ala Tyr Leu Val
195 200 205

Gly Asp His Phe Ile Leu Leu Asn Leu Gly Lys Gln Val Met Asp Lys
210 215 220

Ser Arg Ala Glu Val Glu Leu Glu Glu Leu Thr Leu Ala Met Ser Gly
225 230 235 240

Gly Gly Glu Leu Asp Ser Leu Ser His Glu Leu Lys Arg
245 250

<210> 13
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXA00203

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aggaagctgc tgcagaaatc gaaaacacaa aggaggaccg ttgagcaccg ccgtagtttc 60

acagaagaag tccacaacgg catccaaaat tggacattgg atg ctc aat aac ggt 115
Met Leu Asn Asn Gly
1 5

```
gcg ttg gtg ggg ctg att gca ctg tgt gtt gga ctt ttt att gca aca   163
Ala Leu Val Gly Leu Ile Ala Leu Cys Val Gly Leu Phe Ile Ala Thr
                10                  15                  20

ccc cac ttt ctc acc att cct aac ctg atc aac atc ggt atc caa tcg   211
Pro His Phe Leu Thr Ile Pro Asn Leu Ile Asn Ile Gly Ile Gln Ser
            25                  30                  35

gcg acg gtg gcg atc ctg gcg ttc ggc atg acc ttc gtc atc gtt acc   259
Ala Thr Val Ala Ile Leu Ala Phe Gly Met Thr Phe Val Ile Val Thr
        40                  45                  50

gca ggc att gat ttg tct gtg gga tca gtg gct gcg ttg ggt gcg atg   307
Ala Gly Ile Asp Leu Ser Val Gly Ser Val Ala Ala Leu Gly Ala Met
    55                  60                  65

acc tcg gcg tat ttc ttc gcg gaa gtt ggt ttg ccg ggc tgg atc acg   355
Thr Ser Ala Tyr Phe Phe Ala Glu Val Gly Leu Pro Gly Trp Ile Thr
70                  75                  80                  85

ctg ctg att ggc ctg ttc atc gga ttg ttg gcg ggt gcg atc tct ggc   403
Leu Leu Ile Gly Leu Phe Ile Gly Leu Leu Ala Gly Ala Ile Ser Gly
                90                  95                  100

att tct att gct tat ggc aag ttg cct gcg ttt att gcc acc ttg gcc   451
Ile Ser Ile Ala Tyr Gly Lys Leu Pro Ala Phe Ile Ala Thr Leu Ala
            105                 110                 115

atg atg tcg atc gcc agg gga atc acc ttg gtc att tcc caa ggc tca   499
Met Met Ser Ile Ala Arg Gly Ile Thr Leu Val Ile Ser Gln Gly Ser
        120                 125                 130

cca att ccc agt gca cca gct gtg aac gct ttg ggg cgc acc tac ttt   547
Pro Ile Pro Ser Ala Pro Ala Val Asn Ala Leu Gly Arg Thr Tyr Phe
    135                 140                 145

ggc atc ccg atg ccg att ctg atg atg gca ctg gct ggc att gtg tgt   595
Gly Ile Pro Met Pro Ile Leu Met Met Ala Leu Ala Gly Ile Val Cys
150                 155                 160                 165

tgg ttt att ttg agc cgc acc gtg ctg gga cgg tcc atg tac gcc att   643
Trp Phe Ile Leu Ser Arg Thr Val Leu Gly Arg Ser Met Tyr Ala Ile
                170                 175                 180

ggc gga aac atg gaa gca gcc cga cta tct ggt ctg cca gtg aag aaa   691
Gly Gly Asn Met Glu Ala Ala Arg Leu Ser Gly Leu Pro Val Lys Lys
            185                 190                 195

atc ctg gtc atg gtc tat gca ctg gct ggt gtg tat gca gca ctt gcg   739
Ile Leu Val Met Val Tyr Ala Leu Ala Gly Val Tyr Ala Ala Leu Ala
        200                 205                 210

ggt ctg gtc atg acg gga cgc ttg tcg tcc gcg cag ccg cag gca ggc   787
Gly Leu Val Met Thr Gly Arg Leu Ser Ser Ala Gln Pro Gln Ala Gly
    215                 220                 225

gtg gga tac gaa ctc gat gcg att gcc gcc gtg gtc att ggt ggt gcg   835
Val Gly Tyr Glu Leu Asp Ala Ile Ala Ala Val Val Ile Gly Gly Ala
230                 235                 240                 245

tca ctt gct ggc gga acc gga aaa gca acg ggc act ttg att ggt gcc   883
```

```
Ser Leu Ala Gly Gly Thr Gly Lys Ala Thr Gly Thr Leu Ile Gly Ala
                250                 255                 260

atc ttg ttg gcc gtg atc cgc aat ggc ttg aac att ttg aac gtg tcc   931
Ile Leu Leu Ala Val Ile Arg Asn Gly Leu Asn Ile Leu Asn Val Ser
            265                 270                 275

tcg ttc tgg cag cag att gtc atc ggt tgt gtc atc gcg ctt gcg gtg   979
Ser Phe Trp Gln Gln Ile Val Ile Gly Cys Val Ile Ala Leu Ala Val
        280                 285                 290

ggc ttc gat gtc atc cga aac aaa acc tct aag taattcctga aaggaaattt 1032
Gly Phe Asp Val Ile Arg Asn Lys Thr Ser Lys
    295                 300

tca                                                               1035


<210> 14
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 14
Met Leu Asn Asn Gly Ala Leu Val Gly Leu Ile Ala Leu Cys Val Gly
  1               5                  10                  15

Leu Phe Ile Ala Thr Pro His Phe Leu Thr Ile Pro Asn Leu Ile Asn
             20                  25                  30

Ile Gly Ile Gln Ser Ala Thr Val Ala Ile Leu Ala Phe Gly Met Thr
         35                  40                  45

Phe Val Ile Val Thr Ala Gly Ile Asp Leu Ser Val Gly Ser Val Ala
     50                  55                  60

Ala Leu Gly Ala Met Thr Ser Ala Tyr Phe Phe Ala Glu Val Gly Leu
 65                  70                  75                  80

Pro Gly Trp Ile Thr Leu Leu Ile Gly Leu Phe Ile Gly Leu Leu Ala
                 85                  90                  95

Gly Ala Ile Ser Gly Ile Ser Ile Ala Tyr Gly Lys Leu Pro Ala Phe
            100                 105                 110

Ile Ala Thr Leu Ala Met Met Ser Ile Ala Arg Gly Ile Thr Leu Val
        115                 120                 125

Ile Ser Gln Gly Ser Pro Ile Pro Ser Ala Pro Ala Val Asn Ala Leu
    130                 135                 140

Gly Arg Thr Tyr Phe Gly Ile Pro Met Pro Ile Leu Met Met Ala Leu
145                 150                 155                 160

Ala Gly Ile Val Cys Trp Phe Ile Leu Ser Arg Thr Val Leu Gly Arg
                165                 170                 175

Ser Met Tyr Ala Ile Gly Gly Asn Met Glu Ala Ala Arg Leu Ser Gly
            180                 185                 190

Leu Pro Val Lys Lys Ile Leu Val Met Val Tyr Ala Leu Ala Gly Val
```

```
        195                 200                 205

Tyr Ala Ala Leu Ala Gly Leu Val Met Thr Gly Arg Leu Ser Ser Ala
    210                 215                 220

Gln Pro Gln Ala Gly Val Gly Tyr Glu Leu Asp Ala Ile Ala Ala Val
225                 230                 235                 240

Val Ile Gly Gly Ala Ser Leu Ala Gly Gly Thr Gly Lys Ala Thr Gly
                245                 250                 255

Thr Leu Ile Gly Ala Ile Leu Leu Ala Val Ile Arg Asn Gly Leu Asn
            260                 265                 270

Ile Leu Asn Val Ser Ser Phe Trp Gln Gln Ile Val Ile Gly Cys Val
        275                 280                 285

Ile Ala Leu Ala Val Gly Phe Asp Val Ile Arg Asn Lys Thr Ser Lys
    290                 295                 300
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CURRENT APPLICATION

<210> 15
<211> 1011
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(988)
<223> RXA00270

<400> 15

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tggagatccc tcaagagatt ttggataagg ccgaacgcgt atg atc ggc gct ttt   115
                                               Met Ile Gly Ala Phe
                                                 1               5

gag ttc gga ttg ttg tac gga gtt gtc gca ttg ggc gtc tat ttg acg   163
Glu Phe Gly Leu Leu Tyr Gly Val Val Ala Leu Gly Val Tyr Leu Thr
                  10                  15                  20

ttc cgt gtg ctc aac ttt ccc gac ctc acc gtt gac ggc agc ctg acc   211
Phe Arg Val Leu Asn Phe Pro Asp Leu Thr Val Asp Gly Ser Leu Thr
              25                  30                  35

act ggc gcg gca aca gct gcg aca gct ctt atg tct ggc tgg cct ccc   259
Thr Gly Ala Ala Thr Ala Ala Thr Ala Leu Met Ser Gly Trp Pro Pro
          40                  45                  50

ctt atg gct act gcc gct ggt ttc gtt act ggc ttt atc gct ggc atg   307
Leu Met Ala Thr Ala Ala Gly Phe Val Thr Gly Phe Ile Ala Gly Met
      55                  60                  65

atc acc ggt ttg ctg cac acc aag ggc aag atc gat ggt ttg ctc gca   355
Ile Thr Gly Leu Leu His Thr Lys Gly Lys Ile Asp Gly Leu Leu Ala
  70                  75                  80                  85
```

```
ggt att ttg acc atg att gcg ttg tgg tcg gtt aac ttg cgc atc atg   403
Gly Ile Leu Thr Met Ile Ala Leu Trp Ser Val Asn Leu Arg Ile Met
                 90                  95                 100

ggt ggc gcg aac gtg cca ttg ttg cgc acc gat aac ctc ttc acc ccg   451
Gly Gly Ala Asn Val Pro Leu Leu Arg Thr Asp Asn Leu Phe Thr Pro
            105                 110                 115

ctt cgc gac gcc ggc ctc ctc ggc aca tgg gca ggc ccg gcg atc ctc   499
Leu Arg Asp Ala Gly Leu Leu Gly Thr Trp Ala Gly Pro Ala Ile Leu
        120                 125                 130

gcc gtt gca gtg gga att ttg gga ctc atc gtc atc tgg ttc ctc aac   547
Ala Val Ala Val Gly Ile Leu Gly Leu Ile Val Ile Trp Phe Leu Asn
    135                 140                 145

act gat atc gga ctg tcg ctg cga tcc acc ggc gac aac ggg ccg atg   595
Thr Asp Ile Gly Leu Ser Leu Arg Ser Thr Gly Asp Asn Gly Pro Met
150                 155                 160                 165

gtg cag tcc ttt ggt gtt tca acg gat ttc acc aaa atc ctc acc atc   643
Val Gln Ser Phe Gly Val Ser Thr Asp Phe Thr Lys Ile Leu Thr Ile
                170                 175                 180

tcc ctg tcc aat ggt ttt gtt ggt ctt gcc ggt gca ctc atc gct cag   691
Ser Leu Ser Asn Gly Phe Val Gly Leu Ala Gly Ala Leu Ile Ala Gln
            185                 190                 195

tac cag ggc ttc gca gat att tcg atg ggt att ggc ctc atc gtg atc   739
Tyr Gln Gly Phe Ala Asp Ile Ser Met Gly Ile Gly Leu Ile Val Ile
        200                 205                 210

ggt ctc gca tcg gtt att ttg ggc cag gcc atc ttc ggt cag cgt cgc   787
Gly Leu Ala Ser Val Ile Leu Gly Gln Ala Ile Phe Gly Gln Arg Arg
    215                 220                 225

gtg tgg ttg gct gtg ttg gct gtc atc gtc ggt gcc atc gcg tac cgc   835
Val Trp Leu Ala Val Leu Ala Val Ile Val Gly Ala Ile Ala Tyr Arg
230                 235                 240                 245

ctg atc att ttc gca gca ctg cgc gtt ggc ctt gac ccc aac gat atg   883
Leu Ile Ile Phe Ala Ala Leu Arg Val Gly Leu Asp Pro Asn Asp Met
                250                 255                 260

aag gca att tct gcg atc ttg gtg gtt gtc gcc atg ctg ctg ccg agg   931
Lys Ala Ile Ser Ala Ile Leu Val Val Val Ala Met Leu Leu Pro Arg
            265                 270                 275

tgg cgt gcg aag ttc tcc aag gca ccg aag cct aag caa cca gta gca   979
Trp Arg Ala Lys Phe Ser Lys Ala Pro Lys Pro Lys Gln Pro Val Ala
        280                 285                 290

gtg gag gct taagacatgt tatccatcaa cgg                            1011
Val Glu Ala
    295
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<210> 16
<211> 296
<212> PRT
<213> Corynebacterium glutamicum

<400> 16

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Met Ile Gly Ala Phe Glu Phe Gly Leu Leu Tyr Gly Val Val Ala Leu
 1               5                  10                  15

Gly Val Tyr Leu Thr Phe Arg Val Leu Asn Phe Pro Asp Leu Thr Val
            20                  25                  30

Asp Gly Ser Leu Thr Thr Gly Ala Ala Thr Ala Ala Thr Ala Leu Met
        35                  40                  45

Ser Gly Trp Pro Pro Leu Met Ala Thr Ala Ala Gly Phe Val Thr Gly
    50                  55                  60

Phe Ile Ala Gly Met Ile Thr Gly Leu Leu His Thr Lys Gly Lys Ile
65                  70                  75                  80

Asp Gly Leu Leu Ala Gly Ile Leu Thr Met Ile Ala Leu Trp Ser Val
                85                  90                  95

Asn Leu Arg Ile Met Gly Gly Ala Asn Val Pro Leu Leu Arg Thr Asp
            100                 105                 110

Asn Leu Phe Thr Pro Leu Arg Asp Ala Gly Leu Leu Gly Thr Trp Ala
        115                 120                 125

Gly Pro Ala Ile Leu Ala Val Ala Val Gly Ile Leu Gly Leu Ile Val
    130                 135                 140

Ile Trp Phe Leu Asn Thr Asp Ile Gly Leu Ser Leu Arg Ser Thr Gly
145                 150                 155                 160

Asp Asn Gly Pro Met Val Gln Ser Phe Gly Val Ser Thr Asp Phe Thr
                165                 170                 175

Lys Ile Leu Thr Ile Ser Leu Ser Asn Gly Phe Val Gly Leu Ala Gly
            180                 185                 190

Ala Leu Ile Ala Gln Tyr Gln Gly Phe Ala Asp Ile Ser Met Gly Ile
        195                 200                 205

Gly Leu Ile Val Ile Gly Leu Ala Ser Val Ile Leu Gly Gln Ala Ile
    210                 215                 220

Phe Gly Gln Arg Arg Val Trp Leu Ala Val Leu Ala Val Ile Val Gly
225                 230                 235                 240

Ala Ile Ala Tyr Arg Leu Ile Ile Phe Ala Ala Leu Arg Val Gly Leu
                245                 250                 255

Asp Pro Asn Asp Met Lys Ala Ile Ser Ala Ile Leu Val Val Val Ala
            260                 265                 270

Met Leu Leu Pro Arg Trp Arg Ala Lys Phe Ser Lys Ala Pro Lys Pro
        275                 280                 285

Lys Gln Pro Val Ala Val Glu Ala
    290                 295
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<210> 17

<211> 1146
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1123)
<223> RXA02439

<400> 17

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gcaccactgt tggtggcgga cgacccgtgt acacaggacc agccattgtg gatgccacca 60

acgttgatgt cattgctgaa gccgttgggg agggtctgcg atg aca aaa atc aag   115
                                              Met Thr Lys Ile Lys
                                                1               5

agt ggg gag gcg tcg aca agc att gtt gag cgc gcc tta aag cgc ccc   163
Ser Gly Glu Ala Ser Thr Ser Ile Val Glu Arg Ala Leu Lys Arg Pro
                10                  15                  20

gaa ctg acc agc ctg ctt ggc gcc gtg ctt gtt ttt acg ctg ttt atg   211
Glu Leu Thr Ser Leu Leu Gly Ala Val Leu Val Phe Thr Leu Phe Met
            25                  30                  35

gtg gtc gcg ccg gca ttt agg tca tgg gat tcg atg gcg acc gtg ctg   259
Val Val Ala Pro Ala Phe Arg Ser Trp Asp Ser Met Ala Thr Val Leu
        40                  45                  50

tat gcg agt tcc acg atc ggc atc atg gcg gtt gcc gtg ggc ctg ctg   307
Tyr Ala Ser Ser Thr Ile Gly Ile Met Ala Val Ala Val Gly Leu Leu
    55                  60                  65

atg atc gct gat gaa ttc gac ctg tcc acc ggc gtt gcc gtg aca act   355
Met Ile Ala Asp Glu Phe Asp Leu Ser Thr Gly Val Ala Val Thr Thr
70                  75                  80                  85

gca gcg ctg gcg gcc tcg atg ttt agc tat aac ctg tgg ctg aac acc   403
Ala Ala Leu Ala Ala Ser Met Phe Ser Tyr Asn Leu Trp Leu Asn Thr
                90                  95                  100

tgg gtg ggc gcg ctg att gca ttg gtg att tcg ctg gcc atc ggc ttt   451
Trp Val Gly Ala Leu Ile Ala Leu Val Ile Ser Leu Ala Ile Gly Phe
            105                 110                 115

ttc aac ggc ttt ttg gta gtg aaa acc aag att gca tcc ttc ctg atc   499
Phe Asn Gly Phe Leu Val Val Lys Thr Lys Ile Ala Ser Phe Leu Ile
        120                 125                 130

acc ctt gcc act ttc ctt atg ctg cag ggt att aat ctg gcg gtc acc   547
Thr Leu Ala Thr Phe Leu Met Leu Gln Gly Ile Asn Leu Ala Val Thr
    135                 140                 145

aag ctg att tcc ggc acc gtg gcc acg cca acc atc gcg gat atg gaa   595
Lys Leu Ile Ser Gly Thr Val Ala Thr Pro Thr Ile Ala Asp Met Glu
150                 155                 160                 165

ggt ttt cct tca gcg cgt gcg gtg ttt gcc agc tcg att ccc atc ttt   643
Gly Phe Pro Ser Ala Arg Ala Val Phe Ala Ser Ser Ile Pro Ile Phe
                170                 175                 180

ggt gtg aat att cgc atc act gtt ttt tgg tgg ctg ctg ttt gtt atc   691
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Gly Val Asn Ile Arg Ile Thr Val Phe Trp Trp Leu Leu Phe Val Ile
            185                 190                 195

gtc ggc act ttt gtg ttg ttt aag acg cgc atc ggc aac tgg att ttt   739
Val Gly Thr Phe Val Leu Phe Lys Thr Arg Ile Gly Asn Trp Ile Phe
        200                 205                 210

gcg gtc ggt ggc gat gaa gag gca gct cgc gca gtc ggc gtt ccc gtg   787
Ala Val Gly Gly Asp Glu Glu Ala Ala Arg Ala Val Gly Val Pro Val
    215                 220                 225

cgt ggc gtg aaa atc ggc ctg ttc atg ttc gtt ggt ttt gcc gcc tgg   835
Arg Gly Val Lys Ile Gly Leu Phe Met Phe Val Gly Phe Ala Ala Trp
230                 235                 240                 245

ttt gtg ggc atg cac aac ctg ttc ctc ttt gat tcg att cag gct ggt   883
Phe Val Gly Met His Asn Leu Phe Leu Phe Asp Ser Ile Gln Ala Gly
                250                 255                 260

caa ggc gtg ggt aat gag ttc ctc tac atc atc gct gcg gtg atc gga   931
Gln Gly Val Gly Asn Glu Phe Leu Tyr Ile Ile Ala Ala Val Ile Gly
            265                 270                 275

ggc atc tcc atg act ggt ggc cgc gga aca gtg gtg ggc aca atg att   979
Gly Ile Ser Met Thr Gly Gly Arg Gly Thr Val Val Gly Thr Met Ile
        280                 285                 290

ggt gca ctc atc ttt gga atg acc aac caa ggc att gtt tat gca ggt   1027
Gly Ala Leu Ile Phe Gly Met Thr Asn Gln Gly Ile Val Tyr Ala Gly
    295                 300                 305

tgg aac cct gac tgg ttc atg ttc ttc ctc ggc ggc acc cta ctt ctg   1075
Trp Asn Pro Asp Trp Phe Met Phe Phe Leu Gly Gly Thr Leu Leu Leu
310                 315                 320                 325

gct gtt ttg ctc aat cac cga ttc gag cgt ttc aac aag gag cga tca   1123
Ala Val Leu Leu Asn His Arg Phe Glu Arg Phe Asn Lys Glu Arg Ser
                330                 335                 340

tgacagacct cattcaactc cgc                                        1146
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09/30/05 FRI 09:59 [TX/RX NO 6139]

<210> 18
<211> 341
<212> PRT
<213> Corynebacterium glutamicum

<400> 18

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Met Thr Lys Ile Lys Ser Gly Glu Ala Ser Thr Ser Ile Val Glu Arg
  1               5                  10                  15

Ala Leu Lys Arg Pro Glu Leu Thr Ser Leu Leu Gly Ala Val Leu Val
            20                  25                  30

Phe Thr Leu Phe Met Val Val Ala Pro Ala Phe Arg Ser Trp Asp Ser
        35                  40                  45

Met Ala Thr Val Leu Tyr Ala Ser Ser Thr Ile Gly Ile Met Ala Val
    50                  55                  60

Ala Val Gly Leu Leu Met Ile Ala Asp Glu Phe Asp Leu Ser Thr Gly
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65 70 75 80

Val Ala Val Thr Thr Ala Ala Leu Ala Ala Ser Met Phe Ser Tyr Asn
85 90 95

Leu Trp Leu Asn Thr Trp Val Gly Ala Leu Ile Ala Leu Val Ile Ser
100 105 110

Leu Ala Ile Gly Phe Phe Asn Gly Phe Leu Val Val Lys Thr Lys Ile
115 120 125

Ala Ser Phe Leu Ile Thr Leu Ala Thr Phe Leu Met Leu Gln Gly Ile
130 135 140

Asn Leu Ala Val Thr Lys Leu Ile Ser Gly Thr Val Ala Thr Pro Thr
145 150 155 160

Ile Ala Asp Met Glu Gly Phe Pro Ser Ala Arg Ala Val Phe Ala Ser
165 170 175

Ser Ile Pro Ile Phe Gly Val Asn Ile Arg Ile Thr Val Phe Trp Trp
180 185 190

Leu Leu Phe Val Ile Val Gly Thr Phe Val Leu Phe Lys Thr Arg Ile
195 200 205

Gly Asn Trp Ile Phe Ala Val Gly Gly Asp Glu Glu Ala Ala Arg Ala
210 215 220

Val Gly Val Pro Val Arg Gly Val Lys Ile Gly Leu Phe Met Phe Val
225 230 235 240

Gly Phe Ala Ala Trp Phe Val Gly Met His Asn Leu Phe Leu Phe Asp
245 250 255

Ser Ile Gln Ala Gly Gln Gly Val Gly Asn Glu Phe Leu Tyr Ile Ile
260 265 270

Ala Ala Val Ile Gly Gly Ile Ser Met Thr Gly Gly Arg Gly Thr Val
275 280 285

Val Gly Thr Met Ile Gly Ala Leu Ile Phe Gly Met Thr Asn Gln Gly
290 295 300

Ile Val Tyr Ala Gly Trp Asn Pro Asp Trp Phe Met Phe Phe Leu Gly
305 310 315 320

Gly Thr Leu Leu Leu Ala Val Leu Leu Asn His Arg Phe Glu Arg Phe
325 330 335

Asn Lys Glu Arg Ser
340

<210> 19
<211> 746
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(723)
<223> RXN02994

<400> 19

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atc aag atg acg gga gtg caa aaa tac ttc ggc gac ttt cat gcc ctt   48
Ile Lys Met Thr Gly Val Gln Lys Tyr Phe Gly Asp Phe His Ala Leu
  1               5                  10                  15

acg gat att gat ctt gaa att ccc aga gga caa gtt gtc gtc gta ctt   96
Thr Asp Ile Asp Leu Glu Ile Pro Arg Gly Gln Val Val Val Val Leu
             20                  25                  30

gga cca tcc gga tcc ggc aag tca acc ctt tgc cgc acg atc aac cgt  144
Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg
         35                  40                  45

ctc gaa acc atc gag gaa ggc acc atc gaa atc gat gga aag gtt ctc  192
Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Val Leu
     50                  55                  60

cca gaa gaa ggt aaa ggc tta gcc aat ctc cgc gcc gat gtc gga atg  240
Pro Glu Glu Gly Lys Gly Leu Ala Asn Leu Arg Ala Asp Val Gly Met
 65                  70                  75                  80

gta ttc cag tcc ttc aac ctc ttc ccc cac ctc acc atc aaa gac aac  288
Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn
                 85                  90                  95

gtc act ctt gca ccc atc aaa gtg cga aag atg aaa aag tct gaa gcc  336
Val Thr Leu Ala Pro Ile Lys Val Arg Lys Met Lys Lys Ser Glu Ala
            100                 105                 110

gaa aag ctt gcg atg agc ctg ttg gaa cgc gtc ggc atc gca aac caa  384
Glu Lys Leu Ala Met Ser Leu Leu Glu Arg Val Gly Ile Ala Asn Gln
        115                 120                 125

gct gat aaa tat ccg gcg caa ctg tcc ggc ggt cag caa cag cgt gtg  432
Ala Asp Lys Tyr Pro Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg Val
    130                 135                 140

gcc atc gcg cgc gca ctt gcg atg aac cca aag atc atg ctt ttc gac  480
Ala Ile Ala Arg Ala Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp
145                 150                 155                 160

gag ccc acc tcc gcc ctt gac cct gaa atg gtc aac gaa gtg ttg gac  528
Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp
                165                 170                 175

gtc atg gca agc ctt gcc aag gaa ggc atg acg atg gtg tgt gtt acc  576
Val Met Ala Ser Leu Ala Lys Glu Gly Met Thr Met Val Cys Val Thr
            180                 185                 190

cac gag atg gga ttc gca cgc aaa gca gcc gat cgt gtg ttg ttc atg  624
His Glu Met Gly Phe Ala Arg Lys Ala Ala Asp Arg Val Leu Phe Met
        195                 200                 205

gcg gat ggg ctc att gtg gaa gat acg gaa cca gat tcc ttc ttc acc  672
Ala Asp Gly Leu Ile Val Glu Asp Thr Glu Pro Asp Ser Phe Phe Thr
    210                 215                 220

aac cct aag tct gat cgt gca aaa gac ttc ctc ggc aag atc ctt gcc  720
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Asn Pro Lys Ser Asp Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu Ala
225 230 235 240

cac tagtttttgg ctgcgcctct atc 746
His

<210> 20
<211> 241
<212> PRT
<213> Corynebacterium glutamicum

<400> 20
Ile Lys Met Thr Gly Val Gln Lys Tyr Phe Gly Asp Phe His Ala Leu
1 5 10 15

Thr Asp Ile Asp Leu Glu Ile Pro Arg Gly Gln Val Val Val Val Leu
20 25 30

Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg
35 40 45

Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Val Leu
50 55 60

Pro Glu Glu Gly Lys Gly Leu Ala Asn Leu Arg Ala Asp Val Gly Met
65 70 75 80

Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn
85 90 95

Val Thr Leu Ala Pro Ile Lys Val Arg Lys Met Lys Lys Ser Glu Ala
100 105 110

Glu Lys Leu Ala Met Ser Leu Leu Glu Arg Val Gly Ile Ala Asn Gln
115 120 125

Ala Asp Lys Tyr Pro Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg Val
130 135 140

Ala Ile Ala Arg Ala Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp
145 150 155 160

Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp
165 170 175

Val Met Ala Ser Leu Ala Lys Glu Gly Met Thr Met Val Cys Val Thr
180 185 190

His Glu Met Gly Phe Ala Arg Lys Ala Ala Asp Arg Val Leu Phe Met
195 200 205

Ala Asp Gly Leu Ile Val Glu Asp Thr Glu Pro Asp Ser Phe Phe Thr
210 215 220

Asn Pro Lys Ser Asp Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu Ala
225 230 235 240

His

<210> 21
<211> 1790
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1767)
<223> FRXA01245

<400> 21

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gcc tcc tgg gtc acc acc ctg ggg ctg ggc ggg ttc cac cta gat ttc   48
Ala Ser Trp Val Thr Thr Leu Gly Leu Gly Gly Phe His Leu Asp Phe
  1               5                  10                  15

tgg tgg gaa ctg gcc ctg ctg gtg acc ata atg ctg ttg ggc cac tgg   96
Trp Trp Glu Leu Ala Leu Leu Val Thr Ile Met Leu Leu Gly His Trp
             20                  25                  30

ctg gag atg cgc gct ctt ggt gca gcc tcc tcc gcg ctt gac gcg ctg   144
Leu Glu Met Arg Ala Leu Gly Ala Ala Ser Ser Ala Leu Asp Ala Leu
         35                  40                  45

gca gcg ctc ctg ccc gat gag gcc gag aag gtc gtc gac ggg acc acc   192
Ala Ala Leu Leu Pro Asp Glu Ala Glu Lys Val Val Asp Gly Thr Thr
     50                  55                  60

cgc acc gta gcg atc tca gag ctg gcc gtc gac gat gtc gtg ctg gtc   240
Arg Thr Val Ala Ile Ser Glu Leu Ala Val Asp Asp Val Val Leu Val
 65                  70                  75                  80

cga gca ggt gcc cgc gtc ccg gcc gac ggg acc atc atg gac gga gcg   288
Arg Ala Gly Ala Arg Val Pro Ala Asp Gly Thr Ile Met Asp Gly Ala
                 85                  90                  95

gcc gaa ttc gat gag gcc atg atc acc ggc gaa tcc cga ccc gtc tac   336
Ala Glu Phe Asp Glu Ala Met Ile Thr Gly Glu Ser Arg Pro Val Tyr
            100                 105                 110

cgg gat acc ggt gag acc gtg gtg gcc ggc acc gtg gcc acc gac aac   384
Arg Asp Thr Gly Glu Thr Val Val Ala Gly Thr Val Ala Thr Asp Asn
        115                 120                 125

acc gtc cgt atc cgg gtg gag gcc acc ggt ggg gac acc gcc ctg gca   432
Thr Val Arg Ile Arg Val Glu Ala Thr Gly Gly Asp Thr Ala Leu Ala
    130                 135                 140

ggc atc cag cgc atg gtc gcc gac gcc cag gcc tcc tcc tcc cgg gcc   480
Gly Ile Gln Arg Met Val Ala Asp Ala Gln Ala Ser Ser Ser Arg Ala
145                 150                 155                 160

cag gcc ctg gcc gat cga gcc gca gcc tta ctg ttc tgg ttc gcc ctg   528
Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu Leu Phe Trp Phe Ala Leu
                165                 170                 175

atc acg gcc ctg atc acc gcc gtg gtc tgg acc atc atc ggc agc ccc   576
Ile Thr Ala Leu Ile Thr Ala Val Val Trp Thr Ile Ile Gly Ser Pro
            180                 185                 190
```

```
gac gat gcc gtg gtc cgc gcg gtg acc gtg ctg atc atc gcc tgc ccg   624
Asp Asp Ala Val Val Arg Ala Val Thr Val Leu Ile Ile Ala Cys Pro
        195                 200                 205

cac gcc ctg ggc ctg gcc atc ccg ctg gtc atc gcg atc tcc tcc gag   672
His Ala Leu Gly Leu Ala Ile Pro Leu Val Ile Ala Ile Ser Ser Glu
    210                 215                 220

cgc gcc gcg aaa tcc ggg gtg ctc atc aag gac cgc atg gca ctc gag   720
Arg Ala Ala Lys Ser Gly Val Leu Ile Lys Asp Arg Met Ala Leu Glu
225                 230                 235                 240

cac atg cgc acc atc gac gtc gtc ttg ttc gat aag acc ggc acc ctg   768
His Met Arg Thr Ile Asp Val Val Leu Phe Asp Lys Thr Gly Thr Leu
                245                 250                 255

acc gaa ggc gca cac gcc gtc acc ggc gtg gct ccg gcc acg ggt atc   816
Thr Glu Gly Ala His Ala Val Thr Gly Val Ala Pro Ala Thr Gly Ile
            260                 265                 270

gcc gag ggt gag ctg ctg gcc ctg gcc gcc gcc gct gag gcc gat agt   864
Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala Ala Ala Glu Ala Asp Ser
        275                 280                 285

gag cac ccc gtg gcc cgc gcg atc gtg act gcc gcg gcc gca cac ccg   912
Glu His Pro Val Ala Arg Ala Ile Val Thr Ala Ala Ala Ala His Pro
    290                 295                 300

gag gcc tcg cag cgt cag ctg cgc gca acc ggt ttc acc gcc gcc tcc   960
Glu Ala Ser Gln Arg Gln Leu Arg Ala Thr Gly Phe Thr Ala Ala Ser
305                 310                 315                 320

ggc cgc ggg atc cgg gcc acc gtc gac ggt gcc gaa atc ctc gtg ggc  1008
Gly Arg Gly Ile Arg Ala Thr Val Asp Gly Ala Glu Ile Leu Val Gly
                325                 330                 335

ggg ccg aac atg cta cgc gag ttc aat ctg acc acc ccg ggt gag ctc  1056
Gly Pro Asn Met Leu Arg Glu Phe Asn Leu Thr Thr Pro Gly Glu Leu
            340                 345                 350

gcc gac atc acc ggt tcc tgg gca cag cga ggt gcc gga gtg cta cat  1104
Ala Asp Ile Thr Gly Ser Trp Ala Gln Arg Gly Ala Gly Val Leu His
        355                 360                 365

gtc gtc cgc gac ggt gag atc atc ggt gcg gtg gca gtg gag gac aaa  1152
Val Val Arg Asp Gly Glu Ile Ile Gly Ala Val Ala Val Glu Asp Lys
    370                 375                 380

atc cgc ccc gaa tcc cgc gcg gcg gta cgc gcc ctg cag gcc cgc ggg  1200
Ile Arg Pro Glu Ser Arg Ala Ala Val Arg Ala Leu Gln Ala Arg Gly
385                 390                 395                 400

gtg aag gtg gcg atg atc acc ggt gac gcc acc cag gtc gcc cag gca  1248
Val Lys Val Ala Met Ile Thr Gly Asp Ala Thr Gln Val Ala Gln Ala
                405                 410                 415

gtg ggc aag gat ctg ggg atc gat gag gtc ttc gcc gag gtt ctg ccg  1296
Val Gly Lys Asp Leu Gly Ile Asp Glu Val Phe Ala Glu Val Leu Pro
            420                 425                 430

cag gac aag gac acc aag gtc acc cag ctg cag gag cgc ggt ctg agc  1344
```

```
Gln Asp Lys Asp Thr Lys Val Thr Gln Leu Gln Glu Arg Gly Leu Ser
        435                 440                 445

gtg gcc atg gtc ggc gac ggt gtc aat gac gcc ccg gcc ctg gcc cgg   1392
Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Ala Arg
    450                 455                 460

gcc gag gtc ggt att gcg att ggc gcg ggt aca gat gtg gcg atg gag   1440
Ala Glu Val Gly Ile Ala Ile Gly Ala Gly Thr Asp Val Ala Met Glu
465                 470                 475                 480

tcc gcc ggg gtg gtc ctg gcc agt gat gat ccc cgg gcc gtg ctg tcg   1488
Ser Ala Gly Val Val Leu Ala Ser Asp Asp Pro Arg Ala Val Leu Ser
                485                 490                 495

atg atc gag ctc tcc cat gcc agc tac cgc aag atg gtc cag aac ctg   1536
Met Ile Glu Leu Ser His Ala Ser Tyr Arg Lys Met Val Gln Asn Leu
            500                 505                 510

gtc tgg gcg acc ggg tac aac atc gtg gcc gtt ccg ctg gcc gcc ggt   1584
Val Trp Ala Thr Gly Tyr Asn Ile Val Ala Val Pro Leu Ala Ala Gly
        515                 520                 525

gtg ctc gcc cct atc ggt gtg ctg ctt ccc ccg gcg gcg gcc gcc atc   1632
Val Leu Ala Pro Ile Gly Val Leu Leu Pro Pro Ala Ala Ala Ala Ile
    530                 535                 540

ttg atg tcc ctg tcc acg atc atc gtc gcc ctc aac gcc cag ctg cta   1680
Leu Met Ser Leu Ser Thr Ile Ile Val Ala Leu Asn Ala Gln Leu Leu
545                 550                 555                 560

cgc cgg atc gac ctg gac ccg gct cac cta gct ccg acc gac ggg aag   1728
Arg Arg Ile Asp Leu Asp Pro Ala His Leu Ala Pro Thr Asp Gly Lys
                565                 570                 575

gag gag aag gct gct gtg agc tct gca gcc ccc gtc cgc tgactttcaa    1777
Glu Glu Lys Ala Ala Val Ser Ser Ala Ala Pro Val Arg
            580                 585

tgcttcatgg act                                                   1790
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<210> 22
<211> 589
<212> PRT
<213> Corynebacterium glutamicum

<400> 22

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Ala Ser Trp Val Thr Thr Leu Gly Leu Gly Gly Phe His Leu Asp Phe
  1               5                  10                  15

Trp Trp Glu Leu Ala Leu Leu Val Thr Ile Met Leu Leu Gly His Trp
             20                  25                  30

Leu Glu Met Arg Ala Leu Gly Ala Ala Ser Ser Ala Leu Asp Ala Leu
         35                  40                  45

Ala Ala Leu Leu Pro Asp Glu Ala Glu Lys Val Val Asp Gly Thr Thr
     50                  55                  60

Arg Thr Val Ala Ile Ser Glu Leu Ala Val Asp Asp Val Val Leu Val
```

65 70 75 80

Arg Ala Gly Ala Arg Val Pro Ala Asp Gly Thr Ile Met Asp Gly Ala
85 90 95

Ala Glu Phe Asp Glu Ala Met Ile Thr Gly Glu Ser Arg Pro Val Tyr
100 105 110

Arg Asp Thr Gly Glu Thr Val Val Ala Gly Thr Val Ala Thr Asp Asn
115 120 125

Thr Val Arg Ile Arg Val Glu Ala Thr Gly Gly Asp Thr Ala Leu Ala
130 135 140

Gly Ile Gln Arg Met Val Ala Asp Ala Gln Ala Ser Ser Ser Arg Ala
145 150 155 160

Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu Leu Phe Trp Phe Ala Leu
165 170 175

Ile Thr Ala Leu Ile Thr Ala Val Val Trp Thr Ile Ile Gly Ser Pro
180 185 190

Asp Asp Ala Val Val Arg Ala Val Thr Val Leu Ile Ile Ala Cys Pro
195 200 205

His Ala Leu Gly Leu Ala Ile Pro Leu Val Ile Ala Ile Ser Ser Glu
210 215 220

Arg Ala Ala Lys Ser Gly Val Leu Ile Lys Asp Arg Met Ala Leu Glu
225 230 235 240

His Met Arg Thr Ile Asp Val Val Leu Phe Asp Lys Thr Gly Thr Leu
245 250 255

Thr Glu Gly Ala His Ala Val Thr Gly Val Ala Pro Ala Thr Gly Ile
260 265 270

Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala Ala Ala Glu Ala Asp Ser
275 280 285

Glu His Pro Val Ala Arg Ala Ile Val Thr Ala Ala Ala Ala His Pro
290 295 300

Glu Ala Ser Gln Arg Gln Leu Arg Ala Thr Gly Phe Thr Ala Ala Ser
305 310 315 320

Gly Arg Gly Ile Arg Ala Thr Val Asp Gly Ala Glu Ile Leu Val Gly
325 330 335

Gly Pro Asn Met Leu Arg Glu Phe Asn Leu Thr Thr Pro Gly Glu Leu
340 345 350

Ala Asp Ile Thr Gly Ser Trp Ala Gln Arg Gly Ala Gly Val Leu His
355 360 365

Val Val Arg Asp Gly Glu Ile Ile Gly Ala Val Ala Val Glu Asp Lys
370 375 380

Ile Arg Pro Glu Ser Arg Ala Ala Val Arg Ala Leu Gln Ala Arg Gly
385 390 395 400

09549350 pct 030502

Val Lys Val Ala Met Ile Thr Gly Asp Ala Thr Gln Val Ala Gln Ala
405 410 415

Val Gly Lys Asp Leu Gly Ile Asp Glu Val Phe Ala Glu Val Leu Pro
420 425 430

Gln Asp Lys Asp Thr Lys Val Thr Gln Leu Gln Glu Arg Gly Leu Ser
435 440 445

Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Ala Arg
450 455 460

Ala Glu Val Gly Ile Ala Ile Gly Ala Gly Thr Asp Val Ala Met Glu
465 470 475 480

Ser Ala Gly Val Val Leu Ala Ser Asp Asp Pro Arg Ala Val Leu Ser
485 490 495

Met Ile Glu Leu Ser His Ala Ser Tyr Arg Lys Met Val Gln Asn Leu
500 505 510

Val Trp Ala Thr Gly Tyr Asn Ile Val Ala Val Pro Leu Ala Ala Gly
515 520 525

Val Leu Ala Pro Ile Gly Val Leu Leu Pro Pro Ala Ala Ala Ala Ile
530 535 540

Leu Met Ser Leu Ser Thr Ile Ile Val Ala Leu Asn Ala Gln Leu Leu
545 550 555 560

Arg Arg Ile Asp Leu Asp Pro Ala His Leu Ala Pro Thr Asp Gly Lys
565 570 575

Glu Glu Lys Ala Ala Val Ser Ser Ala Ala Pro Val Arg
580 585

<210> 23
<211> 807
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(784)
<223> RXA00002

<400> 23
ctgacttctt gggcttcggt gctgcaatat ctaggttcac gccccggatg gcaccggaga 60

ggctgcagac aagctcgctg ctgaggattc tcacctgcac gtg ctg cac cgc gaa 115
Val Leu His Arg Glu
1 5

ggc aag ggt ggc ctt ctt ggc gct tat atc gcc ggc ttc gag tgg ggc 163
Gly Lys Gly Gly Leu Leu Gly Ala Tyr Ile Ala Gly Phe Glu Trp Gly
10 15 20

cta gag aag gat tac cat gtt ctg tgc gaa atg gat gcc gac ggc tcc 211
Leu Glu Lys Asp Tyr His Val Leu Cys Glu Met Asp Ala Asp Gly Ser

```
                25                  30                  35

cac gca cca gaa cag ctc cac ctc ttg ctt gag gaa att gaa aag ggc   259
His Ala Pro Glu Gln Leu His Leu Leu Leu Glu Glu Ile Glu Lys Gly
         40                  45                  50

gca gat ctg gtc att ggc tcc cgc tac gta ccg ggt gga gag aca gtg   307
Ala Asp Leu Val Ile Gly Ser Arg Tyr Val Pro Gly Gly Glu Thr Val
     55                  60                  65

aac tgg cct gcc aac cgc gaa ctg ctg tcc cgc ttg ggc aac aag tac   355
Asn Trp Pro Ala Asn Arg Glu Leu Leu Ser Arg Leu Gly Asn Lys Tyr
 70                  75                  80                  85

att tct gtt gcc ctg ggt gcc ggc atc aat gac atg act gcc ggc tac   403
Ile Ser Val Ala Leu Gly Ala Gly Ile Asn Asp Met Thr Ala Gly Tyr
                 90                  95                 100

cgt gct ttc cgg cgt gag ctg ctt gag cac ctc gac ttt gag gag ctt   451
Arg Ala Phe Arg Arg Glu Leu Leu Glu His Leu Asp Phe Glu Glu Leu
            105                 110                 115

tcc aac gcc gga tac atc ttc cag gtg gac gtt gcc ttc cgc gcc atc   499
Ser Asn Ala Gly Tyr Ile Phe Gln Val Asp Val Ala Phe Arg Ala Ile
        120                 125                 130

aag gat ggc ttc gat gtc cgc gag gtt ccg atc acc ttc acc gag cgc   547
Lys Asp Gly Phe Asp Val Arg Glu Val Pro Ile Thr Phe Thr Glu Arg
    135                 140                 145

gag ctt ggt gaa tcc aag ctg gac ggc tcc ttt gtc aag gat tcc ctg   595
Glu Leu Gly Glu Ser Lys Leu Asp Gly Ser Phe Val Lys Asp Ser Leu
150                 155                 160                 165

ctc gaa gta acc aag tgg gga gtg gct cac cgc tcc gag cag atc agc   643
Leu Glu Val Thr Lys Trp Gly Val Ala His Arg Ser Glu Gln Ile Ser
                170                 175                 180

gat ttc aca tcg gaa gta tcc aag atc gcc tcc cgc acg gtc aag gac   691
Asp Phe Thr Ser Glu Val Ser Lys Ile Ala Ser Arg Thr Val Lys Asp
            185                 190                 195

atg gag ctt ggc cct aag gcc acc acg gcc aag aac gct gta ccg gac   739
Met Glu Leu Gly Pro Lys Ala Thr Thr Ala Lys Asn Ala Val Pro Asp
        200                 205                 210

ttc gtt tcc gaa gtc tct aac cta gct aaa ggc acc ttc aag aag       784
Phe Val Ser Glu Val Ser Asn Leu Ala Lys Gly Thr Phe Lys Lys
    215                 220                 225

taactcgatg cccgcggcgt ctc                                        807
```

<210> 24
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 24

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Val Leu His Arg Glu Gly Lys Gly Gly Leu Leu Gly Ala Tyr Ile Ala
  1               5                  10                  15
```

Gly Phe Glu Trp Gly Leu Glu Lys Asp Tyr His Val Leu Cys Glu Met
20 25 30

Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu Leu Leu Glu
35 40 45

Glu Ile Glu Lys Gly Ala Asp Leu Val Ile Gly Ser Arg Tyr Val Pro
50 55 60

Gly Gly Glu Thr Val Asn Trp Pro Ala Asn Arg Glu Leu Leu Ser Arg
65 70 75 80

Leu Gly Asn Lys Tyr Ile Ser Val Ala Leu Gly Ala Gly Ile Asn Asp
85 90 95

Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Leu Leu Glu His Leu
100 105 110

Asp Phe Glu Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln Val Asp Val
115 120 125

Ala Phe Arg Ala Ile Lys Asp Gly Phe Asp Val Arg Glu Val Pro Ile
130 135 140

Thr Phe Thr Glu Arg Glu Leu Gly Glu Ser Lys Leu Asp Gly Ser Phe
145 150 155 160

Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Val Ala His Arg
165 170 175

Ser Glu Gln Ile Ser Asp Phe Thr Ser Glu Val Ser Lys Ile Ala Ser
180 185 190

Arg Thr Val Lys Asp Met Glu Leu Gly Pro Lys Ala Thr Thr Ala Lys
195 200 205

Asn Ala Val Pro Asp Phe Val Ser Glu Val Ser Asn Leu Ala Lys Gly
210 215 220

Thr Phe Lys Lys
225

<210> 25
<211> 696
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)
<223> RXA00160

<400> 25
tacaggggtg gggttacccc ctaaggtggt cacaacttga taacggactg gttaataaat 60

ggccaatctg accattttaa cctccataaa aaggattctc atg cta aac atc gca 115
Met Leu Asn Ile Ala
1 5

```
cgc aac cgc aac atg aag cgt cga cta gca att gct gct ttc gtc gcc   163
Arg Asn Arg Asn Met Lys Arg Arg Leu Ala Ile Ala Ala Phe Val Ala
                 10                  15                  20

acc gca acc gct acc gcc acc atg gca cca gca tcc gcg caa acc gac   211
Thr Ala Thr Ala Thr Ala Thr Met Ala Pro Ala Ser Ala Gln Thr Asp
             25                  30                  35

tac gca ggc ctt tcc tcc ggc gtt gcc gac acc gtc gca gaa gct gca   259
Tyr Ala Gly Leu Ser Ser Gly Val Ala Asp Thr Val Ala Glu Ala Ala
         40                  45                  50

gga gtc gca acc acc gcc gtc gca cca gcc gcc acc gta gcg cgc cca   307
Gly Val Ala Thr Thr Ala Val Ala Pro Ala Ala Thr Val Ala Arg Pro
     55                  60                  65

gca aac ggc acc ttc acc tca gga ttc gga cca cgt tgg gga acc ttc   355
Ala Asn Gly Thr Phe Thr Ser Gly Phe Gly Pro Arg Trp Gly Thr Phe
 70                  75                  80                  85

cac aac ggc atc gac atc gca aac tca atc ggc acc cca atc tac gcc   403
His Asn Gly Ile Asp Ile Ala Asn Ser Ile Gly Thr Pro Ile Tyr Ala
                 90                  95                 100

gtc atg gcc ggc act gtc atc agc tct ggc cca gca tcc ggc tat gga   451
Val Met Ala Gly Thr Val Ile Ser Ser Gly Pro Ala Ser Gly Tyr Gly
             105                 110                 115

cag tgg atc cgc atc cag cac gac gac gga tcc atc tcc atc tac gga   499
Gln Trp Ile Arg Ile Gln His Asp Asp Gly Ser Ile Ser Ile Tyr Gly
         120                 125                 130

cac atg gaa tac ctc tac gtc tcc gtc ggc gaa cgc gtc gca gca ggc   547
His Met Glu Tyr Leu Tyr Val Ser Val Gly Glu Arg Val Ala Ala Gly
     135                 140                 145

cag gaa atc gca gga atg ggc agc caa gga ttc tcc acc ggc tcc cac   595
Gln Glu Ile Ala Gly Met Gly Ser Gln Gly Phe Ser Thr Gly Ser His
150                 155                 160                 165

ctc cac ttc gag atc cac cca gac ggc gtc acc cca gtc gac cca cag   643
Leu His Phe Glu Ile His Pro Asp Gly Val Thr Pro Val Asp Pro Gln
                 170                 175                 180

gca tgg ctc gca aac cac ggc atc tac gtt taagcgctag ccgttcgtgg     693
Ala Trp Leu Ala Asn His Gly Ile Tyr Val
             185                 190

gat                                                              696
```

<210> 26
<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 26

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Met Leu Asn Ile Ala Arg Asn Arg Asn Met Lys Arg Arg Leu Ala Ile
  1               5                  10                  15

Ala Ala Phe Val Ala Thr Ala Thr Ala Thr Ala Thr Met Ala Pro Ala
```

20 25 30

Ser Ala Gln Thr Asp Tyr Ala Gly Leu Ser Ser Gly Val Ala Asp Thr
35 40 45

Val Ala Glu Ala Ala Gly Val Ala Thr Thr Ala Val Ala Pro Ala Ala
50 55 60

Thr Val Ala Arg Pro Ala Asn Gly Thr Phe Thr Ser Gly Phe Gly Pro
65 70 75 80

Arg Trp Gly Thr Phe His Asn Gly Ile Asp Ile Ala Asn Ser Ile Gly
85 90 95

Thr Pro Ile Tyr Ala Val Met Ala Gly Thr Val Ile Ser Ser Gly Pro
100 105 110

Ala Ser Gly Tyr Gly Gln Trp Ile Arg Ile Gln His Asp Asp Gly Ser
115 120 125

Ile Ser Ile Tyr Gly His Met Glu Tyr Leu Tyr Val Ser Val Gly Glu
130 135 140

Arg Val Ala Ala Gly Gln Glu Ile Ala Gly Met Gly Ser Gln Gly Phe
145 150 155 160

Ser Thr Gly Ser His Leu His Phe Glu Ile His Pro Asp Gly Val Thr
165 170 175

Pro Val Asp Pro Gln Ala Trp Leu Ala Asn His Gly Ile Tyr Val
180 185 190

<210> 27
<211> 1063
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (90)..(1040)
<223> RXA00345

<400> 27
agtgacccat atggcgtatc cgaggtctaa cgcgattttg cgattttcaa taagttttca 60

tgttgacatc ctttttcaat aagcatttaatg gca ggt atg aaa aag ctt ctt 113
Met Ala Gly Met Lys Lys Leu Leu
1 5

tgg aca ctc ccc atc ctc cca ctg gta cta gct ggc tgc tca act gga 161
Trp Thr Leu Pro Ile Leu Pro Leu Val Leu Ala Gly Cys Ser Thr Gly
10 15 20

tca gca gat tcc gcg gat tcc acc aac gct gcc gga tcc aat tcc ctt 209
Ser Ala Asp Ser Ala Asp Ser Thr Asn Ala Ala Gly Ser Asn Ser Leu
25 30 35 40

aaa gtg gtc acc tcc acc cag gtg tgg gct gac gtc gcc gaa gct gtc 257
Lys Val Val Thr Ser Thr Gln Val Trp Ala Asp Val Ala Glu Ala Val
45 50 55

```
gcc cca gat gta gac att gaa gca att att acc ggt ggc gac atc gac   305
Ala Pro Asp Val Asp Ile Glu Ala Ile Ile Thr Gly Gly Asp Ile Asp
            60                  65                  70

cct cat tcc ttc gag cct tcc gct acc gat atg gct aaa gtt tcc gaa   353
Pro His Ser Phe Glu Pro Ser Ala Thr Asp Met Ala Lys Val Ser Glu
        75                  80                  85

gct gac atc att atc gtc ggt ggc ggc ggc tat gat tcc tgg ctc tac   401
Ala Asp Ile Ile Ile Val Gly Gly Gly Gly Tyr Asp Ser Trp Leu Tyr
    90                  95                  100

ggc acc ttg gaa gac gat gat cgc atc atc cac gca ttg gat ctc tca   449
Gly Thr Leu Glu Asp Asp Asp Arg Ile Ile His Ala Leu Asp Leu Ser
105                 110                 115                 120

gag cat gac cac agc gag cat gat gat cac gag cac gaa gcc gaa gaa   497
Glu His Asp His Ser Glu His Asp Asp His Glu His Glu Ala Glu Glu
                125                 130                 135

gcc cac gaa cac gac cac gat gaa gag ggc cac gat cat gac gtc gac   545
Ala His Glu His Asp His Asp Glu Glu Gly His Asp His Asp Val Asp
            140                 145                 150

aac gag cac gtc tgg tac tcc act gaa tac gtc tct gag gta gct gaa   593
Asn Glu His Val Trp Tyr Ser Thr Glu Tyr Val Ser Glu Val Ala Glu
        155                 160                 165

gag ttc gca gaa aaa gtc acc gag ctt gat ccc gag gca cag gcc gat   641
Glu Phe Ala Glu Lys Val Thr Glu Leu Asp Pro Glu Ala Gln Ala Asp
    170                 175                 180

gca acg gct gtg acc acc aag atg gac gag ctg cac aat cag att cac   689
Ala Thr Ala Val Thr Thr Lys Met Asp Glu Leu His Asn Gln Ile His
185                 190                 195                 200

gat ctt cca gca gtt cgc att gct cag acc gag ccg atc gcc gat cac   737
Asp Leu Pro Ala Val Arg Ile Ala Gln Thr Glu Pro Ile Ala Asp His
                205                 210                 215

att ttg tcc cac tcc gac atg gtg gaa tcc acc cct gag ggt tac cgc   785
Ile Leu Ser His Ser Asp Met Val Glu Ser Thr Pro Glu Gly Tyr Arg
            220                 225                 230

gca acc acg ttg agc gag agc gag cca acc gca gca gat gtt gcg tcg   833
Ala Thr Thr Leu Ser Glu Ser Glu Pro Thr Ala Ala Asp Val Ala Ser
        235                 240                 245

ttc cag gat gca att aac aac ggt gac ctc gat gtt ttg atc tac aac   881
Phe Gln Asp Ala Ile Asn Asn Gly Asp Leu Asp Val Leu Ile Tyr Asn
    250                 255                 260

cca cag tcc gcg tcg act gtc gcg acc agc ttg aag gat ttg gca gaa   929
Pro Gln Ser Ala Ser Thr Val Ala Thr Ser Leu Lys Asp Leu Ala Glu
265                 270                 275                 280

gaa aaa ggc atc cca gtt gtt gag atc tat gag acc cct caa aac acc   977
Glu Lys Gly Ile Pro Val Val Glu Ile Tyr Glu Thr Pro Gln Asn Thr
                285                 290                 295
```

```
gag aat ttc ctc gat gca ttc acc aag gca gtt gat gat ctc acc gct   1025
Glu Asn Phe Leu Asp Ala Phe Thr Lys Ala Val Asp Asp Leu Thr Ala
            300                 305                 310

gcc act aac cag gtt tagaattatt taaatgctgt tga                    1063
Ala Thr Asn Gln Val
        315
```

<210> 28
<211> 317
<212> PRT
<213> Corynebacterium glutamicum

<400> 28

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Met Ala Gly Met Lys Lys Leu Leu Trp Thr Leu Pro Ile Leu Pro Leu
  1               5                  10                  15

Val Leu Ala Gly Cys Ser Thr Gly Ser Ala Asp Ser Ala Asp Ser Thr
             20                  25                  30

Asn Ala Ala Gly Ser Asn Ser Leu Lys Val Val Thr Ser Thr Gln Val
         35                  40                  45

Trp Ala Asp Val Ala Glu Ala Val Ala Pro Asp Val Asp Ile Glu Ala
     50                  55                  60

Ile Ile Thr Gly Gly Asp Ile Asp Pro His Ser Phe Glu Pro Ser Ala
 65                  70                  75                  80

Thr Asp Met Ala Lys Val Ser Glu Ala Asp Ile Ile Ile Val Gly Gly
                 85                  90                  95

Gly Gly Tyr Asp Ser Trp Leu Tyr Gly Thr Leu Glu Asp Asp Asp Arg
            100                 105                 110

Ile Ile His Ala Leu Asp Leu Ser Glu His Asp His Ser Glu His Asp
        115                 120                 125

Asp His Glu His Glu Ala Glu Glu Ala His Glu His Asp His Asp Glu
    130                 135                 140

Glu Gly His Asp His Asp Val Asp Asn Glu His Val Trp Tyr Ser Thr
145                 150                 155                 160

Glu Tyr Val Ser Glu Val Ala Glu Glu Phe Ala Glu Lys Val Thr Glu
                165                 170                 175

Leu Asp Pro Glu Ala Gln Ala Asp Ala Thr Ala Val Thr Thr Lys Met
            180                 185                 190

Asp Glu Leu His Asn Gln Ile His Asp Leu Pro Ala Val Arg Ile Ala
        195                 200                 205

Gln Thr Glu Pro Ile Ala Asp His Ile Leu Ser His Ser Asp Met Val
    210                 215                 220

Glu Ser Thr Pro Glu Gly Tyr Arg Ala Thr Thr Leu Ser Glu Ser Glu
225                 230                 235                 240

Pro Thr Ala Ala Asp Val Ala Ser Phe Gln Asp Ala Ile Asn Asn Gly
```

```
                245                 250                 255

Asp Leu Asp Val Leu Ile Tyr Asn Pro Gln Ser Ala Ser Thr Val Ala
            260                 265                 270

Thr Ser Leu Lys Asp Leu Ala Glu Glu Lys Gly Ile Pro Val Val Glu
        275                 280                 285

Ile Tyr Glu Thr Pro Gln Asn Thr Glu Asn Phe Leu Asp Ala Phe Thr
    290                 295                 300

Lys Ala Val Asp Asp Leu Thr Ala Ala Thr Asn Gln Val
305                 310                 315
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<210> 29
<211> 1020
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(997)
<223> RXA00413

<400> 29

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ctgtacagat cgcggtctat ggtgctaatc tcctaaatac ttgaatgacc atttcatgat 60

ccattcacaa aaactttccc aaacaaggac gtatttgaaa atg aaa ctt cgt cgc   115
                                              Met Lys Leu Arg Arg
                                                1               5

atc aca acc acc gcc atc gct ggc ctc ttc gcc gca acc gca ctt gtt   163
Ile Thr Thr Thr Ala Ile Ala Gly Leu Phe Ala Ala Thr Ala Leu Val
                  10                  15                  20

gcc tgt ggc tcc gat tcc gat gga agc agc acc act gtt gct gaa ggc   211
Ala Cys Gly Ser Asp Ser Asp Gly Ser Ser Thr Thr Val Ala Glu Gly
              25                  30                  35

acc gaa ggc gtg acc atc cgc atc ggc acc acc gac gct gcg aag gaa   259
Thr Glu Gly Val Thr Ile Arg Ile Gly Thr Thr Asp Ala Ala Lys Glu
          40                  45                  50

gca tgg acc gta ttc gaa gac aag gca gct gaa gag ggc atc acc ctc   307
Ala Trp Thr Val Phe Glu Asp Lys Ala Ala Glu Glu Gly Ile Thr Leu
      55                  60                  65

gac atc gtt cct ttc tct gac tac tcc acc cca aat gag gct ctt gcc   355
Asp Ile Val Pro Phe Ser Asp Tyr Ser Thr Pro Asn Glu Ala Leu Ala
 70                  75                  80                  85

cag gat cag ctg gac gtt aac ctc ttc cag cac ctg aag ttc ctg gct   403
Gln Asp Gln Leu Asp Val Asn Leu Phe Gln His Leu Lys Phe Leu Ala
                  90                  95                 100

gag tac aac gtc ggc tcc ggc gca gac ctc acc cca gtt ggc tcc agc   451
Glu Tyr Asn Val Gly Ser Gly Ala Asp Leu Thr Pro Val Gly Ser Ser
              105                 110                 115

gaa atc gtg cca ctg gca cta ttc tgg aag gac cac gac tcc atc gac   499
```

```
Glu Ile Val Pro Leu Ala Leu Phe Trp Lys Asp His Asp Ser Ile Asp
        120                 125                 130

ggc att gac ggc gag tcc gtt gcc atc cct aac gat cct tcc aac cag   547
Gly Ile Asp Gly Glu Ser Val Ala Ile Pro Asn Asp Pro Ser Asn Gln
    135                 140                 145

ggc cgc gcc atc aac gtt ctc gtt cag gca ggt ctg gtc acc ctg aag   595
Gly Arg Ala Ile Asn Val Leu Val Gln Ala Gly Leu Val Thr Leu Lys
150                 155                 160                 165

acc cca ggt ctg gtc acc cca gct cca gtc gat atc gac gag gca gct   643
Thr Pro Gly Leu Val Thr Pro Ala Pro Val Asp Ile Asp Glu Ala Ala
                170                 175                 180

tcc aag gtt tcc gtc atc cca gtc gac gca gct cag gca cca acc gct   691
Ser Lys Val Ser Val Ile Pro Val Asp Ala Ala Gln Ala Pro Thr Ala
            185                 190                 195

tac cag gag ggt cgc cca gcg atc atc aac aac tcc ttc ctt gac cgc   739
Tyr Gln Glu Gly Arg Pro Ala Ile Ile Asn Asn Ser Phe Leu Asp Arg
        200                 205                 210

gca ggc atc gat cca aac ctc gcg gtc ttc gaa gat gat cct gag tct   787
Ala Gly Ile Asp Pro Asn Leu Ala Val Phe Glu Asp Asp Pro Glu Ser
    215                 220                 225

gaa gaa gca gag cca tac atc aac gtc ttc gtc acc aag gct gag gac   835
Glu Glu Ala Glu Pro Tyr Ile Asn Val Phe Val Thr Lys Ala Glu Asp
230                 235                 240                 245

aag gac gat gcc aac atc gcc cgc ctc gtt gag ctg tgg cac gac cca   883
Lys Asp Asp Ala Asn Ile Ala Arg Leu Val Glu Leu Trp His Asp Pro
                250                 255                 260

gag gtt ctg gct gca gta gac cgc gac tct gag ggc acc tcc gtc cca   931
Glu Val Leu Ala Ala Val Asp Arg Asp Ser Glu Gly Thr Ser Val Pro
            265                 270                 275

gtt gat cgt cca gga gct gac ctt cag gaa atc ctt gat cgc ctt gag   979
Val Asp Arg Pro Gly Ala Asp Leu Gln Glu Ile Leu Asp Arg Leu Glu
        280                 285                 290

gct gat cag gaa aac gca taatctcttt tgagttcttt gca                1020
Ala Asp Gln Glu Asn Ala
    295
```

<210> 30
<211> 299
<212> PRT
<213> Corynebacterium glutamicum

<400> 30

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Met Lys Leu Arg Arg Ile Thr Thr Thr Ala Ile Ala Gly Leu Phe Ala
  1               5                  10                  15

Ala Thr Ala Leu Val Ala Cys Gly Ser Asp Ser Asp Gly Ser Ser Thr
             20                  25                  30

Thr Val Ala Glu Gly Thr Glu Gly Val Thr Ile Arg Ile Gly Thr Thr
```

```
         35                  40                  45

Asp Ala Ala Lys Glu Ala Trp Thr Val Phe Glu Asp Lys Ala Ala Glu
      50                  55                  60

Glu Gly Ile Thr Leu Asp Ile Val Pro Phe Ser Asp Tyr Ser Thr Pro
 65                  70                  75                  80

Asn Glu Ala Leu Ala Gln Asp Gln Leu Asp Val Asn Leu Phe Gln His
                 85                  90                  95

Leu Lys Phe Leu Ala Glu Tyr Asn Val Gly Ser Gly Ala Asp Leu Thr
            100                 105                 110

Pro Val Gly Ser Ser Glu Ile Val Pro Leu Ala Leu Phe Trp Lys Asp
        115                 120                 125

His Asp Ser Ile Asp Gly Ile Asp Gly Glu Ser Val Ala Ile Pro Asn
    130                 135                 140

Asp Pro Ser Asn Gln Gly Arg Ala Ile Asn Val Leu Val Gln Ala Gly
145                 150                 155                 160

Leu Val Thr Leu Lys Thr Pro Gly Leu Val Thr Pro Ala Pro Val Asp
                165                 170                 175

Ile Asp Glu Ala Ala Ser Lys Val Ser Val Ile Pro Val Asp Ala Ala
            180                 185                 190

Gln Ala Pro Thr Ala Tyr Gln Glu Gly Arg Pro Ala Ile Ile Asn Asn
        195                 200                 205

Ser Phe Leu Asp Arg Ala Gly Ile Asp Pro Asn Leu Ala Val Phe Glu
    210                 215                 220

Asp Asp Pro Glu Ser Glu Glu Ala Glu Pro Tyr Ile Asn Val Phe Val
225                 230                 235                 240

Thr Lys Ala Glu Asp Lys Asp Asp Ala Asn Ile Ala Arg Leu Val Glu
                245                 250                 255

Leu Trp His Asp Pro Glu Val Leu Ala Ala Val Asp Arg Asp Ser Glu
            260                 265                 270

Gly Thr Ser Val Pro Val Asp Arg Pro Gly Ala Asp Leu Gln Glu Ile
        275                 280                 285

Leu Asp Arg Leu Glu Ala Asp Gln Glu Asn Ala
    290                 295
```

<210> 31
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXA00482

<400> 31

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gcgatttcta tgaaattctt cacccatcca caactatcta ctatactttt agaagtaata 60

actattgagt taatataaac atgaagaaag gatttgcttt atg cgc att tca agc   115
                                              Met Arg Ile Ser Ser
                                                1               5

aaa ctt gtc acc aca gca cta ctc gca gcc att tca ctt ttc ggg ata   163
Lys Leu Val Thr Thr Ala Leu Leu Ala Ala Ile Ser Leu Phe Gly Ile
                   10                  15                  20

tcc acg gca caa gcc caa gac att ttt gac ggc gga cga ctt gca ggt   211
Ser Thr Ala Gln Ala Gln Asp Ile Phe Asp Gly Gly Arg Leu Ala Gly
               25                  30                  35

ggc tcc tcg cag gta tct aac cta agt tcg gtt cct gaa aac cta gcg   259
Gly Ser Ser Gln Val Ser Asn Leu Ser Ser Val Pro Glu Asn Leu Ala
          40                  45                  50

ctg ccc gaa att gaa aat agc att gac cta gaa cgc tac aaa ggc aag   307
Leu Pro Glu Ile Glu Asn Ser Ile Asp Leu Glu Arg Tyr Lys Gly Lys
     55                  60                  65

tgg tat caa gtc gca gca att ccc caa cca ttc tct tta cag tgc tca   355
Trp Tyr Gln Val Ala Ala Ile Pro Gln Pro Phe Ser Leu Gln Cys Ser
 70                  75                  80                  85

cat gac gtt acc gct gat tac ggc gtg atc gac tcg gac aca atc tct   403
His Asp Val Thr Ala Asp Tyr Gly Val Ile Asp Ser Asp Thr Ile Ser
                   90                  95                 100

gta aca aat aag tgt ggc act ttc ttt ggg cct tca gtt att gaa ggc   451
Val Thr Asn Lys Cys Gly Thr Phe Phe Gly Pro Ser Val Ile Glu Gly
               105                 110                 115

agc gct aaa gta gtt tcc aat gct tca tta aag gtt agc ttc cca ggt   499
Ser Ala Lys Val Val Ser Asn Ala Ser Leu Lys Val Ser Phe Pro Gly
          120                 125                 130

att cca ttt cag agt gaa gac aat caa gca aac tac cgc gtg acc tat   547
Ile Pro Phe Gln Ser Glu Asp Asn Gln Ala Asn Tyr Arg Val Thr Tyr
     135                 140                 145

atc gaa gat gat tat tca cta gca atc gtc ggc agc cca agc cgg tcc   595
Ile Glu Asp Asp Tyr Ser Leu Ala Ile Val Gly Ser Pro Ser Arg Ser
150                 155                 160                 165

tca gga ttt ata cta tcc cgc acg cca cag ctc agt agt gac caa tgg   643
Ser Gly Phe Ile Leu Ser Arg Thr Pro Gln Leu Ser Ser Asp Gln Trp
                   170                 175                 180

tct cac gtt cgg aac att aca gag gac agt ggg tgg tgg cca tgc gca   691
Ser His Val Arg Asn Ile Thr Glu Asp Ser Gly Trp Trp Pro Cys Ala
               185                 190                 195

ttc att aca gtc cca gcg aca ggt ggc tta aac acc gcc act ccg ctc   739
Phe Ile Thr Val Pro Ala Thr Gly Gly Leu Asn Thr Ala Thr Pro Leu
          200                 205                 210

tgc aca ctt taattaacgt agatggtcat cta                            771
Cys Thr Leu
```

215

<210> 32
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 32

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Met Arg Ile Ser Ser Lys Leu Val Thr Thr Ala Leu Leu Ala Ala Ile
  1               5                  10                  15

Ser Leu Phe Gly Ile Ser Thr Ala Gln Ala Gln Asp Ile Phe Asp Gly
            20                  25                  30

Gly Arg Leu Ala Gly Gly Ser Ser Gln Val Ser Asn Leu Ser Ser Val
        35                  40                  45

Pro Glu Asn Leu Ala Leu Pro Glu Ile Glu Asn Ser Ile Asp Leu Glu
    50                  55                  60

Arg Tyr Lys Gly Lys Trp Tyr Gln Val Ala Ala Ile Pro Gln Pro Phe
65                  70                  75                  80

Ser Leu Gln Cys Ser His Asp Val Thr Ala Asp Tyr Gly Val Ile Asp
                85                  90                  95

Ser Asp Thr Ile Ser Val Thr Asn Lys Cys Gly Thr Phe Phe Gly Pro
            100                 105                 110

Ser Val Ile Glu Gly Ser Ala Lys Val Val Ser Asn Ala Ser Leu Lys
        115                 120                 125

Val Ser Phe Pro Gly Ile Pro Phe Gln Ser Glu Asp Asn Gln Ala Asn
    130                 135                 140

Tyr Arg Val Thr Tyr Ile Glu Asp Asp Tyr Ser Leu Ala Ile Val Gly
145                 150                 155                 160

Ser Pro Ser Arg Ser Ser Gly Phe Ile Leu Ser Arg Thr Pro Gln Leu
                165                 170                 175

Ser Ser Asp Gln Trp Ser His Val Arg Asn Ile Thr Glu Asp Ser Gly
            180                 185                 190

Trp Trp Pro Cys Ala Phe Ile Thr Val Pro Ala Thr Gly Gly Leu Asn
        195                 200                 205

Thr Ala Thr Pro Leu Cys Thr Leu
    210                 215
```

<210> 33
<211> 1758
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1735)
<223> RXN01164

<400> 33
gccgatcgtg attgatgaag acgagatcca agcctggact tctgatctca aacctgaaga 60

tttcaccaaa ggtaaagatg aatccgacgg tgagaaataa gtg aca ctg ttt gtt 115
Val Thr Leu Phe Val
1 5

cgg ctc gcc ctt gct gct gtg ggc ggg ctt ttt gtc ttt gct tcc aat 163
Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe Val Phe Ala Ser Asn
10 15 20

gaa ccg atc ggc tgg ttt gtc gcg gga att gtt ggc act gca tta ttt 211
Glu Pro Ile Gly Trp Phe Val Ala Gly Ile Val Gly Thr Ala Leu Phe
25 30 35

ttt atc tcc ctt gcg ccg tgg gat ctg gga gtt ccc caa aag cgg cgg 259
Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val Pro Gln Lys Arg Arg
40 45 50

aag aag aat gag cca gtc cca ttt ttg caa cag atg tcc acg ggc cca 307
Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln Met Ser Thr Gly Pro
55 60 65

act gtt gta cag ggc atg ctt tta ggt ttt gtc cat ggc ctg gtg aca 355
Thr Val Val Gln Gly Met Leu Leu Gly Phe Val His Gly Leu Val Thr
70 75 80 85

tat ttg cag ctg ttg ccg tgg atc ggt gag ttt gtt ggc tca ctg cct 403
Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe Val Gly Ser Leu Pro
90 95 100

tat gtc gcg ttg tca gtt gtc gag gcg ctt tat tcc att gct ctt ggt 451
Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr Ser Ile Ala Leu Gly
105 110 115

gct ttc ggc gtg ctc att gcg cgt tgg agg gac tgg aag gtt ctc ctg 499
Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp Trp Lys Val Leu Leu
120 125 130

ttt ccg gcg atg tat gtg gct gtg gag tat cta aga agc tcg tgg cca 547
Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu Arg Ser Ser Trp Pro
135 140 145

ttt gat gga ttc gcg tgg gtt cgc ctg gca tgg ggt caa att aac ggt 595
Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp Gly Gln Ile Asn Gly
150 155 160 165

ccg ttg gct aat ctc gca gcg ctt ggt ggg gta gcg ttt gtc act ttt 643
Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val Ala Phe Val Thr Phe
170 175 180

tcc acg gtg ctg gct gcc gtg ggt gtg gcc atg gtg att att tcc aag 691
Ser Thr Val Leu Ala Ala Val Gly Val Ala Met Val Ile Ile Ser Lys
185 190 195

aag cga ctg gcc ggc gca atc atc acc gcg agt gtg att gct atc ggc 739
Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser Val Ile Ala Ile Gly
200 205 210

gcg gtg tca tcc ctg tac gtt gac cgc aat ggc acg agc gat gaa agc 787

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    215                 220                 225

atc gaa gta gcc gca att cag ggc aat gtg cct cgg atg gga ttg gac   835
Ile Glu Val Ala Ala Ile Gln Gly Asn Val Pro Arg Met Gly Leu Asp
230                 235                 240                 245

ttc aat gca cag cgc cgc gcg gtg ctg gcg aat cac gca cgg gaa acc   883
Phe Asn Ala Gln Arg Arg Ala Val Leu Ala Asn His Ala Arg Glu Thr
                250                 255                 260

ctc aag ctg gat gaa caa gtg gat ttg gtg atc tgg ccg gag aat tcc   931
Leu Lys Leu Asp Glu Gln Val Asp Leu Val Ile Trp Pro Glu Asn Ser
            265                 270                 275

tca gac gtc aac cca ttt tcc gat gca caa gca aga gcc att atc gat   979
Ser Asp Val Asn Pro Phe Ser Asp Ala Gln Ala Arg Ala Ile Ile Asp
        280                 285                 290

gga gca gtg gaa cat gtt cag gca cct att ttg gtg ggc acg atc acc   1027
Gly Ala Val Glu His Val Gln Ala Pro Ile Leu Val Gly Thr Ile Thr
    295                 300                 305

gtc gat gag gtt ggt cca cgc aac acc atg cag gta ttt gat cct gtt   1075
Val Asp Glu Val Gly Pro Arg Asn Thr Met Gln Val Phe Asp Pro Val
310                 315                 320                 325

gaa ggt gcc gcg gag tac cac aat aag aag ttc ttg cag ccg ttt ggt   1123
Glu Gly Ala Ala Glu Tyr His Asn Lys Lys Phe Leu Gln Pro Phe Gly
                330                 335                 340

gaa tac atg ccg ttt cgc gaa ttc ctg aga att ttc tcg ccc tac gtt   1171
Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile Phe Ser Pro Tyr Val
            345                 350                 355

gat tcc gct gga aac ttc cag ccc ggt gat ggc acc ggc gta gtg gag   1219
Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly Thr Gly Val Val Glu
        360                 365                 370

atg aat gct gcg aac tta ggc cgc gct gtg aca gtg ggc gtg atg acg   1267
Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr Val Gly Val Met Thr
    375                 380                 385

tgt tac gag gtc atc ttc gac cgt gct ggc cgc gac gcc atc gcc aat   1315
Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg Asp Ala Ile Ala Asn
390                 395                 400                 405

ggg gct gaa ttt ttg acc acg ccc acc aac aac gcc acc ttc gga ttc   1363
Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn Ala Thr Phe Gly Phe
                410                 415                 420

acg gac atg acg tat cag caa tta gca atg agc agg atg cgt gcc atc   1411
Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser Arg Met Arg Ala Ile
            425                 430                 435

gaa ttt gat agg gcg gtg gtt gtt gca gct aca tcg ggt gtt tcg gct   1459
Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr Ser Gly Val Ser Ala
        440                 445                 450

atc gtc aac cct gat gga agc att tcc caa aac acc cga att ttt gag   1507
Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn Thr Arg Ile Phe Glu
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    455                 460                 465

gcc gcc acc ttg acg gaa tcc att cca ctc aag gac act gtc acc atc   1555
Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys Asp Thr Val Thr Ile
470                 475                 480                 485

gca gcg cgg gtt ggt ttc tat gtt gaa tta ctg ttg gtt atc att ggt   1603
Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu Leu Val Ile Ile Gly
                490                 495                 500

gta tta gct gga cta ttc gcc att cga atg aat agc cgt tca aag tct   1651
Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn Ser Arg Ser Lys Ser
            505                 510                 515

gcg aaa ggt tcc gct cgg ccc gca caa gtt cgg gtt aag aag gtg cct   1699
Ala Lys Gly Ser Ala Arg Pro Ala Gln Val Arg Val Lys Lys Val Pro
        520                 525                 530

gcg aaa aag gca gca act aat cgt cga aaa gta aaa taaaaacgtc        1745
Ala Lys Lys Ala Ala Thr Asn Arg Arg Lys Val Lys
    535                 540                 545

ccgaagggac gag                                                   1758


<210> 34
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<213> Corynebacterium glutamicum

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Val Thr Leu Phe Val Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe
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            20                  25                  30

Gly Thr Ala Leu Phe Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val
        35                  40                  45

Pro Gln Lys Arg Arg Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln
    50                  55                  60

Met Ser Thr Gly Pro Thr Val Val Gln Gly Met Leu Leu Gly Phe Val
65                  70                  75                  80

His Gly Leu Val Thr Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe
                85                  90                  95

Val Gly Ser Leu Pro Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr
            100                 105                 110

Ser Ile Ala Leu Gly Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp
        115                 120                 125

Trp Lys Val Leu Leu Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu
    130                 135                 140

Arg Ser Ser Trp Pro Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp
145                 150                 155                 160
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Gly Gln Ile Asn Gly Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val
165 170 175

Ala Phe Val Thr Phe Ser Thr Val Leu Ala Ala Val Gly Val Ala Met
180 185 190

Val Ile Ile Ser Lys Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser
195 200 205

Val Ile Ala Ile Gly Ala Val Ser Ser Leu Tyr Val Asp Arg Asn Gly
210 215 220

Thr Ser Asp Glu Ser Ile Glu Val Ala Ala Ile Gln Gly Asn Val Pro
225 230 235 240

Arg Met Gly Leu Asp Phe Asn Ala Gln Arg Arg Ala Val Leu Ala Asn
245 250 255

His Ala Arg Glu Thr Leu Lys Leu Asp Glu Gln Val Asp Leu Val Ile
260 265 270

Trp Pro Glu Asn Ser Ser Asp Val Asn Pro Phe Ser Asp Ala Gln Ala
275 280 285

Arg Ala Ile Ile Asp Gly Ala Val Glu His Val Gln Ala Pro Ile Leu
290 295 300

Val Gly Thr Ile Thr Val Asp Glu Val Gly Pro Arg Asn Thr Met Gln
305 310 315 320

Val Phe Asp Pro Val Glu Gly Ala Ala Glu Tyr His Asn Lys Lys Phe
325 330 335

Leu Gln Pro Phe Gly Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile
340 345 350

Phe Ser Pro Tyr Val Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly
355 360 365

Thr Gly Val Val Glu Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr
370 375 380

Val Gly Val Met Thr Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg
385 390 395 400

Asp Ala Ile Ala Asn Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn
405 410 415

Ala Thr Phe Gly Phe Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser
420 425 430

Arg Met Arg Ala Ile Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr
435 440 445

Ser Gly Val Ser Ala Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn
450 455 460

Thr Arg Ile Phe Glu Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys
465 470 475 480

Asp Thr Val Thr Ile Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu

485 490 495

Leu Val Ile Ile Gly Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn
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Ser Arg Ser Lys Ser Ala Lys Gly Ser Ala Arg Pro Ala Gln Val Arg
515 520 525

Val Lys Lys Val Pro Ala Lys Lys Ala Ala Thr Asn Arg Arg Lys Val
530 535 540

Lys
545

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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1675)
<223> FRXA01164

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tttcaccaaa ggtaaagatg aatccgacgg tgagaaataa gtg aca ctg ttt gtt 115
Val Thr Leu Phe Val
1 5

cgg ctc gcc ctt gct gct gtg ggc ggg ctt ttt gtc ttt gct tcc aat 163
Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe Val Phe Ala Ser Asn
10 15 20

gaa ccg atc ggc tgg ttt gtc gcg gga att gtt ggc act gca tta ttt 211
Glu Pro Ile Gly Trp Phe Val Ala Gly Ile Val Gly Thr Ala Leu Phe
25 30 35

ttt atc tcc ctt gcg ccg tgg gat ctg gga gtt ccc caa aag cgg cgg 259
Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val Pro Gln Lys Arg Arg
40 45 50

aag aag aat gag cca gtc cca ttt ttg caa cag atg tcc acg ggc cca 307
Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln Met Ser Thr Gly Pro
55 60 65

act gtt gta cag ggc atg ctt tta ggt ttt gtc cat ggc ctg gtg aca 355
Thr Val Val Gln Gly Met Leu Leu Gly Phe Val His Gly Leu Val Thr
70 75 80 85

tat ttg cag ctg ttg ccg tgg atc ggt gag ttt gtt ggc tca ctg cct 403
Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe Val Gly Ser Leu Pro
90 95 100

tat gtc gcg ttg tca gtt gtc gag gcg ctt tat tcc att gct ctt ggt 451
Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr Ser Ile Ala Leu Gly
105 110 115

gct ttc ggc gtg ctc att gcg cgt tgg agg gac tgg aag gtt ctc ctg 499

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Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp Trp Lys Val Leu Leu
        120                 125                 130

ttt ccg gcg atg tat gtg gct gtg gag tat cta aga agc tcg tgg cca   547
Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu Arg Ser Ser Trp Pro
    135                 140                 145

ttt gat gga ttc gcg tgg gtt cgc ctg gca tgg ggt caa att aac ggt   595
Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp Gly Gln Ile Asn Gly
150                 155                 160                 165

ccg ttg gct aat ctc gca gcg ctt ggt ggg gta gcg ttt gtc act ttt   643
Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val Ala Phe Val Thr Phe
                170                 175                 180

tcc acg gtg ctg gct gcc gtg ggt gtg gcc atg gtg att att tcc aag   691
Ser Thr Val Leu Ala Ala Val Gly Val Ala Met Val Ile Ile Ser Lys
            185                 190                 195

aag cga ctg gcc ggc gca atc atc acc gcg agt gtg att gct atc ggc   739
Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser Val Ile Ala Ile Gly
        200                 205                 210

gcg gtg tca tcc ctg tac gtt gac cgc aat ggc acg agc gat gaa agc   787
Ala Val Ser Ser Leu Tyr Val Asp Arg Asn Gly Thr Ser Asp Glu Ser
    215                 220                 225

atc gaa gta gcc gca att cag ggc aat gtg cct cgg atg gga ttg gac   835
Ile Glu Val Ala Ala Ile Gln Gly Asn Val Pro Arg Met Gly Leu Asp
230                 235                 240                 245

ttc aat gca cag cgc cgc gcg gtg ctg gcg aat cac gca cgg gaa acc   883
Phe Asn Ala Gln Arg Arg Ala Val Leu Ala Asn His Ala Arg Glu Thr
                250                 255                 260

ctc aag ctg gat gaa caa gtg gat ttg gtg atc tgg ccg gag aat tcc   931
Leu Lys Leu Asp Glu Gln Val Asp Leu Val Ile Trp Pro Glu Asn Ser
            265                 270                 275

tca gac gtc aac cca ttt tcc gat gca caa gca aga gcc att atc gat   979
Ser Asp Val Asn Pro Phe Ser Asp Ala Gln Ala Arg Ala Ile Ile Asp
        280                 285                 290

gga gca gtg gaa cat gtt cag gca cct att ttg gtg ggc acg atc acc   1027
Gly Ala Val Glu His Val Gln Ala Pro Ile Leu Val Gly Thr Ile Thr
    295                 300                 305

gtc gat gag gtt ggt cca cgc aac acc atg cag gta ttt gat cct gtt   1075
Val Asp Glu Val Gly Pro Arg Asn Thr Met Gln Val Phe Asp Pro Val
310                 315                 320                 325

gaa ggt gcc gcg gag tac cac aat aag aag ttc ttg cag ccg ttt ggt   1123
Glu Gly Ala Ala Glu Tyr His Asn Lys Lys Phe Leu Gln Pro Phe Gly
                330                 335                 340

gaa tac atg ccg ttt cgc gaa ttc ctg aga att ttc tcg ccc tac gtt   1171
Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile Phe Ser Pro Tyr Val
            345                 350                 355

gat tcc gct gga aac ttc cag ccc ggt gat ggc acc ggc gta gtg gag   1219
Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly Thr Gly Val Val Glu
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        360                 365                 370

atg aat gct gcg aac tta ggc cgc gct gtg aca gtg ggc gtg atg acg   1267
Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr Val Gly Val Met Thr
    375                 380                 385

tgt tac gag gtc atc ttc gac cgt gct ggc cgc gac gcc atc gcc aat   1315
Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg Asp Ala Ile Ala Asn
390                 395                 400                 405

ggg gct gaa ttt ttg acc acg ccc acc aac aac gcc acc ttc gga ttc   1363
Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn Ala Thr Phe Gly Phe
                410                 415                 420

acg gac atg acg tat cag caa tta gca atg agc agg atg cgt gcc atc   1411
Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser Arg Met Arg Ala Ile
            425                 430                 435

gaa ttt gat agg gcg gtg gtt gtt gca gct aca tcg ggt gtt tcg gct   1459
Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr Ser Gly Val Ser Ala
        440                 445                 450

atc gtc aac cct gat gga agc att tcc caa aac acc cga att ttt gag   1507
Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn Thr Arg Ile Phe Glu
    455                 460                 465

gcc gcc acc ttg acg gaa tcc att cca ctc aag gac act gtc acc atc   1555
Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys Asp Thr Val Thr Ile
470                 475                 480                 485

gca gcg cgg gtt ggt ttc tat gtt gaa tta ctg ttg gtt atc att ggt   1603
Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu Leu Val Ile Ile Gly
                490                 495                 500

gta tta gct gga cta ttc gcc att cga atg aat agc cgt tca aag tct   1651
Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn Ser Arg Ser Lys Ser
            505                 510                 515

gcg aaa ggt tcc gct cgg ccc gca                                  1675
Ala Lys Gly Ser Ala Arg Pro Ala
        520                 525
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<210> 36
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<213> Corynebacterium glutamicum

<400> 36

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Val Thr Leu Phe Val Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe
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             20                  25                  30

Gly Thr Ala Leu Phe Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val
         35                  40                  45

Pro Gln Lys Arg Arg Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln
     50                  55                  60
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Met Ser Thr Gly Pro Thr Val Val Gln Gly Met Leu Leu Gly Phe Val
65 70 75 80

His Gly Leu Val Thr Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe
85 90 95

Val Gly Ser Leu Pro Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr
100 105 110

Ser Ile Ala Leu Gly Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp
115 120 125

Trp Lys Val Leu Leu Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu
130 135 140

Arg Ser Ser Trp Pro Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp
145 150 155 160

Gly Gln Ile Asn Gly Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val
165 170 175

Ala Phe Val Thr Phe Ser Thr Val Leu Ala Ala Val Gly Val Ala Met
180 185 190

Val Ile Ile Ser Lys Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser
195 200 205

Val Ile Ala Ile Gly Ala Val Ser Ser Leu Tyr Val Asp Arg Asn Gly
210 215 220

Thr Ser Asp Glu Ser Ile Glu Val Ala Ala Ile Gln Gly Asn Val Pro
225 230 235 240

Arg Met Gly Leu Asp Phe Asn Ala Gln Arg Arg Ala Val Leu Ala Asn
245 250 255

His Ala Arg Glu Thr Leu Lys Leu Asp Glu Gln Val Asp Leu Val Ile
260 265 270

Trp Pro Glu Asn Ser Ser Asp Val Asn Pro Phe Ser Asp Ala Gln Ala
275 280 285

Arg Ala Ile Ile Asp Gly Ala Val Glu His Val Gln Ala Pro Ile Leu
290 295 300

Val Gly Thr Ile Thr Val Asp Glu Val Gly Pro Arg Asn Thr Met Gln
305 310 315 320

Val Phe Asp Pro Val Glu Gly Ala Ala Glu Tyr His Asn Lys Lys Phe
325 330 335

Leu Gln Pro Phe Gly Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile
340 345 350

Phe Ser Pro Tyr Val Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly
355 360 365

Thr Gly Val Val Glu Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr
370 375 380

Val Gly Val Met Thr Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg

385 390 395 400

Asp Ala Ile Ala Asn Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn
405 410 415

Ala Thr Phe Gly Phe Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser
420 425 430

Arg Met Arg Ala Ile Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr
435 440 445

Ser Gly Val Ser Ala Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn
450 455 460

Thr Arg Ile Phe Glu Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys
465 470 475 480

Asp Thr Val Thr Ile Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu
485 490 495

Leu Val Ile Ile Gly Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn
500 505 510

Ser Arg Ser Lys Ser Ala Lys Gly Ser Ala Arg Pro Ala
515 520 525

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<222> (101)..(910)
<223> RXN01168

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taaaataaaa acgtcccgaa gggacgagga ggacaacacc atg agc agt gag gca 115
Met Ser Ser Glu Ala
1 5

gta gat gct acg acg ctg gtg att att cca acg tac aac gag ctg gaa 163
Val Asp Ala Thr Thr Leu Val Ile Ile Pro Thr Tyr Asn Glu Leu Glu
10 15 20

aac ctt cca ctc atc gtg gat cgc gtg cgc acc gca acc cct gac gtt 211
Asn Leu Pro Leu Ile Val Asp Arg Val Arg Thr Ala Thr Pro Asp Val
25 30 35

cac gta ctc atc gtg gac gac aac agc cca gac ggc acc ggc gag cgc 259
His Val Leu Ile Val Asp Asp Asn Ser Pro Asp Gly Thr Gly Glu Arg
40 45 50

gca gac aag ctt gct gct gac gac gac cac att ttt gtc ctc cac cgc 307
Ala Asp Lys Leu Ala Ala Asp Asp Asp His Ile Phe Val Leu His Arg
55 60 65

gaa ggc aaa ggc ggc ctg tgc gca gag tac atg gct ggc ttc cag tgg 355

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Glu Gly Lys Gly Gly Leu Cys Ala Glu Tyr Met Ala Gly Phe Gln Trp
 70                  75                  80                  85

ggc ctg gag cgc gac tac cag gtc ctg tgc gaa atg gac gcc gac ggc   403
Gly Leu Glu Arg Asp Tyr Gln Val Leu Cys Glu Met Asp Ala Asp Gly
                 90                  95                 100

tcc cac gca cca gaa cag ctg cac ctg ctg ctc gct gag atc acc aat   451
Ser His Ala Pro Glu Gln Leu His Leu Leu Leu Ala Glu Ile Thr Asn
            105                 110                 115

ggc gct gac ctg gtc atc ggc tcg cgc tac gtg cca ggc ggc cgc gta   499
Gly Ala Asp Leu Val Ile Gly Ser Arg Tyr Val Pro Gly Gly Arg Val
        120                 125                 130

gtc aac tgg ccc aag aac cgt tgg ctc ttg tcc aag ggc ggc aac gtc   547
Val Asn Trp Pro Lys Asn Arg Trp Leu Leu Ser Lys Gly Gly Asn Val
    135                 140                 145

tac atc agc gtc gcg ctc ggc gcc ggc ttg acc gat atg acc gca ggg   595
Tyr Ile Ser Val Ala Leu Gly Ala Gly Leu Thr Asp Met Thr Ala Gly
150                 155                 160                 165

tac cgc gct ttt cga cgt gaa gtg cta gaa gca ctg ccg ctt gat gag   643
Tyr Arg Ala Phe Arg Arg Glu Val Leu Glu Ala Leu Pro Leu Asp Glu
                170                 175                 180

ctc tcc aac gct ggg tac att ttc caa gtt gag att gcc tac cgt gca   691
Leu Ser Asn Ala Gly Tyr Ile Phe Gln Val Glu Ile Ala Tyr Arg Ala
            185                 190                 195

gtt gaa gcc gga ttc gat gtt cgt gaa gtt ccc atc act ttc acc gag   739
Val Glu Ala Gly Phe Asp Val Arg Glu Val Pro Ile Thr Phe Thr Glu
        200                 205                 210

cgt gag atc ggc gaa tcc aag ctg gac ggc agc ttt gtc aag gat tcc   787
Arg Glu Ile Gly Glu Ser Lys Leu Asp Gly Ser Phe Val Lys Asp Ser
    215                 220                 225

ctg ctc gag gta acc aag tgg ggc ctc aag cac cgc ggt ggc cag gcc   835
Leu Leu Glu Val Thr Lys Trp Gly Leu Lys His Arg Gly Gly Gln Ala
230                 235                 240                 245

aag gaa ctg tcc aag gaa atg gtc ggc ctg ctg aac tat gag tgg aag   883
Lys Glu Leu Ser Lys Glu Met Val Gly Leu Leu Asn Tyr Glu Trp Lys
                250                 255                 260

cac ttc aaa aag cgc aac acc tgg ctc taaactgctt gccggttagt         930
His Phe Lys Lys Arg Asn Thr Trp Leu
            265                 270

gaa                                                               933


<210> 38
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 38
Met Ser Ser Glu Ala Val Asp Ala Thr Thr Leu Val Ile Ile Pro Thr
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            20                  25                  30

Ala Thr Pro Asp Val His Val Leu Ile Val Asp Asp Asn Ser Pro Asp
        35                  40                  45

Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp His Ile
    50                  55                  60

Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu Tyr Met
65                  70                  75                  80

Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu Cys Glu
                85                  90                  95

Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu Leu Leu
            100                 105                 110

Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg Tyr Val
        115                 120                 125

Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu Leu Ser
    130                 135                 140

Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly Leu Thr
145                 150                 155                 160

Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu Glu Ala
                165                 170                 175

Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln Val Glu
            180                 185                 190

Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu Val Pro
        195                 200                 205

Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp Gly Ser
    210                 215                 220

Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu Lys His
225                 230                 235                 240

Arg Gly Gly Gln Ala Lys Glu Leu Ser Lys Glu Met Val Gly Leu Leu
                245                 250                 255

Asn Tyr Glu Trp Lys His Phe Lys Lys Arg Asn Thr Trp Leu
            260                 265                 270
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<210> 39
<211> 743
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(720)
<223> FRXA01168

<400> 39

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cgc acc gca acc cct gac gtt cac gta ctc atc gtg gac gac aac agc   48
Arg Thr Ala Thr Pro Asp Val His Val Leu Ile Val Asp Asp Asn Ser
  1               5                  10                  15

cca gac ggc acc ggc gag cgc gca gac aag ctt gct gct gac gac gac   96
Pro Asp Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp
            20                  25                  30

cac att ttt gtc ctc cac cgc gaa ggc aaa ggc ggc ctg tgc gca gag  144
His Ile Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu
        35                  40                  45

tac atg gct ggc ttc cag tgg ggc ctg gag cgc gac tac cag gtc ctg  192
Tyr Met Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu
    50                  55                  60

tgc gaa atg gac gcc gac ggc tcc cac gca cca gaa cag ctg cac ctg  240
Cys Glu Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu
65                  70                  75                  80

ctg ctc gct gag atc acc aat ggc gct gac ctg gtc atc ggc tcg cgc  288
Leu Leu Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg
                85                  90                  95

tac gtg cca ggc ggc cgc gta gtc aac tgg ccc aag aac cgt tgg ctc  336
Tyr Val Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu
            100                 105                 110

ttg tcc aag ggc ggc aac gtc tac atc agc gtc gcg ctc ggc gcc ggc  384
Leu Ser Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly
        115                 120                 125

ttg acc gat atg acc gca ggg tac cgc gct ttt cga cgt gaa gtg cta  432
Leu Thr Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu
    130                 135                 140

gaa gca ctg ccg ctt gat gag ctc tcc aac gct ggg tac att ttc caa  480
Glu Ala Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln
145                 150                 155                 160

gtt gag att gcc tac cgt gca gtt gaa gcc gga ttc gat gtt cgt gaa  528
Val Glu Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu
                165                 170                 175

gtt ccc atc act ttc acc gag cgt gag atc ggc gaa tcc aag ctg gac  576
Val Pro Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp
            180                 185                 190

ggc agc ttt gtc aag gat tcc ctg ctc gag gta acc aag tgg ggc ctc  624
Gly Ser Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu
        195                 200                 205

aag cac cgc ggt ggc cag gcc aag gaa ctg tcc aag gaa atg gtc ggc  672
Lys His Arg Gly Gly Gln Ala Lys Glu Leu Ser Lys Glu Met Val Gly
    210                 215                 220

ctg ctg aac tat gag tgg aag cac ttc aaa aag cgc aac acc tgg ctc  720
Leu Leu Asn Tyr Glu Trp Lys His Phe Lys Lys Arg Asn Thr Trp Leu
225                 230                 235                 240
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US-10-664-050-39 = pgu15650

taaactgctt gccggttagt gaa 743

<210> 40
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 40

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Arg Thr Ala Thr Pro Asp Val His Val Leu Ile Val Asp Asp Asn Ser
  1               5                  10                  15

Pro Asp Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp
             20                  25                  30

His Ile Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu
         35                  40                  45

Tyr Met Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu
     50                  55                  60

Cys Glu Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu
 65                  70                  75                  80

Leu Leu Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg
                85                  90                  95

Tyr Val Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu
            100                 105                 110

Leu Ser Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly
        115                 120                 125

Leu Thr Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu
    130                 135                 140

Glu Ala Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln
145                 150                 155                 160

Val Glu Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu
                165                 170                 175

Val Pro Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp
            180                 185                 190

Gly Ser Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu
        195                 200                 205

Lys His Arg Gly Gly Gln Ala Lys Glu Leu Ser Lys Glu Met Val Gly
    210                 215                 220

Leu Leu Asn Tyr Glu Trp Lys His Phe Lys Lys Arg Asn Thr Trp Leu
225                 230                 235                 240
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<210> 41
<211> 1293
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1270)
<223> RXN02062

<400> 41

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ttgtctaaac atcgttttgg ggtccgaatg atagcccctt ttaatgcccc catttcggta 60

tcgctgcgca actgttttta gatggctaat ctttgaaatt atg aga gtc gga atg   115
                                            Met Arg Val Gly Met
                                              1               5

atg aca aga gag tat cca cca gag gtt tac ggc ggc gct ggc gtg cac   163
Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly Gly Ala Gly Val His
                  10                  15                  20

gtc acc gaa ttg acc cga ttc atg cgt gag atc gct gaa gtt gat gtt   211
Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile Ala Glu Val Asp Val
              25                  30                  35

cac tgc atg ggt gca cct cgc gat atg gag gga gtt ttc gtc cac ggc   259
His Cys Met Gly Ala Pro Arg Asp Met Glu Gly Val Phe Val His Gly
          40                  45                  50

gtc gat cct gcc ttg gaa agc gcg aac cct gcg att aag aca ctg tcc   307
Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala Ile Lys Thr Leu Ser
      55                  60                  65

acc ggt tta cgc atg gca gaa gct gca aac aac gtg gat gtc gtg cac   355
Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn Val Asp Val Val His
  70                  75                  80                  85

tca cac act tgg tat gca ggt ctt ggc ggc cac ctt gca gct cgt ctc   403
Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His Leu Ala Ala Arg Leu
                  90                  95                 100

cac ggc att cct cac gtg gct acc gcg cac tct ttg gag cca gat cgc   451
His Gly Ile Pro His Val Ala Thr Ala His Ser Leu Glu Pro Asp Arg
              105                 110                 115

cca tgg aag cgt gag cag ctt ggc ggt gga tac gac gtg tcc tcc tgg   499
Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr Asp Val Ser Ser Trp
          120                 125                 130

tct gaa aaa aat gcc atg gaa tac gct gac gcg gtc atc gct gtg tcg   547
Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala Val Ile Ala Val Ser
      135                 140                 145

gct cgc atg aaa gat tcc atc ctc gct gcg tac cct cgc atc gag ccg   595
Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr Pro Arg Ile Glu Pro
150                 155                 160                 165

gac aac gtg cgt gtt gtc ctc aac ggc atc gac act gag ttg tgg cag   643
Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp Thr Glu Leu Trp Gln
                  170                 175                 180

cct cgc ccg act ttc gat gac gcg gaa gat tcc gta ctc cgc tcc cta   691
Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser Val Leu Arg Ser Leu
              185                 190                 195
```

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ggc gtt gac cca cag cgg ccc atc gtc gca ttt gtc ggc cgc atc acc   739
Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe Val Gly Arg Ile Thr
        200                 205                 210

cgc caa aaa ggc gtc gag cac ctc atc aag gca gca gcg ctt ttc gac   787
Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala Ala Ala Leu Phe Asp
    215                 220                 225

gag tcc gtg cag ctt gtg ctc tgt gcc ggc gcg cca gac acc ccc gaa   835
Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala Pro Asp Thr Pro Glu
230                 235                 240                 245

atc gca gct cgc acc acc gcc ctg gtg gaa gaa ctc cag gca aag cgc   883
Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu Leu Gln Ala Lys Arg
                250                 255                 260

gaa ggc att ttc tgg gtt cag gac atg ctg ggc aag gac aaa atc caa   931
Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly Lys Asp Lys Ile Gln
            265                 270                 275

gag att ctc acc gct gct gac acc ttc gtg tgc cca tcc att tac gag   979
Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys Pro Ser Ile Tyr Glu
        280                 285                 290

cca ctg ggc atc gtg aac ttg gaa gca atg gcc tgc aac acc gca gtt   1027
Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala Cys Asn Thr Ala Val
    295                 300                 305

gtc gca tcc gac gtt gga ggc atc cct gag gtt gtt gtc gac ggc acc   1075
Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val Val Val Asp Gly Thr
310                 315                 320                 325

acc ggc gcc ctc gtt cac tac gac gaa aat gat gtc gaa acc ttc gag   1123
Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp Val Glu Thr Phe Glu
                330                 335                 340

cgc gat atc gcc gaa gcg gtg aat aaa atg gtc gct gat cga gag acc   1171
Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val Ala Asp Arg Glu Thr
            345                 350                 355

gca gcc aaa ttt ggt ctc gca ggg cgc gaa cgt gct atc aat gat ttc   1219
Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg Ala Ile Asn Asp Phe
        360                 365                 370

tcc tgg gca acg att gct cag cag acc att gat gtg tac aaa tcc ttg   1267
Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp Val Tyr Lys Ser Leu
    375                 380                 385

atg taaaaccgaa agccggggaa cct                                    1293
Met
390
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<210> 42
<211> 390
<212> PRT
<213> Corynebacterium glutamicum

<400> 42
Met Arg Val Gly Met Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly

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  1               5                  10                  15

Gly Ala Gly Val His Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile
            20                  25                  30

Ala Glu Val Asp Val His Cys Met Gly Ala Pro Arg Asp Met Glu Gly
        35                  40                  45

Val Phe Val His Gly Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala
    50                  55                  60

Ile Lys Thr Leu Ser Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn
65                  70                  75                  80

Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His
                85                  90                  95

Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr Ala His Ser
            100                 105                 110

Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr
        115                 120                 125

Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala
    130                 135                 140

Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr
145                 150                 155                 160

Pro Arg Ile Glu Pro Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp
                165                 170                 175

Thr Glu Leu Trp Gln Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser
            180                 185                 190

Val Leu Arg Ser Leu Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe
        195                 200                 205

Val Gly Arg Ile Thr Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala
    210                 215                 220

Ala Ala Leu Phe Asp Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala
225                 230                 235                 240

Pro Asp Thr Pro Glu Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu
                245                 250                 255

Leu Gln Ala Lys Arg Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly
            260                 265                 270

Lys Asp Lys Ile Gln Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys
        275                 280                 285

Pro Ser Ile Tyr Glu Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala
    290                 295                 300

Cys Asn Thr Ala Val Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val
305                 310                 315                 320

Val Val Asp Gly Thr Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp
                325                 330                 335
```

```
Val Glu Thr Phe Glu Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val
            340                 345                 350

Ala Asp Arg Glu Thr Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg
        355                 360                 365

Ala Ile Asn Asp Phe Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp
    370                 375                 380

Val Tyr Lys Ser Leu Met
385                 390


<210> 43
<211> 1293
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1270)
<223> FRXA02062

<400> 43
ttgtctaaac atcgttttgg ggtccgaatg atagcccctt ttaatgcccc catttcggta 60

tcgctgcgca actgttttta gatggctaat ctttgaaatt atg aga gtc gga atg   115
                                        Met Arg Val Gly Met
                                          1               5

atg aca aga gag tat cca cca gag gtt tac ggc ggc gct ggc gtg cac   163
Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly Gly Ala Gly Val His
                10                  15                  20

gtc acc gaa ttg acc cga ttc atg cgt gag atc gct gaa gtt gat gtt   211
Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile Ala Glu Val Asp Val
            25                  30                  35

cac tgc atg ggt gca cct cgc gat atg gag gga gtt ttc gtc cac ggc   259
His Cys Met Gly Ala Pro Arg Asp Met Glu Gly Val Phe Val His Gly
        40                  45                  50

gtc gat cct gcc ttg gaa agc gcg aac cct gcg att aag aca ctg tcc   307
Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala Ile Lys Thr Leu Ser
    55                  60                  65

acc ggt tta cgc atg gca gaa gct gca aac aac gtg gat gtc gtg cac   355
Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn Val Asp Val Val His
70                  75                  80                  85

tca cac act tgg tat gca ggt ctt ggc ggc cac ctt gca gct cgt ctc   403
Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His Leu Ala Ala Arg Leu
                90                  95                  100

cac ggc att cct cac gtg gct acc gcg cac tct ttg gag cca gat cgc   451
His Gly Ile Pro His Val Ala Thr Ala His Ser Leu Glu Pro Asp Arg
            105                 110                 115

cca tgg aag cgt gag cag ctt ggc ggt gga tac gac gtg tcc tcc tgg   499
Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr Asp Val Ser Ser Trp
```

```
        120                 125                 130

tct gaa aaa aat gcc atg gaa tac gct gac gcg gtc atc gct gtg tcg   547
Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala Val Ile Ala Val Ser
    135                 140                 145

gct cgc atg aaa gat tcc atc ctc gct gcg tac cct cgc atc gag ccg   595
Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr Pro Arg Ile Glu Pro
150                 155                 160                 165

gac aac gtg cgt gtt gtc ctc aac ggc atc gac act gag ttg tgg cag   643
Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp Thr Glu Leu Trp Gln
                170                 175                 180

cct cgc ccg act ttc gat gac gcg gaa gat tcc gta ctc cgc tcc cta   691
Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser Val Leu Arg Ser Leu
            185                 190                 195

ggc gtt gac cca cag cgg ccc atc gtc gca ttt gtc ggc cgc atc acc   739
Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe Val Gly Arg Ile Thr
        200                 205                 210

cgc caa aaa ggc gtc gag cac ctc atc aag gca gca gcg ctt ttc gac   787
Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala Ala Ala Leu Phe Asp
    215                 220                 225

gag tcc gtg cag ctt gtg ctc tgt gcc ggc gcg cca gac acc ccc gaa   835
Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala Pro Asp Thr Pro Glu
230                 235                 240                 245

atc gca gct cgc acc acc gcc ctg gtg gaa gaa ctc cag gca aag cgc   883
Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu Leu Gln Ala Lys Arg
                250                 255                 260

gaa ggc att ttc tgg gtt cag gac atg ctg ggc aag gac aaa atc caa   931
Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly Lys Asp Lys Ile Gln
            265                 270                 275

gag att ctc acc gct gct gac acc ttc gtg tgc cca tcc att tac gag   979
Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys Pro Ser Ile Tyr Glu
        280                 285                 290

cca ctg ggc atc gtg aac ttg gaa gca atg gcc tgc aac acc gca gtt  1027
Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala Cys Asn Thr Ala Val
    295                 300                 305

gtc gca tcc gac gtt gga ggc atc cct gag gtt gtt gtc gac ggc acc  1075
Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val Val Val Asp Gly Thr
310                 315                 320                 325

acc ggc gcc ctc gtt cac tac gac gaa aat gat gtc gaa acc ttc gag  1123
Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp Val Glu Thr Phe Glu
                330                 335                 340

cgc gat atc gcc gaa gcg gtg aat aaa atg gtc gct gat cga gag acc  1171
Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val Ala Asp Arg Glu Thr
            345                 350                 355

gca gcc aaa ttt ggt ctc gca ggg cgc gaa cgt gct atc aat gat ttc  1219
Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg Ala Ile Asn Asp Phe
        360                 365                 370
```

```
tcc tgg gca acg att gct cag cag acc att gat gtg tac aaa tcc ttg   1267
Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp Val Tyr Lys Ser Leu
    375                 380                 385

atg taaaaccgaa agccggggaa cct                                     1293
Met
390
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<210> 44
<211> 390
<212> PRT
<213> Corynebacterium glutamicum

<400> 44

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Met Arg Val Gly Met Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly
  1               5                  10                  15

Gly Ala Gly Val His Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile
             20                  25                  30

Ala Glu Val Asp Val His Cys Met Gly Ala Pro Arg Asp Met Glu Gly
         35                  40                  45

Val Phe Val His Gly Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala
     50                  55                  60

Ile Lys Thr Leu Ser Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn
 65                  70                  75                  80

Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His
                 85                  90                  95

Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr Ala His Ser
            100                 105                 110

Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr
        115                 120                 125

Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala
    130                 135                 140

Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr
145                 150                 155                 160

Pro Arg Ile Glu Pro Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp
                165                 170                 175

Thr Glu Leu Trp Gln Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser
            180                 185                 190

Val Leu Arg Ser Leu Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe
        195                 200                 205

Val Gly Arg Ile Thr Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala
    210                 215                 220

Ala Ala Leu Phe Asp Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala
225                 230                 235                 240
```

US 2005/0153417 A1

```
Pro Asp Thr Pro Glu Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu
                245                 250                 255

Leu Gln Ala Lys Arg Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly
            260                 265                 270

Lys Asp Lys Ile Gln Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys
        275                 280                 285

Pro Ser Ile Tyr Glu Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala
    290                 295                 300

Cys Asn Thr Ala Val Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val
305                 310                 315                 320

Val Val Asp Gly Thr Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp
                325                 330                 335

Val Glu Thr Phe Glu Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val
            340                 345                 350

Ala Asp Arg Glu Thr Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg
        355                 360                 365

Ala Ile Asn Asp Phe Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp
    370                 375                 380

Val Tyr Lys Ser Leu Met
385                 390
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09/15/2005 15:20 [ Doc: 2005-0915_US_NP_BGI-131CP_Sequence_Listing.txt ]

<210> 45
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXA02222

<400> 45

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aagattgcaa aaaccttgaa aaagtgtatg gcagcgatgg ttg ggt cga cct ccc   115
                                              Leu Gly Arg Pro Pro
                                                1               5

cca gga gac gtt cat act ctc cta gac gat atc gga gca gag gaa tct   163
Pro Gly Asp Val His Thr Leu Leu Asp Asp Ile Gly Ala Glu Glu Ser
                10                  15                  20

gaa gca gat aaa gtt cca att gaa tgg caa aac gcc ctg act aag gca   211
Glu Ala Asp Lys Val Pro Ile Glu Trp Gln Asn Ala Leu Thr Lys Ala
            25                  30                  35

gac agg tat gca aac cgg caa cac atg tct cag gca cga ctc tat cgc   259
Asp Arg Tyr Ala Asn Arg Gln His Met Ser Gln Ala Arg Leu Tyr Arg
        40                  45                  50

caa tta acc agt gat gtt gga gag ggc ttc act gaa gaa gct gcc caa   307
```

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Gln Leu Thr Ser Asp Val Gly Glu Gly Phe Thr Glu Glu Ala Ala Gln
     55                  60                  65

tac gca atc gaa aat gtg aac gca gac tgg aac gct aac gcc cta gta   355
Tyr Ala Ile Glu Asn Val Asn Ala Asp Trp Asn Ala Asn Ala Leu Val
 70                  75                  80                  85

aaa gca aga aat tac cag gag cgc caa gca atg tca gta gac cgc att   403
Lys Ala Arg Asn Tyr Gln Glu Arg Gln Ala Met Ser Val Asp Arg Ile
                 90                  95                 100

tac agg caa ctt act agt gaa cac ggt gaa ggg ttt acc cca gag cag   451
Tyr Arg Gln Leu Thr Ser Glu His Gly Glu Gly Phe Thr Pro Glu Gln
            105                 110                 115

gca caa tac gcg atc gac aac cta taaggcataa agatcctagt att         498
Ala Gln Tyr Ala Ile Asp Asn Leu
        120                 125
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Date Recue/Date Received

<210> 46
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 46

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Leu Gly Arg Pro Pro Pro Gly Asp Val His Thr Leu Leu Asp Asp Ile
  1               5                  10                  15

Gly Ala Glu Glu Ser Glu Ala Asp Lys Val Pro Ile Glu Trp Gln Asn
            20                  25                  30

Ala Leu Thr Lys Ala Asp Arg Tyr Ala Asn Arg Gln His Met Ser Gln
        35                  40                  45

Ala Arg Leu Tyr Arg Gln Leu Thr Ser Asp Val Gly Glu Gly Phe Thr
     50                  55                  60

Glu Glu Ala Ala Gln Tyr Ala Ile Glu Asn Val Asn Ala Asp Trp Asn
 65                  70                  75                  80

Ala Asn Ala Leu Val Lys Ala Arg Asn Tyr Gln Glu Arg Gln Ala Met
                85                  90                  95

Ser Val Asp Arg Ile Tyr Arg Gln Leu Thr Ser Glu His Gly Glu Gly
            100                 105                 110

Phe Thr Pro Glu Gln Ala Gln Tyr Ala Ile Asp Asn Leu
        115                 120                 125
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<210> 47
<211> 1344
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1321)
<223> RXA02313

<400> 47
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ttaactgcga tgtaggcatg atgtggagat aataaggccc atg cgg gta gca att 115
Met Arg Val Ala Ile
1 5

gtt gca gag tcg ttc ctt cca aat gtc aac gga gtc acc aac tcg gtg 163
Val Ala Glu Ser Phe Leu Pro Asn Val Asn Gly Val Thr Asn Ser Val
10 15 20

ctc cgg gtg ttg gag cat ttg aaa gcc aac gga cac gac gcg ctc gtc 211
Leu Arg Val Leu Glu His Leu Lys Ala Asn Gly His Asp Ala Leu Val
25 30 35

atc gcg ccg ggt gcc cgg gat ttt gaa gaa gaa atc ggc cac tac ctg 259
Ile Ala Pro Gly Ala Arg Asp Phe Glu Glu Glu Ile Gly His Tyr Leu
40 45 50

ggc ttt gaa att gtg cgc gtc ccc acc gtt cgg gtc cca ctg att gat 307
Gly Phe Glu Ile Val Arg Val Pro Thr Val Arg Val Pro Leu Ile Asp
55 60 65

tca ctg ccc atc ggt gtt cct ctg ccc tca gtt acc tct gtg ctg cgc 355
Ser Leu Pro Ile Gly Val Pro Leu Pro Ser Val Thr Ser Val Leu Arg
70 75 80 85

gag tac aac cca gac atc att cac ctg gca tcc cca ttt gtg ctc ggt 403
Glu Tyr Asn Pro Asp Ile Ile His Leu Ala Ser Pro Phe Val Leu Gly
90 95 100

gga gcg gca gca ttc gca gca agg cag ctg cgc atc cca gca att gct 451
Gly Ala Ala Ala Phe Ala Ala Arg Gln Leu Arg Ile Pro Ala Ile Ala
105 110 115

atc tat caa act gat gtc gca ggg ttc tcc cag cgc tac cac ctg gca 499
Ile Tyr Gln Thr Asp Val Ala Gly Phe Ser Gln Arg Tyr His Leu Ala
120 125 130

ccg ttg gcc act gca agc tgg gaa tgg atc aag acg gtc cac aac atg 547
Pro Leu Ala Thr Ala Ser Trp Glu Trp Ile Lys Thr Val His Asn Met
135 140 145

tgc cag cgc acc ctt gct ccc tca tcc atg agc att gac gag ctg cgt 595
Cys Gln Arg Thr Leu Ala Pro Ser Ser Met Ser Ile Asp Glu Leu Arg
150 155 160 165

gac cac gga att aat gat att ttc cac tgg gct cgg ggc gtg gac tcc 643
Asp His Gly Ile Asn Asp Ile Phe His Trp Ala Arg Gly Val Asp Ser
170 175 180

aag cgt ttc cac cct gga aag cgt tcc gta gcg cta cgt aag tct tgg 691
Lys Arg Phe His Pro Gly Lys Arg Ser Val Ala Leu Arg Lys Ser Trp
185 190 195

gat cca agt gga gca aag aag atc gtt ggt ttc gtt ggg cgc ctt gca 739
Asp Pro Ser Gly Ala Lys Lys Ile Val Gly Phe Val Gly Arg Leu Ala
200 205 210

tcc gaa aag ggc gtg gag cgc ctt gct gga tta tcc gga cgc tca gac 787
Ser Glu Lys Gly Val Glu Arg Leu Ala Gly Leu Ser Gly Arg Ser Asp

```
    215                 220                 225

atc caa ttg gtc atc gtc ggt gat ggc cca gag gcc aag tac ctg cag   835
Ile Gln Leu Val Ile Val Gly Asp Gly Pro Glu Ala Lys Tyr Leu Gln
230                 235                 240                 245

gaa atg atg ccg gat gcg atc ttc aca gga gct ctc ggc ggc gag gaa   883
Glu Met Met Pro Asp Ala Ile Phe Thr Gly Ala Leu Gly Gly Glu Glu
                250                 255                 260

cta gcc acc acc tac gca tca ctc gat ctg ttt gtg cac cca ggt gag   931
Leu Ala Thr Thr Tyr Ala Ser Leu Asp Leu Phe Val His Pro Gly Glu
            265                 270                 275

ttt gaa acc ttc tgc cag gcg atc cag gaa gcc caa gca tca ggt gtg   979
Phe Glu Thr Phe Cys Gln Ala Ile Gln Glu Ala Gln Ala Ser Gly Val
        280                 285                 290

ccc acc att ggc cca cgc gca ggt ggt ccc att gat ttg atc aac gaa   1027
Pro Thr Ile Gly Pro Arg Ala Gly Gly Pro Ile Asp Leu Ile Asn Glu
    295                 300                 305

ggc gtc aac ggc ctg ctt ctt gat gtt gta gat ttc aag gaa acc ctc   1075
Gly Val Asn Gly Leu Leu Leu Asp Val Val Asp Phe Lys Glu Thr Leu
310                 315                 320                 325

ccc gct gca gcc gaa tgg att ttg gac gat tcc cgc cac tcc gaa atg   1123
Pro Ala Ala Ala Glu Trp Ile Leu Asp Asp Ser Arg His Ser Glu Met
                330                 335                 340

tgc gca gct gct tgg gaa ggt gtg aaa gac aag acc tgg gaa gct ttg   1171
Cys Ala Ala Ala Trp Glu Gly Val Lys Asp Lys Thr Trp Glu Ala Leu
            345                 350                 355

tgc acc cag ctt ctc cag cac tac gcg gat gta atc gca ttg tca cag   1219
Cys Thr Gln Leu Leu Gln His Tyr Ala Asp Val Ile Ala Leu Ser Gln
        360                 365                 370

cgc atc cca ctg aca ttc ttt ggc cct agc gct gaa gta gca aag ctt   1267
Arg Ile Pro Leu Thr Phe Phe Gly Pro Ser Ala Glu Val Ala Lys Leu
    375                 380                 385

cca ctg tgg gtt gct cgc gcg ctg ggt gtt cgc acc cgc atc agc atc   1315
Pro Leu Trp Val Ala Arg Ala Leu Gly Val Arg Thr Arg Ile Ser Ile
390                 395                 400                 405

gag gct taactctgca gaattaatcc atg                                1344
Glu Ala
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<210> 48
<211> 407
<212> PRT
<213> Corynebacterium glutamicum

<400> 48

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Met Arg Val Ala Ile Val Ala Glu Ser Phe Leu Pro Asn Val Asn Gly
  1               5                  10                  15

Val Thr Asn Ser Val Leu Arg Val Leu Glu His Leu Lys Ala Asn Gly
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                20                  25                  30

His Asp Ala Leu Val Ile Ala Pro Gly Ala Arg Asp Phe Glu Glu Glu
          35                  40                  45

Ile Gly His Tyr Leu Gly Phe Glu Ile Val Arg Val Pro Thr Val Arg
     50                  55                  60

Val Pro Leu Ile Asp Ser Leu Pro Ile Gly Val Pro Leu Pro Ser Val
 65                  70                  75                  80

Thr Ser Val Leu Arg Glu Tyr Asn Pro Asp Ile Ile His Leu Ala Ser
                 85                  90                  95

Pro Phe Val Leu Gly Gly Ala Ala Ala Phe Ala Ala Arg Gln Leu Arg
            100                 105                 110

Ile Pro Ala Ile Ala Ile Tyr Gln Thr Asp Val Ala Gly Phe Ser Gln
        115                 120                 125

Arg Tyr His Leu Ala Pro Leu Ala Thr Ala Ser Trp Glu Trp Ile Lys
    130                 135                 140

Thr Val His Asn Met Cys Gln Arg Thr Leu Ala Pro Ser Ser Met Ser
145                 150                 155                 160

Ile Asp Glu Leu Arg Asp His Gly Ile Asn Asp Ile Phe His Trp Ala
                165                 170                 175

Arg Gly Val Asp Ser Lys Arg Phe His Pro Gly Lys Arg Ser Val Ala
            180                 185                 190

Leu Arg Lys Ser Trp Asp Pro Ser Gly Ala Lys Lys Ile Val Gly Phe
        195                 200                 205

Val Gly Arg Leu Ala Ser Glu Lys Gly Val Glu Arg Leu Ala Gly Leu
    210                 215                 220

Ser Gly Arg Ser Asp Ile Gln Leu Val Ile Val Gly Asp Gly Pro Glu
225                 230                 235                 240

Ala Lys Tyr Leu Gln Glu Met Met Pro Asp Ala Ile Phe Thr Gly Ala
                245                 250                 255

Leu Gly Gly Glu Glu Leu Ala Thr Thr Tyr Ala Ser Leu Asp Leu Phe
            260                 265                 270

Val His Pro Gly Glu Phe Glu Thr Phe Cys Gln Ala Ile Gln Glu Ala
        275                 280                 285

Gln Ala Ser Gly Val Pro Thr Ile Gly Pro Arg Ala Gly Gly Pro Ile
    290                 295                 300

Asp Leu Ile Asn Glu Gly Val Asn Gly Leu Leu Leu Asp Val Val Asp
305                 310                 315                 320

Phe Lys Glu Thr Leu Pro Ala Ala Ala Glu Trp Ile Leu Asp Asp Ser
                325                 330                 335

Arg His Ser Glu Met Cys Ala Ala Ala Trp Glu Gly Val Lys Asp Lys
            340                 345                 350
```

Thr Trp Glu Ala Leu Cys Thr Gln Leu Leu Gln His Tyr Ala Asp Val
355 360 365

Ile Ala Leu Ser Gln Arg Ile Pro Leu Thr Phe Phe Gly Pro Ser Ala
370 375 380

Glu Val Ala Lys Leu Pro Leu Trp Val Ala Arg Ala Leu Gly Val Arg
385 390 395 400

Thr Arg Ile Ser Ile Glu Ala
405

<210> 49
<211> 1377
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1354)
<223> RXA02491

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agacgtcccg ctgctttctt cggcgatcta gaatgtgggc atg cgc gta gct atg 115
Met Arg Val Ala Met
1 5

att tcc atg cac acc tct cca ttg cag cag ccc gga act ggt gat tca 163
Ile Ser Met His Thr Ser Pro Leu Gln Gln Pro Gly Thr Gly Asp Ser
10 15 20

ggc ggc atg aac gtc tac att ctt tcg acc gcg act gag cta gcg aaa 211
Gly Gly Met Asn Val Tyr Ile Leu Ser Thr Ala Thr Glu Leu Ala Lys
25 30 35

cag ggt atc gag gtc gat att tac act cgt gcc acg agg cct tct cag 259
Gln Gly Ile Glu Val Asp Ile Tyr Thr Arg Ala Thr Arg Pro Ser Gln
40 45 50

ggt gag atc gtg aga gta gct gag aat ttg cgg gtc att aat atc gct 307
Gly Glu Ile Val Arg Val Ala Glu Asn Leu Arg Val Ile Asn Ile Ala
55 60 65

gcg ggg ccg tat gag ggg ctt tcc aaa gag gag ctt cct act cag ttg 355
Ala Gly Pro Tyr Glu Gly Leu Ser Lys Glu Glu Leu Pro Thr Gln Leu
70 75 80 85

gcg gcg ttt acc ggc gga atg ttg tcg ttt acg cgc cgg gag aag gtt 403
Ala Ala Phe Thr Gly Gly Met Leu Ser Phe Thr Arg Arg Glu Lys Val
90 95 100

act tat gat ctg atc cat tct cac tat tgg ctg tct ggt cag gtg ggg 451
Thr Tyr Asp Leu Ile His Ser His Tyr Trp Leu Ser Gly Gln Val Gly
105 110 115

tgg ttg ctg cgc gat ttg tgg cgg att ccc ctt att cat acg gca cac 499
Trp Leu Leu Arg Asp Leu Trp Arg Ile Pro Leu Ile His Thr Ala His

```
        120                 125                 130

act ttg gcg gcg gtg aag aat tct tat cgg gat gat tcg gac act ccg   547
Thr Leu Ala Ala Val Lys Asn Ser Tyr Arg Asp Asp Ser Asp Thr Pro
    135                 140                 145

gag tcg gag gcg cgt cgc att tgt gag cag cag ctg gtg gat aac gct   595
Glu Ser Glu Ala Arg Arg Ile Cys Glu Gln Gln Leu Val Asp Asn Ala
150                 155                 160                 165

gac gtg ttg gcg gtg aac act cag gag gag atg cag gat ttg atg cat   643
Asp Val Leu Ala Val Asn Thr Gln Glu Glu Met Gln Asp Leu Met His
                170                 175                 180

cac tac gat gcg gat ccg gat cgg att tct gtg gtg tca ccg ggt gcg   691
His Tyr Asp Ala Asp Pro Asp Arg Ile Ser Val Val Ser Pro Gly Ala
            185                 190                 195

gac gtg gaa ctt tat agc cct gga aat gat cgc gcg acg gaa cgt tcc   739
Asp Val Glu Leu Tyr Ser Pro Gly Asn Asp Arg Ala Thr Glu Arg Ser
        200                 205                 210

cgt cgt gag ctg ggc att ccg ctg cac aca aag gta gtg gct ttt gtg   787
Arg Arg Glu Leu Gly Ile Pro Leu His Thr Lys Val Val Ala Phe Val
    215                 220                 225

ggt cgg ttg cag ccg ttt aag ggc ccg cag gtg ctg atc aag gcg gtt   835
Gly Arg Leu Gln Pro Phe Lys Gly Pro Gln Val Leu Ile Lys Ala Val
230                 235                 240                 245

gcg gcg ttg ttt gat cgc gat ccg gac cga aat ctg cgc gtc att att   883
Ala Ala Leu Phe Asp Arg Asp Pro Asp Arg Asn Leu Arg Val Ile Ile
                250                 255                 260

tgt ggc ggc cct tct ggt ccg aat gcg aca ccg gat acc tat agg cat   931
Cys Gly Gly Pro Ser Gly Pro Asn Ala Thr Pro Asp Thr Tyr Arg His
            265                 270                 275

atg gca gag gaa ctg ggc gtc gaa aag cga att cgc ttt ttg gac ccg   979
Met Ala Glu Glu Leu Gly Val Glu Lys Arg Ile Arg Phe Leu Asp Pro
        280                 285                 290

cgc ccg ccg agc gag cta gtg gcc gtg tat cgg gcg gcg gac atc gtg   1027
Arg Pro Pro Ser Glu Leu Val Ala Val Tyr Arg Ala Ala Asp Ile Val
    295                 300                 305

gcc gtg cca agt ttt aat gag tcc ttc gga ctc gtc gcc atg gag gcg   1075
Ala Val Pro Ser Phe Asn Glu Ser Phe Gly Leu Val Ala Met Glu Ala
310                 315                 320                 325

caa gcc agc ggc aca ccg gtc att gcg gcc cgg gtt ggc ggc ctg ccc   1123
Gln Ala Ser Gly Thr Pro Val Ile Ala Ala Arg Val Gly Gly Leu Pro
                330                 335                 340

atc gca gtc gcg gaa ggg gag acg gga ttg ctt gtc gac ggc cac tcc   1171
Ile Ala Val Ala Glu Gly Glu Thr Gly Leu Leu Val Asp Gly His Ser
            345                 350                 355

ccg cat gcc tgg gcc gac gcc tta gcc aca ctc ttg gac gat gac gaa   1219
Pro His Ala Trp Ala Asp Ala Leu Ala Thr Leu Leu Asp Asp Asp Glu
        360                 365                 370
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Sequence Listing.ST25

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acg cgc atc aga atg ggt gaa gac gcc gtc gaa cac gcc aga aca ttc   1267
Thr Arg Ile Arg Met Gly Glu Asp Ala Val Glu His Ala Arg Thr Phe
    375                 380                 385

tcc tgg gcg gcc acc gcc gca cag cta tcg tcg ctg tac aac gac gct   1315
Ser Trp Ala Ala Thr Ala Ala Gln Leu Ser Ser Leu Tyr Asn Asp Ala
390                 395                 400                 405

att gcc aac gaa aat gtc gac ggt gaa acg cat cac ggc taagtaaacg    1364
Ile Ala Asn Glu Asn Val Asp Gly Glu Thr His His Gly
                410                 415

cgcgtcgtgg aac                                                   1377
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<210> 50
<211> 418
<212> PRT
<213> Corynebacterium glutamicum

<400> 50

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Met Arg Val Ala Met Ile Ser Met His Thr Ser Pro Leu Gln Gln Pro
  1               5                  10                  15

Gly Thr Gly Asp Ser Gly Gly Met Asn Val Tyr Ile Leu Ser Thr Ala
             20                  25                  30

Thr Glu Leu Ala Lys Gln Gly Ile Glu Val Asp Ile Tyr Thr Arg Ala
         35                  40                  45

Thr Arg Pro Ser Gln Gly Glu Ile Val Arg Val Ala Glu Asn Leu Arg
     50                  55                  60

Val Ile Asn Ile Ala Ala Gly Pro Tyr Glu Gly Leu Ser Lys Glu Glu
 65                  70                  75                  80

Leu Pro Thr Gln Leu Ala Ala Phe Thr Gly Gly Met Leu Ser Phe Thr
                 85                  90                  95

Arg Arg Glu Lys Val Thr Tyr Asp Leu Ile His Ser His Tyr Trp Leu
            100                 105                 110

Ser Gly Gln Val Gly Trp Leu Leu Arg Asp Leu Trp Arg Ile Pro Leu
        115                 120                 125

Ile His Thr Ala His Thr Leu Ala Ala Val Lys Asn Ser Tyr Arg Asp
    130                 135                 140

Asp Ser Asp Thr Pro Glu Ser Glu Ala Arg Arg Ile Cys Glu Gln Gln
145                 150                 155                 160

Leu Val Asp Asn Ala Asp Val Leu Ala Val Asn Thr Gln Glu Glu Met
                165                 170                 175

Gln Asp Leu Met His His Tyr Asp Ala Asp Pro Asp Arg Ile Ser Val
            180                 185                 190

Val Ser Pro Gly Ala Asp Val Glu Leu Tyr Ser Pro Gly Asn Asp Arg
        195                 200                 205
```

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Ala Thr Glu Arg Ser Arg Arg Glu Leu Gly Ile Pro Leu His Thr Lys
    210                 215                 220

Val Val Ala Phe Val Gly Arg Leu Gln Pro Phe Lys Gly Pro Gln Val
225                 230                 235                 240

Leu Ile Lys Ala Val Ala Ala Leu Phe Asp Arg Asp Pro Asp Arg Asn
                245                 250                 255

Leu Arg Val Ile Ile Cys Gly Gly Pro Ser Gly Pro Asn Ala Thr Pro
            260                 265                 270

Asp Thr Tyr Arg His Met Ala Glu Glu Leu Gly Val Glu Lys Arg Ile
        275                 280                 285

Arg Phe Leu Asp Pro Arg Pro Pro Ser Glu Leu Val Ala Val Tyr Arg
    290                 295                 300

Ala Ala Asp Ile Val Ala Val Pro Ser Phe Asn Glu Ser Phe Gly Leu
305                 310                 315                 320

Val Ala Met Glu Ala Gln Ala Ser Gly Thr Pro Val Ile Ala Ala Arg
                325                 330                 335

Val Gly Gly Leu Pro Ile Ala Val Ala Glu Gly Glu Thr Gly Leu Leu
            340                 345                 350

Val Asp Gly His Ser Pro His Ala Trp Ala Asp Ala Leu Ala Thr Leu
        355                 360                 365

Leu Asp Asp Asp Glu Thr Arg Ile Arg Met Gly Glu Asp Ala Val Glu
    370                 375                 380

His Ala Arg Thr Phe Ser Trp Ala Ala Thr Ala Ala Gln Leu Ser Ser
385                 390                 395                 400

Leu Tyr Asn Asp Ala Ile Ala Asn Glu Asn Val Asp Gly Glu Thr His
                405                 410                 415

His Gly
```

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<210> 51
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1264)
<223> RXN02595

<400> 51
gtgggtaaag gggactccga ggaagtccac gtcgtcttct ttcgcggcgc tgaggatggt 60

ttcgcggatt tgtgcggggg agtgggtggg agagaaaacg gtg atc gtt gtg gcc 115
                                        Val Ile Val Val Ala
                                          1               5

atg gct tcc att atg gct tgt tta aaa gca gct aga ctg aat aac cct 163

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Met Ala Ser Ile Met Ala Cys Leu Lys Ala Ala Arg Leu Asn Asn Pro
                 10                  15                  20

atg aag atc ctt ttg ttg tgc tgg cgt gat acc act cat cct caa ggt   211
Met Lys Ile Leu Leu Leu Cys Trp Arg Asp Thr Thr His Pro Gln Gly
            25                  30                  35

ggc gga agt gaa cgc tat ctg gag cgg gtg ggt gag ttt ttg gcg gat   259
Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly Glu Phe Leu Ala Asp
        40                  45                  50

cag ggc cat gag gtg gtg ttt cgt act gct ggg cac acg gat gcg cca   307
Gln Gly His Glu Val Val Phe Arg Thr Ala Gly His Thr Asp Ala Pro
    55                  60                  65

cgg cgt tct ttc cgc gat ggt gtg agg tat tcc agg agc ggt ggg aag   355
Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser Arg Ser Gly Gly Lys
70                  75                  80                  85

ttt agt gtg tat ccc aag gcg tgg gtg gcc atg atg ttg ggt cgt gtg   403
Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met Met Leu Gly Arg Val
                90                  95                  100

ggg att ggc acg ttt tcc aag gtt gat gtg gtg gtg gat acg cag aat   451
Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val Val Asp Thr Gln Asn
            105                 110                 115

ggc att ccg ttt ttt gga aag ttt ttc tcc ggt aag ccg act gtg ttg   499
Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly Lys Pro Thr Val Leu
        120                 125                 130

ctc acg cat cat tgc cat aag gag cag tgg ccg gtg gtg ggt cgg gtg   547
Leu Thr His His Cys His Lys Glu Gln Trp Pro Val Val Gly Arg Val
    135                 140                 145

ctg gcg aag gtt ggt tgg ctg att gag agc cag atc gcg ccg cgc gct   595
Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln Ile Ala Pro Arg Ala
150                 155                 160                 165

tac aaa act gcg ccg tat gtg act gtt tca gag ccg agc gct gag gag   643
Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu Pro Ser Ala Glu Glu
                170                 175                 180

ctc att gcg ttg ggt gtg gat cag cag cgg att cat atc gtg cgc aat   691
Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile His Ile Val Arg Asn
            185                 190                 195

ggc gtg gat ccc gtg ccg ctg cac acg ccg aag ctg gat cgc gat ggc   739
Gly Val Asp Pro Val Pro Leu His Thr Pro Lys Leu Asp Arg Asp Gly
        200                 205                 210

cag cat gcg gtg acg ttg tcg cgc ctg gtt ccg cac aag cag att gag   787
Gln His Ala Val Thr Leu Ser Arg Leu Val Pro His Lys Gln Ile Glu
    215                 220                 225

cat gcg atg gat gtc gtc gcg gcg ctc gac ggc gtg gtg ctg gat gta   835
His Ala Met Asp Val Val Ala Ala Leu Asp Gly Val Val Leu Asp Val
230                 235                 240                 245

gtc gaa agc ggt tgg tgg cag aag gaa ctg gtc gat tat gcc cgc acg   883
Val Glu Ser Gly Trp Trp Gln Lys Glu Leu Val Asp Tyr Ala Arg Thr
```

```
                  250                 255                 260

ctg ggt gtg agc gat cgc gtg gtt ttc cac ggc cag gtc gcc gag gat   931
Leu Gly Val Ser Asp Arg Val Val Phe His Gly Gln Val Ala Glu Asp
            265                 270                 275

cac aag cac gcc ctg ttg gag cgc gcc acg att cat ctc atg cct tcg   979
His Lys His Ala Leu Leu Glu Arg Ala Thr Ile His Leu Met Pro Ser
        280                 285                 290

cgc aag gaa ggc tgg ggc ctg gcg gtc acg gag gcg gcg cag cac ggc   1027
Arg Lys Glu Gly Trp Gly Leu Ala Val Thr Glu Ala Ala Gln His Gly
    295                 300                 305

gtt ccg acg atc ggt tac cga agc tca ggc ggc ctg cgc gat tcc gtc   1075
Val Pro Thr Ile Gly Tyr Arg Ser Ser Gly Gly Leu Arg Asp Ser Val
310                 315                 320                 325

gtc gac ggc gaa acc ggc ctg ctt gtc gac tcc aag gcc gag ctt att   1123
Val Asp Gly Glu Thr Gly Leu Leu Val Asp Ser Lys Ala Glu Leu Ile
                330                 335                 340

tca gcc acc aaa acc ctg ctt atc gac gcc tcc ctc cgc tcc aag ctc   1171
Ser Ala Thr Lys Thr Leu Leu Ile Asp Ala Ser Leu Arg Ser Lys Leu
            345                 350                 355

ggc gcc agc gcg aag cag cgc gcc gaa aac tac aag tgg gac acc gcg   1219
Gly Ala Ser Ala Lys Gln Arg Ala Glu Asn Tyr Lys Trp Asp Thr Ala
        360                 365                 370

gga gcg cag ttc gag gaa cta ctt ctt ggt ctt gcg tcg aaa aag       1264
Gly Ala Gln Phe Glu Glu Leu Leu Leu Gly Leu Ala Ser Lys Lys
    375                 380                 385

tagtcccagc ggcaacgcca tcc                                        1287
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<210> 52
<211> 388
<212> PRT
<213> Corynebacterium glutamicum

<400> 52

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Val Ile Val Val Ala Met Ala Ser Ile Met Ala Cys Leu Lys Ala Ala
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Arg Leu Asn Asn Pro Met Lys Ile Leu Leu Leu Cys Trp Arg Asp Thr
             20                  25                  30

Thr His Pro Gln Gly Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly
         35                  40                  45

Glu Phe Leu Ala Asp Gln Gly His Glu Val Val Phe Arg Thr Ala Gly
     50                  55                  60

His Thr Asp Ala Pro Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser
 65                  70                  75                  80

Arg Ser Gly Gly Lys Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met
                 85                  90                  95
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Met Leu Gly Arg Val Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val
100 105 110

Val Asp Thr Gln Asn Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly
115 120 125

Lys Pro Thr Val Leu Leu Thr His His Cys His Lys Glu Gln Trp Pro
130 135 140

Val Val Gly Arg Val Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln
145 150 155 160

Ile Ala Pro Arg Ala Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu
165 170 175

Pro Ser Ala Glu Glu Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile
180 185 190

His Ile Val Arg Asn Gly Val Asp Pro Val Pro Leu His Thr Pro Lys
195 200 205

Leu Asp Arg Asp Gly Gln His Ala Val Thr Leu Ser Arg Leu Val Pro
210 215 220

His Lys Gln Ile Glu His Ala Met Asp Val Val Ala Ala Leu Asp Gly
225 230 235 240

Val Val Leu Asp Val Val Glu Ser Gly Trp Trp Gln Lys Glu Leu Val
245 250 255

Asp Tyr Ala Arg Thr Leu Gly Val Ser Asp Arg Val Val Phe His Gly
260 265 270

Gln Val Ala Glu Asp His Lys His Ala Leu Leu Glu Arg Ala Thr Ile
275 280 285

His Leu Met Pro Ser Arg Lys Glu Gly Trp Gly Leu Ala Val Thr Glu
290 295 300

Ala Ala Gln His Gly Val Pro Thr Ile Gly Tyr Arg Ser Ser Gly Gly
305 310 315 320

Leu Arg Asp Ser Val Val Asp Gly Glu Thr Gly Leu Leu Val Asp Ser
325 330 335

Lys Ala Glu Leu Ile Ser Ala Thr Lys Thr Leu Leu Ile Asp Ala Ser
340 345 350

Leu Arg Ser Lys Leu Gly Ala Ser Ala Lys Gln Arg Ala Glu Asn Tyr
355 360 365

Lys Trp Asp Thr Ala Gly Ala Gln Phe Glu Glu Leu Leu Gly Leu
370 375 380

Ala Ser Lys Lys
385

<210> 53
<211> 751
<212> DNA

<213> Corynebacterium glutamicum

<220>
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<222> (101)..(751)
<223> FRXA02595

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Val Ile Val Val Ala
1 5

atg gct tcc att atg gct tgt tta aaa gca gct aga ctg aat aac cct 163
Met Ala Ser Ile Met Ala Cys Leu Lys Ala Ala Arg Leu Asn Asn Pro
10 15 20

atg aag atc ctt ttg ttg tgc tgg cgt gat acc act cat cct caa ggt 211
Met Lys Ile Leu Leu Leu Cys Trp Arg Asp Thr Thr His Pro Gln Gly
25 30 35

ggc gga agt gaa cgc tat ctg gag cgg gtg ggt gag ttt ttg gcg gat 259
Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly Glu Phe Leu Ala Asp
40 45 50

cag ggc cat gag gtg gtg ttt cgt act gct ggg cac acg gat gcg cca 307
Gln Gly His Glu Val Val Phe Arg Thr Ala Gly His Thr Asp Ala Pro
55 60 65

cgg cgt tct ttc cgc gat ggt gtg agg tat tcc agg agc ggt ggg aag 355
Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser Arg Ser Gly Gly Lys
70 75 80 85

ttt agt gtg tat ccc aag gcg tgg gtg gcc atg atg ttg ggt cgt gtg 403
Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met Met Leu Gly Arg Val
90 95 100

ggg att ggc acg ttt tcc aag gtt gat gtg gtg gtg gat acg cag aat 451
Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val Val Asp Thr Gln Asn
105 110 115

ggc att ccg ttt ttt gga aag ttt ttc tcc ggt aag ccg act gtg ttg 499
Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly Lys Pro Thr Val Leu
120 125 130

ctc acg cat cat tgc cat aag gag cag tgg ccg gtg gtg ggt cgg gtg 547
Leu Thr His His Cys His Lys Glu Gln Trp Pro Val Val Gly Arg Val
135 140 145

ctg gcg aag gtt ggt tgg ctg att gag agc cag atc gcg ccg cgc gct 595
Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln Ile Ala Pro Arg Ala
150 155 160 165

tac aaa act gcg ccg tat gtg act gtt tca gag ccg agc gct gag gag 643
Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu Pro Ser Ala Glu Glu
170 175 180

ctc att gcg ttg ggt gtg gat cag cag cgg att cat atc gtg cgc aat 691
Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile His Ile Val Arg Asn
185 190 195

```
ggc gtg gat ccc gtg ccg ctg cac acg ccg aag ctg gat cgc gat ggc   739
Gly Val Asp Pro Val Pro Leu His Thr Pro Lys Leu Asp Arg Asp Gly
        200                 205                 210

cag cat gcg gtg                                                  751
Gln His Ala Val
    215
```

<210> 54
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 54

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Val Ile Val Val Ala Met Ala Ser Ile Met Ala Cys Leu Lys Ala Ala
  1               5                  10                  15

Arg Leu Asn Asn Pro Met Lys Ile Leu Leu Leu Cys Trp Arg Asp Thr
            20                  25                  30

Thr His Pro Gln Gly Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly
        35                  40                  45

Glu Phe Leu Ala Asp Gln Gly His Glu Val Val Phe Arg Thr Ala Gly
    50                  55                  60

His Thr Asp Ala Pro Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser
65                  70                  75                  80

Arg Ser Gly Gly Lys Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met
                85                  90                  95

Met Leu Gly Arg Val Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val
            100                 105                 110

Val Asp Thr Gln Asn Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly
        115                 120                 125

Lys Pro Thr Val Leu Leu Thr His His Cys His Lys Glu Gln Trp Pro
    130                 135                 140

Val Val Gly Arg Val Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln
145                 150                 155                 160

Ile Ala Pro Arg Ala Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu
                165                 170                 175

Pro Ser Ala Glu Glu Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile
            180                 185                 190

His Ile Val Arg Asn Gly Val Asp Pro Val Pro Leu His Thr Pro Lys
        195                 200                 205

Leu Asp Arg Asp Gly Gln His Ala Val
    210                 215
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<210> 55
<211> 834

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(811)
<223> RXA02616

<400> 55
agtgttactt ccggtagata acaagatggt ctcaattaaa cttcgatagc gtgatataag 60

cttcgaaaag ttttgtggca agaatcggaa gcaggcgaaa ttg cag aag cac act 115
Leu Gln Lys His Thr
1 5

cga ggt ggc aag cac cgc aag cag act acc tcc cca gta act aag ggt 163
Arg Gly Gly Lys His Arg Lys Gln Thr Thr Ser Pro Val Thr Lys Gly
10 15 20

ggt gtc gct ttt gtt gca gta gct acc ggt gcc gtg tca act gca ggc 211
Gly Val Ala Phe Val Ala Val Ala Thr Gly Ala Val Ser Thr Ala Gly
25 30 35

gca ggc gga gca gtt gct gca cag gct tcc aat cag ccc gtt gag gtc 259
Ala Gly Gly Ala Val Ala Ala Gln Ala Ser Asn Gln Pro Val Glu Val
40 45 50

aac ttc gag ctt act gca aac gac aca act gac ctc gtg gct gga agc 307
Asn Phe Glu Leu Thr Ala Asn Asp Thr Thr Asp Leu Val Ala Gly Ser
55 60 65

tcc gcc cct cag atc ctg tcc atc gct gag ttc aag cca gtt gtg aac 355
Ser Ala Pro Gln Ile Leu Ser Ile Ala Glu Phe Lys Pro Val Val Asn
70 75 80 85

ttg ggc gat cag atc gtt aag acc att cag tac aac gct gac cgc att 403
Leu Gly Asp Gln Ile Val Lys Thr Ile Gln Tyr Asn Ala Asp Arg Ile
90 95 100

cag gct gac ctg gac gct cgt ggc cct tca gtg gtt cgc cct gct gaa 451
Gln Ala Asp Leu Asp Ala Arg Gly Pro Ser Val Val Arg Pro Ala Glu
105 110 115

ggt tct tac acc tcc ggc ttc ggt gct cgt tgg ggc acc aac cac aac 499
Gly Ser Tyr Thr Ser Gly Phe Gly Ala Arg Trp Gly Thr Asn His Asn
120 125 130

ggt gtg gat atc gct aac gca atc ggc act cca atc ctc gct gcc atg 547
Gly Val Asp Ile Ala Asn Ala Ile Gly Thr Pro Ile Leu Ala Ala Met
135 140 145

gac ggc act gtt atc gat gca ggt cct gct tcc ggt ttc ggt aac tgg 595
Asp Gly Thr Val Ile Asp Ala Gly Pro Ala Ser Gly Phe Gly Asn Trp
150 155 160 165

gtt cgc ctc cag cac gaa gat ggc acc atc acc gtg tac ggc cac atg 643
Val Arg Leu Gln His Glu Asp Gly Thr Ile Thr Val Tyr Gly His Met
170 175 180

gaa acc gtt gag gtg acc gtt ggt cag act gtt aag gct ggc gag cgc 691
Glu Thr Val Glu Val Thr Val Gly Gln Thr Val Lys Ala Gly Glu Arg

```
            185                 190                 195

atc gca ggc atg ggt agc cga gga ttc tcc acc ggc tcc cac ctc cac   739
Ile Ala Gly Met Gly Ser Arg Gly Phe Ser Thr Gly Ser His Leu His
        200                 205                 210

ttc gag gtt tac cct gca ggc ggt ggc gct gtt gat cca gct cct tgg   787
Phe Glu Val Tyr Pro Ala Gly Gly Gly Ala Val Asp Pro Ala Pro Trp
    215                 220                 225

ctt gca gag cgc ggc att act ctt taattaactt ttgggcgacc ctt        834
Leu Ala Glu Arg Gly Ile Thr Leu
230                 235
```

<210> 56
<211> 237
<212> PRT
<213> Corynebacterium glutamicum

<400> 56

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Leu Gln Lys His Thr Arg Gly Gly Lys His Arg Lys Gln Thr Thr Ser
  1               5                  10                  15

Pro Val Thr Lys Gly Gly Val Ala Phe Val Ala Val Ala Thr Gly Ala
            20                  25                  30

Val Ser Thr Ala Gly Ala Gly Gly Ala Val Ala Ala Gln Ala Ser Asn
        35                  40                  45

Gln Pro Val Glu Val Asn Phe Glu Leu Thr Ala Asn Asp Thr Thr Asp
    50                  55                  60

Leu Val Ala Gly Ser Ser Ala Pro Gln Ile Leu Ser Ile Ala Glu Phe
65                  70                  75                  80

Lys Pro Val Val Asn Leu Gly Asp Gln Ile Val Lys Thr Ile Gln Tyr
                85                  90                  95

Asn Ala Asp Arg Ile Gln Ala Asp Leu Asp Ala Arg Gly Pro Ser Val
            100                 105                 110

Val Arg Pro Ala Glu Gly Ser Tyr Thr Ser Gly Phe Gly Ala Arg Trp
        115                 120                 125

Gly Thr Asn His Asn Gly Val Asp Ile Ala Asn Ala Ile Gly Thr Pro
    130                 135                 140

Ile Leu Ala Ala Met Asp Gly Thr Val Ile Asp Ala Gly Pro Ala Ser
145                 150                 155                 160

Gly Phe Gly Asn Trp Val Arg Leu Gln His Glu Asp Gly Thr Ile Thr
                165                 170                 175

Val Tyr Gly His Met Glu Thr Val Glu Val Thr Val Gly Gln Thr Val
            180                 185                 190

Lys Ala Gly Glu Arg Ile Ala Gly Met Gly Ser Arg Gly Phe Ser Thr
        195                 200                 205

Gly Ser His Leu His Phe Glu Val Tyr Pro Ala Gly Gly Gly Ala Val
```

```
    210                 215                 220

Asp Pro Ala Pro Trp Leu Ala Glu Arg Gly Ile Thr Leu
225                 230                 235


<210> 57
<211> 866
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(843)
<223> RXA02627

<400> 57
gat gtc act gtg gaa agc caa cca gaa cgc gtc gtt gcc ctg ggt tgg   48
Asp Val Thr Val Glu Ser Gln Pro Glu Arg Val Val Ala Leu Gly Trp
  1               5                  10                  15

gga gat gct gag gct gcg ctg gaa ttc ggt gtg cag cct gtg ggt gca   96
Gly Asp Ala Glu Ala Ala Leu Glu Phe Gly Val Gln Pro Val Gly Ala
             20                  25                  30

tca gat tgg ctc gca ttc ggt ggt gaa ggc gtg gga ccg tgg att gag   144
Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu
         35                  40                  45

gat tct gcc tac gat gaa gcg cca gaa ata atc gga acc atg gaa ccg   192
Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro
     50                  55                  60

gag tat gaa aag att gca gcg ctt gaa ccg gat ctg att ttg gac gtg   240
Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val
 65                  70                  75                  80

cgc agc tct ggc gac cag gaa cgc tat gac aag ttg tct tca atc gca   288
Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala
                 85                  90                  95

ctg acc atc ggc gtt cca gaa ggt ggc gat agc tac ctc acc cca cgc   336
Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg
            100                 105                 110

gct gag cag gta acc atg atc gcc act gct ctg ggg cag gct gaa cgt   384
Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg
        115                 120                 125

ggt gaa gaa gtg aac gct gaa tac gag cag ctc act gct gat att cgt   432
Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg
    130                 135                 140

gca gct cac ccg ggc tgg cct gag aag acc gcg gct gct gta tct gca   480
Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Ala Val Ser Ala
145                 150                 155                 160

acg gca acc agc tgg ggt gca tac atc aag ggc tcc aac cgt gta gat   528
Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp
                165                 170                 175
```

```
act ttg ctg gac ctg ggc ttc cag gaa aac cct gag ctg gct aaa cag   576
Thr Leu Leu Asp Leu Gly Phe Gln Glu Asn Pro Glu Leu Ala Lys Gln
            180                 185                 190

caa cct ggc gat acg ggt ttc tcc atc aaa ttc agt gaa gag act ttc   624
Gln Pro Gly Asp Thr Gly Phe Ser Ile Lys Phe Ser Glu Glu Thr Phe
        195                 200                 205

ggc gtt gtg gat tcc gac ctg gtt gtc ggc ttt gcc atc ggt atg act   672
Gly Val Val Asp Ser Asp Leu Val Val Gly Phe Ala Ile Gly Met Thr
    210                 215                 220

cct gag gaa atg gca gag cag gtt cca tgg cag atg ttg acc gcc act   720
Pro Glu Glu Met Ala Glu Gln Val Pro Trp Gln Met Leu Thr Ala Thr
225                 230                 235                 240

cgt gac ggc cgt tcc ttt gtg atg ccc cgt gag att tcc aat gcg ttt   768
Arg Asp Gly Arg Ser Phe Val Met Pro Arg Glu Ile Ser Asn Ala Phe
                245                 250                 255

tct ttg ggt tcc ccg cag tcc act cgg ttc gcg tta gac gcc ttg gtg   816
Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val
            260                 265                 270

cca ctt ctg gag gag cat gca ggg gag tagtggtccg gtggtgcggg         863
Pro Leu Leu Glu Glu His Ala Gly Glu
        275                 280

cag                                                               866
```

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<210> 58
<211> 281
<212> PRT
<213> Corynebacterium glutamicum

<400> 58

```
Asp Val Thr Val Glu Ser Gln Pro Glu Arg Val Val Ala Leu Gly Trp
  1               5                  10                  15

Gly Asp Ala Glu Ala Ala Leu Glu Phe Gly Val Gln Pro Val Gly Ala
            20                  25                  30

Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu
        35                  40                  45

Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro
    50                  55                  60

Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val
65                  70                  75                  80

Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala
                85                  90                  95

Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg
            100                 105                 110

Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg
        115                 120                 125
```

```
Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg
    130                 135                 140

Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Ala Val Ser Ala
145                 150                 155                 160

Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp
                165                 170                 175

Thr Leu Leu Asp Leu Gly Phe Gln Glu Asn Pro Glu Leu Ala Lys Gln
            180                 185                 190

Gln Pro Gly Asp Thr Gly Phe Ser Ile Lys Phe Ser Glu Glu Thr Phe
        195                 200                 205

Gly Val Val Asp Ser Asp Leu Val Val Gly Phe Ala Ile Gly Met Thr
    210                 215                 220

Pro Glu Glu Met Ala Glu Gln Val Pro Trp Gln Met Leu Thr Ala Thr
225                 230                 235                 240

Arg Asp Gly Arg Ser Phe Val Met Pro Arg Glu Ile Ser Asn Ala Phe
                245                 250                 255

Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val
            260                 265                 270

Pro Leu Leu Glu Glu His Ala Gly Glu
        275                 280
```

09/15/2005 15:39 FAX 001/009

<210> 59
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXA02650

<400> 59

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gaatttttgc tgcaactgtg taaaaaccag cgctgaatta aagatcacct ttcacccttа 60

attgagcctg ggtggaagtt tctaccgctc atggggaaag atg gtc aac gtg acc   115
                                              Met Val Asn Val Thr
                                                1               5

tca aag gat gca ggg gca aac gtg acc ccc atg agt aag aaa gaa aag   163
Ser Lys Asp Ala Gly Ala Asn Val Thr Pro Met Ser Lys Lys Glu Lys
                10                  15                  20

agg aca acc gtt aaa cag gtg gtt gcc ttg atg gcc gcc atc gtt gtg   211
Arg Thr Thr Val Lys Gln Val Val Ala Leu Met Ala Ala Ile Val Val
            25                  30                  35

gtg att gcg tcc cta gac caa ata gtc aag cag att atg ctt agt tgg   259
Val Ile Ala Ser Leu Asp Gln Ile Val Lys Gln Ile Met Leu Ser Trp
        40                  45                  50

ttg gaa cct ggc gtt ccc gtt ccc atc att ggg gat tgg ttc cgc ttc   307
```

```
Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly Asp Trp Phe Arg Phe
     55                  60                  65

tac ctc ctg ttt aac ccc gga gcc gca ttt tcg atg ggt ggg gaa aac   355
Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser Met Gly Gly Glu Asn
 70                  75                  80                  85

agc acc tgg atc ttt aca acc atc cag ttg agc ttc gtc atc ggt atc   403
Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser Phe Val Ile Gly Ile
                 90                  95                 100

gca att tat gcc cca cgc atc aaa cac aag tgg atc gcg gca gga ctt   451
Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp Ile Ala Ala Gly Leu
            105                 110                 115

gcc ctt gtt gcc ggt gga gcc ttg gga aac gtg ttg gac cgg ttg ttc   499
Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val Leu Asp Arg Leu Phe
        120                 125                 130

aga gat cct tcc ttc ttc ttc gga cat gtt gtt gat tac atc tcc gta   547
Arg Asp Pro Ser Phe Phe Phe Gly His Val Val Asp Tyr Ile Ser Val
    135                 140                 145

gga aac ttt gca gta ttt aat atc gcc gat gcc tcg att tct tgc ggc   595
Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala Ser Ile Ser Cys Gly
150                 155                 160                 165

gtc gtg gtg ttc ctg atc gga atg ttc ctt gag gac cgt gaa aac gcc   643
Val Val Val Phe Leu Ile Gly Met Phe Leu Glu Asp Arg Glu Asn Ala
                170                 175                 180

cag cat gcc aaa gca act gac gag aag gat gag gcc tgatgaacaa        689
Gln His Ala Lys Ala Thr Asp Glu Lys Asp Glu Ala
            185                 190

ccgacaaagc aga                                                   702
```

<210> 60
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

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<400> 60
Met Val Asn Val Thr Ser Lys Asp Ala Gly Ala Asn Val Thr Pro Met
  1               5                  10                  15

Ser Lys Lys Glu Lys Arg Thr Thr Val Lys Gln Val Val Ala Leu Met
             20                  25                  30

Ala Ala Ile Val Val Val Ile Ala Ser Leu Asp Gln Ile Val Lys Gln
         35                  40                  45

Ile Met Leu Ser Trp Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly
     50                  55                  60

Asp Trp Phe Arg Phe Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser
 65                  70                  75                  80

Met Gly Gly Glu Asn Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser
                 85                  90                  95
```

```
Phe Val Ile Gly Ile Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp
            100                 105                 110

Ile Ala Ala Gly Leu Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val
        115                 120                 125

Leu Asp Arg Leu Phe Arg Asp Pro Ser Phe Phe Phe Gly His Val Val
    130                 135                 140

Asp Tyr Ile Ser Val Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala
145                 150                 155                 160

Ser Ile Ser Cys Gly Val Val Val Phe Leu Ile Gly Met Phe Leu Glu
                165                 170                 175

Asp Arg Glu Asn Ala Gln His Ala Lys Ala Thr Asp Glu Lys Asp Glu
            180                 185                 190

Ala
```

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<210> 61
<211> 1071
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1048)
<223> RXA01094

<400> 61

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gtcagctgac cggggtagcg ggcggtgggc ggacaagtct tgctagattg aagtgcatta 60

cttgtcgcct gactgttagg tttacgttgt tgtggatgtc atg act ttg gcc acg   115
                                            Met Thr Leu Ala Thr
                                              1               5

att ccc tca cca ccg cag ggt gtg tgg tac ttg ggt ccc att ccg att   163
Ile Pro Ser Pro Pro Gln Gly Val Trp Tyr Leu Gly Pro Ile Pro Ile
                 10                  15                  20

agg gcc tat gcg atg tgc atc atc gct ggc att att gtt gcc att tgg   211
Arg Ala Tyr Ala Met Cys Ile Ile Ala Gly Ile Ile Val Ala Ile Trp
             25                  30                  35

ctg acg aga aag cgc tac gcc gcc cgc ggt gga aac cct gaa atc gtc   259
Leu Thr Arg Lys Arg Tyr Ala Ala Arg Gly Gly Asn Pro Glu Ile Val
         40                  45                  50

ctt gat gca gcg atc gtg gca gtt cct gcc gga atc atc ggt gga cgc   307
Leu Asp Ala Ala Ile Val Ala Val Pro Ala Gly Ile Ile Gly Gly Arg
     55                  60                  65

att tat cac gtc att acc gac aac caa aag tac ttc tgc gat acc tgt   355
Ile Tyr His Val Ile Thr Asp Asn Gln Lys Tyr Phe Cys Asp Thr Cys
 70                  75                  80                  85

aac ccc gtc gac gcc ttc aaa atc acc aac ggt ggt ctg ggc atc tgg   403
```

```
Asn Pro Val Asp Ala Phe Lys Ile Thr Asn Gly Gly Leu Gly Ile Trp
                 90                  95                 100

ggt gca gtg atc ctc ggt ggc ctg gca gtg gcc gta ttc ttc cgg tac   451
Gly Ala Val Ile Leu Gly Gly Leu Ala Val Ala Val Phe Phe Arg Tyr
            105                 110                 115

aaa aag ctt cct ctt gca cct ttc gca gat gcc gtg gca cct gca gtt   499
Lys Lys Leu Pro Leu Ala Pro Phe Ala Asp Ala Val Ala Pro Ala Val
        120                 125                 130

atc ctg gcg cag gga att ggt cgt ctg ggc aac tgg ttt aac cag gag   547
Ile Leu Ala Gln Gly Ile Gly Arg Leu Gly Asn Trp Phe Asn Gln Glu
    135                 140                 145

ctc tac ggt gca gaa act acc gtt cca tgg gct ttg gaa atc tac tat   595
Leu Tyr Gly Ala Glu Thr Thr Val Pro Trp Ala Leu Glu Ile Tyr Tyr
150                 155                 160                 165

cgg gta gat gaa aat gga aaa ttc gca ccg gtg aca gga aca tcc acc   643
Arg Val Asp Glu Asn Gly Lys Phe Ala Pro Val Thr Gly Thr Ser Thr
                170                 175                 180

ggt gaa gta atg gct act gtt cat cca aca ttc ctc tat gaa ctg ttg   691
Gly Glu Val Met Ala Thr Val His Pro Thr Phe Leu Tyr Glu Leu Leu
            185                 190                 195

tgg aac cta ctg atc ttc gct ttg ttg atg tgg gct gac aag cga ttc   739
Trp Asn Leu Leu Ile Phe Ala Leu Leu Met Trp Ala Asp Lys Arg Phe
        200                 205                 210

aag ctg gaa cat ggc cga gta ttt gct ctc tac gta gct ggt tac acc   787
Lys Leu Glu His Gly Arg Val Phe Ala Leu Tyr Val Ala Gly Tyr Thr
    215                 220                 225

ttg ggc cgt ttc tgg att gaa caa atg cgc gtt gat gaa gcc acg ctt   835
Leu Gly Arg Phe Trp Ile Glu Gln Met Arg Val Asp Glu Ala Thr Leu
230                 235                 240                 245

att ggc ggc atc cga atc aac acc atc gtc tcc gca gta gtg ttt gcc   883
Ile Gly Gly Ile Arg Ile Asn Thr Ile Val Ser Ala Val Val Phe Ala
                250                 255                 260

ggc gcg atc atc gtg ttc ttc ctg ttg aag aag ggt agg gaa act ccc   931
Gly Ala Ile Ile Val Phe Phe Leu Leu Lys Lys Gly Arg Glu Thr Pro
            265                 270                 275

gaa gag gta gat ccg act ttc gca gcg tct gtt gca gca gat gct gta   979
Glu Glu Val Asp Pro Thr Phe Ala Ala Ser Val Ala Ala Asp Ala Val
        280                 285                 290

gct tcg cca gat aga aaa ccc ttg ccg aaa gca ggg gag ggc att gat   1027
Ala Ser Pro Asp Arg Lys Pro Leu Pro Lys Ala Gly Glu Gly Ile Asp
    295                 300                 305

gga gaa acg ccc tca acg cga taggtttcaa ccataggcct gac             1071
Gly Glu Thr Pro Ser Thr Arg
310                 315
```

<210> 62

<211> 316
<212> PRT
<213> Corynebacterium glutamicum

<400> 62

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Met Thr Leu Ala Thr Ile Pro Ser Pro Pro Gln Gly Val Trp Tyr Leu
  1               5                  10                  15

Gly Pro Ile Pro Ile Arg Ala Tyr Ala Met Cys Ile Ile Ala Gly Ile
             20                  25                  30

Ile Val Ala Ile Trp Leu Thr Arg Lys Arg Tyr Ala Ala Arg Gly Gly
         35                  40                  45

Asn Pro Glu Ile Val Leu Asp Ala Ala Ile Val Ala Val Pro Ala Gly
     50                  55                  60

Ile Ile Gly Gly Arg Ile Tyr His Val Ile Thr Asp Asn Gln Lys Tyr
 65                  70                  75                  80

Phe Cys Asp Thr Cys Asn Pro Val Asp Ala Phe Lys Ile Thr Asn Gly
                 85                  90                  95

Gly Leu Gly Ile Trp Gly Ala Val Ile Leu Gly Gly Leu Ala Val Ala
            100                 105                 110

Val Phe Phe Arg Tyr Lys Lys Leu Pro Leu Ala Pro Phe Ala Asp Ala
        115                 120                 125

Val Ala Pro Ala Val Ile Leu Ala Gln Gly Ile Gly Arg Leu Gly Asn
    130                 135                 140

Trp Phe Asn Gln Glu Leu Tyr Gly Ala Glu Thr Thr Val Pro Trp Ala
145                 150                 155                 160

Leu Glu Ile Tyr Tyr Arg Val Asp Glu Asn Gly Lys Phe Ala Pro Val
                165                 170                 175

Thr Gly Thr Ser Thr Gly Glu Val Met Ala Thr Val His Pro Thr Phe
            180                 185                 190

Leu Tyr Glu Leu Leu Trp Asn Leu Leu Ile Phe Ala Leu Leu Met Trp
        195                 200                 205

Ala Asp Lys Arg Phe Lys Leu Glu His Gly Arg Val Phe Ala Leu Tyr
    210                 215                 220

Val Ala Gly Tyr Thr Leu Gly Arg Phe Trp Ile Glu Gln Met Arg Val
225                 230                 235                 240

Asp Glu Ala Thr Leu Ile Gly Gly Ile Arg Ile Asn Thr Ile Val Ser
                245                 250                 255

Ala Val Val Phe Ala Gly Ala Ile Ile Val Phe Phe Leu Leu Lys Lys
            260                 265                 270

Gly Arg Glu Thr Pro Glu Glu Val Asp Pro Thr Phe Ala Ala Ser Val
        275                 280                 285

Ala Ala Asp Ala Val Ala Ser Pro Asp Arg Lys Pro Leu Pro Lys Ala
    290                 295                 300
```

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Gly Glu Gly Ile Asp Gly Glu Thr Pro Ser Thr Arg
305                 310                 315


<210> 63
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> RXN00934

<400> 63
ccaacccctg tggtttggtg atttggatcc ggagcgtctc aagcgctcta gggagcagac 60

aaatgttcac aaaccggtgg cattacagga ggacaattag gtg cga att gga atg   115
                                            Val Arg Ile Gly Met
                                              1               5

gtc tgc ccg tac tcc ttc gat gag ccg ggc ggt gtt caa gcg cat atc   163
Val Cys Pro Tyr Ser Phe Asp Glu Pro Gly Gly Val Gln Ala His Ile
                10                  15                  20

ctt gac tta gcg cga acc ttc att gcc caa ggc cat gag gtt cag gtg   211
Leu Asp Leu Ala Arg Thr Phe Ile Ala Gln Gly His Glu Val Gln Val
            25                  30                  35

ctt ggt ccg tgt agt gcg gat acg cag gtg ccc gat ttc gtg gtg cgc   259
Leu Gly Pro Cys Ser Ala Asp Thr Gln Val Pro Asp Phe Val Val Arg
        40                  45                  50

ggt ggt ggc agc atc ccg att ccg tac aat ggc tcg gtt gcc cgc ttg   307
Gly Gly Gly Ser Ile Pro Ile Pro Tyr Asn Gly Ser Val Ala Arg Leu
    55                  60                  65

agc ttt ggg ccg aaa atg ttc aag gcc gtg cgc acg ttc ctc cgc gaa   355
Ser Phe Gly Pro Lys Met Phe Lys Ala Val Arg Thr Phe Leu Arg Glu
70                  75                  80                  85

ggc aac ttc gat gtg ctg cat atc cat gaa ccg aat tca cca agt ttt   403
Gly Asn Phe Asp Val Leu His Ile His Glu Pro Asn Ser Pro Ser Phe
                90                  95                  100

tcc atg gcg gcg cta cgc ttt gcg gaa ggc ccc atc gtt gct act tac   451
Ser Met Ala Ala Leu Arg Phe Ala Glu Gly Pro Ile Val Ala Thr Tyr
            105                 110                 115

cac gcc tcc agt agc gga tcg aag ctg ctc aag gct ttc tta cca gtg   499
His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys Ala Phe Leu Pro Val
        120                 125                 130

ctt tcg ccc atg ctg gag aaa gtg cgc gca ggc atc gcc gtg tct gaa   547
Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala Val Ser Glu
    135                 140                 145

atg gct cgg cgc tgg cag gtg gag caa gtc ggc ggc gat ccc gtg ctg   595
Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp Pro Val Leu
150                 155                 160                 165
```

```
atc ccc aac ggg gta gag acc tcc atg ttc aaa gcc gcg cgc caa atc   643
Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala Arg Gln Ile
                170                 175                 180

gaa ccg aat gat cct gta gag atc gtc ttt ttg ggt cgc ctc gat gag   691
Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg Leu Asp Glu
            185                 190                 195

tcc cgc aaa ggc ctc gac atc ctc ctg cgc gct ctg acc agg ctg gat   739
Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala Leu Thr Arg Leu Asp
        200                 205                 210

cgc ccg ttt acc tgc acc gtc att ggc ggc ggc acc ccg cga gaa gtc   787
Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro Arg Glu Val
    215                 220                 225

gcc ggc atc aac ttt gtg ggc cgc gtc agc gat gag gaa aag gca gca   835
Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp Glu Glu Lys Ala Ala
230                 235                 240                 245

atc tta ggt cgc gca gac atc tat gtc gca ccc aac acc ggc ggc gaa   883
Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro Asn Thr Gly Gly Glu
                250                 255                 260

agc ttc ggc atc gtg cta gtt gaa gcg atg gcc gcg gga tgc gct gtc   931
Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly Cys Ala Val
            265                 270                 275

gtc gcc agc gac cta gaa gcg ttc tcc ctg gtc acc gat tct gaa gcc   979
Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp Ser Glu Ala
        280                 285                 290

gca cag cca gcg ggc gtg cta ttt aaa acc ggc tca gac gcc gac cta   1027
Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp Ala Asp Leu
    295                 300                 305

gcc aaa aaa ctt caa gcg ctt atc gac gac ccc tcc tcc cgt tcc acg   1075
Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser Arg Ser Thr
310                 315                 320                 325

ctt atc gcc gcg ggg cta aag cgc gca aac gcc tac gac tgg tcg aca   1123
Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp Trp Ser Thr
                330                 335                 340

gta tcc acc cag gtc atg gca gtc tat gaa acc att gcg atc gac aaa   1171
Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr Ile Ala Ile Asp Lys
            345                 350                 355

gtg agg ctt gga tgacccttgt ttacctcctc atc                        1206
Val Arg Leu Gly
        360
```

<210> 64
<211> 361
<212> PRT
<213> Corynebacterium glutamicum

<400> 64
Val Arg Ile Gly Met Val Cys Pro Tyr Ser Phe Asp Glu Pro Gly Gly

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  1               5                  10                  15

Val Gln Ala His Ile Leu Asp Leu Ala Arg Thr Phe Ile Ala Gln Gly
            20                  25                  30

His Glu Val Gln Val Leu Gly Pro Cys Ser Ala Asp Thr Gln Val Pro
        35                  40                  45

Asp Phe Val Val Arg Gly Gly Gly Ser Ile Pro Ile Pro Tyr Asn Gly
    50                  55                  60

Ser Val Ala Arg Leu Ser Phe Gly Pro Lys Met Phe Lys Ala Val Arg
65                  70                  75                  80

Thr Phe Leu Arg Glu Gly Asn Phe Asp Val Leu His Ile His Glu Pro
                85                  90                  95

Asn Ser Pro Ser Phe Ser Met Ala Ala Leu Arg Phe Ala Glu Gly Pro
            100                 105                 110

Ile Val Ala Thr Tyr His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys
        115                 120                 125

Ala Phe Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly
    130                 135                 140

Ile Ala Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly
145                 150                 155                 160

Gly Asp Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys
                165                 170                 175

Ala Ala Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu
            180                 185                 190

Gly Arg Leu Asp Glu Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala
        195                 200                 205

Leu Thr Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly
    210                 215                 220

Thr Pro Arg Glu Val Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp
225                 230                 235                 240

Glu Glu Lys Ala Ala Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro
                245                 250                 255

Asn Thr Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala
            260                 265                 270

Ala Gly Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val
        275                 280                 285

Thr Asp Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly
    290                 295                 300

Ser Asp Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro
305                 310                 315                 320

Ser Ser Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala
                325                 330                 335
```

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```
Tyr Asp Trp Ser Thr Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr
            340                 345                 350

Ile Ala Ile Asp Lys Val Arg Leu Gly
        355                 360
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<210> 65
<211> 812
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(789)
<223> FRXA00934

<400> 65

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cca agt ttt tcc atg gcg gcg cta ccc ttt gcg gaa ggc ccc atc gtt   48
Pro Ser Phe Ser Met Ala Ala Leu Pro Phe Ala Glu Gly Pro Ile Val
  1               5                  10                  15

gct act tac cac gcc tcc agt agc gga tcg aag ctg ctc aag gct ttc   96
Ala Thr Tyr His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys Ala Phe
             20                  25                  30

tta cca gtg ctt tcg ccc atg ctg gag aaa gtg cgc gca ggc atc gcc   144
Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala
         35                  40                  45

gtg tct gaa atg gct cgg cgc tgg cag gtg gag caa gtc ggc ggc gat   192
Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp
     50                  55                  60

ccc gtg ctg atc ccc aac ggg gta gag acc tcc atg ttc aaa gcc gcg   240
Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala
 65                  70                  75                  80

cgc caa atc gaa ccg aat gat cct gta gag atc gtc ttt ttg ggt cgc   288
Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg
                 85                  90                  95

ctc gat gag tcc cgc aaa ggc ctc gac atc ctc ctg cgc gct ctg acc   336
Leu Asp Glu Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala Leu Thr
            100                 105                 110

agg ctg gat cgc ccg ttt acc tgc acc gtc att ggc ggc ggc acc ccg   384
Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro
        115                 120                 125

cga gaa gtc gcc ggc atc aac ttt gtg ggc cgc gtc agc gat gag gaa   432
Arg Glu Val Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp Glu Glu
    130                 135                 140

aag gca gca atc tta ggt cgc gca gac atc tat gtc gca ccc aac acc   480
Lys Ala Ala Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro Asn Thr
145                 150                 155                 160

ggc ggc gaa agc ttc ggc atc gtg cta gtt gaa gcg atg gcc gcg gga   528
Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly
```

```
                  165                 170                 175

tgc gct gtc gtc gcc agc gac cta gaa gcg ttc tcc ctg gtc acc gat   576
Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp
            180                 185                 190

tct gaa gcc gca cag cca gcg ggc gtg cta ttt aaa acc ggc tca gac   624
Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp
        195                 200                 205

gcc gac cta gcc aaa aaa ctt caa gcg ctt atc gac gac ccc tcc tcc   672
Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser
    210                 215                 220

cgt tcc acg ctt atc gcc gcg ggg cta aag cgc gca aac gcc tac gac   720
Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp
225                 230                 235                 240

tgg tcg aca gta tcc acc cag gtc atg gca gtc tat gaa acc att gcg   768
Trp Ser Thr Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr Ile Ala
                245                 250                 255

atc gac aaa gtg agg ctt gga tgacccttgt ttacctcctc atc             812
Ile Asp Lys Val Arg Leu Gly
            260
```

<210> 66
<211> 263
<212> PRT
<213> Corynebacterium glutamicum

<400> 66

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Pro Ser Phe Ser Met Ala Ala Leu Pro Phe Ala Glu Gly Pro Ile Val
  1               5                  10                  15

Ala Thr Tyr His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys Ala Phe
             20                  25                  30

Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala
         35                  40                  45

Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp
     50                  55                  60

Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala
 65                  70                  75                  80

Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg
                 85                  90                  95

Leu Asp Glu Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala Leu Thr
            100                 105                 110

Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro
        115                 120                 125

Arg Glu Val Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp Glu Glu
    130                 135                 140

Lys Ala Ala Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro Asn Thr
```

```
145                 150                 155                 160

Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly
                165                 170                 175

Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp
            180                 185                 190

Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp
        195                 200                 205

Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser
    210                 215                 220

Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp
225                 230                 235                 240

Trp Ser Thr Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr Ile Ala
                245                 250                 255

Ile Asp Lys Val Arg Leu Gly
            260
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CORRECTED SHEET (RULE 91)

<210> 67
<211> 618
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(595)
<223> RXA02605

<400> 67

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tccgatcctg tcatctacat gtgggagact ttccttaccc aggaattgcc tgcatacctt 60

gagcagaact tcggcgttgc gcgaaacaac aactccattg gtg gcc tgt cca tgg   115
                                              Val Ala Cys Pro Trp
                                                1               5

gcg gga act gcc gcg ctg aac ctc gca gca aag cac cca gat cag ttc   163
Ala Gly Thr Ala Ala Leu Asn Leu Ala Ala Lys His Pro Asp Gln Phe
            10                  15                  20

cgc cag gct atg tct tgg tcc ggc tac ttg aac acc act gcg cca ggc   211
Arg Gln Ala Met Ser Trp Ser Gly Tyr Leu Asn Thr Thr Ala Pro Gly
        25                  30                  35

atg caa acc ctg ctg cgt gtg gcc atg ctg gac acc ggt gga ttc aac   259
Met Gln Thr Leu Leu Arg Val Ala Met Leu Asp Thr Gly Gly Phe Asn
    40                  45                  50

gtc aac gca atg tat ggc tca atc att aac cca cgt cgt ttt gaa aac   307
Val Asn Ala Met Tyr Gly Ser Ile Ile Asn Pro Arg Arg Phe Glu Asn
55                  60                  65

gac cca ttc tgg aac atg ggc ggc ttg gct aac acc gac gtc tac atc   355
Asp Pro Phe Trp Asn Met Gly Gly Leu Ala Asn Thr Asp Val Tyr Ile
70                  75                  80                  85
```

```
tct gca gct tcc ggc ctg tgg agc cct cag gat gat gga gtt cgc gta   403
Ser Ala Ala Ser Gly Leu Trp Ser Pro Gln Asp Asp Gly Val Arg Val
                 90                  95                 100

gac cac cgc ctc act ggt tct gtg ctt gaa ttc gtg gca atg aca tcc   451
Asp His Arg Leu Thr Gly Ser Val Leu Glu Phe Val Ala Met Thr Ser
            105                 110                 115

acc agg att tgg gaa gca aag gca agg ctt cag ggt ctg aac cca act   499
Thr Arg Ile Trp Glu Ala Lys Ala Arg Leu Gln Gly Leu Asn Pro Thr
        120                 125                 130

gcg gat tac cca atg tat ggc att cac ggc tgg gct cag ttc aac tcc   547
Ala Asp Tyr Pro Met Tyr Gly Ile His Gly Trp Ala Gln Phe Asn Ser
    135                 140                 145

cag ctg gag aga act cag ggt cgt gtt cta gac gtc atg aac gcc tgg   595
Gln Leu Glu Arg Thr Gln Gly Arg Val Leu Asp Val Met Asn Ala Trp
150                 155                 160                 165

tagagccaca ccaaaggcca cac                                        618


<210> 68
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 68
Val Ala Cys Pro Trp Ala Gly Thr Ala Ala Leu Asn Leu Ala Ala Lys
  1               5                  10                  15

His Pro Asp Gln Phe Arg Gln Ala Met Ser Trp Ser Gly Tyr Leu Asn
             20                  25                  30

Thr Thr Ala Pro Gly Met Gln Thr Leu Leu Arg Val Ala Met Leu Asp
         35                  40                  45

Thr Gly Gly Phe Asn Val Asn Ala Met Tyr Gly Ser Ile Ile Asn Pro
     50                  55                  60

Arg Arg Phe Glu Asn Asp Pro Phe Trp Asn Met Gly Gly Leu Ala Asn
 65                  70                  75                  80

Thr Asp Val Tyr Ile Ser Ala Ala Ser Gly Leu Trp Ser Pro Gln Asp
                 85                  90                  95

Asp Gly Val Arg Val Asp His Arg Leu Thr Gly Ser Val Leu Glu Phe
            100                 105                 110

Val Ala Met Thr Ser Thr Arg Ile Trp Glu Ala Lys Ala Arg Leu Gln
        115                 120                 125

Gly Leu Asn Pro Thr Ala Asp Tyr Pro Met Tyr Gly Ile His Gly Trp
    130                 135                 140

Ala Gln Phe Asn Ser Gln Leu Glu Arg Thr Gln Gly Arg Val Leu Asp
145                 150                 155                 160

Val Met Asn Ala Trp
                165
```

<210> 69
<211> 1386
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1363)
<223> RXN00525

<400> 69
ccatcgtgtt tattactcac aaccctgagc ttgctgatga atctgatcgg gtggtcacca 60

tggttgacgg gcgcatcatt gggtctgagg tgaaacactc atg agc ctt gca gaa 115
Met Ser Leu Ala Glu
1 5

tca att ctt ttg gcg ctc acc agc ctg aga agc aac aag atg cgt gca 163
Ser Ile Leu Leu Ala Leu Thr Ser Leu Arg Ser Asn Lys Met Arg Ala
10 15 20

ttg ttg acg ctg tta gga gtc atc att ggt atc gca tca gtc atc gga 211
Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile Ala Ser Val Ile Gly
25 30 35

att ttg acc att ggt aaa gcc ctg cag gat caa act ttg aat agt ttg 259
Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln Thr Leu Asn Ser Leu
40 45 50

gaa agc ttg ggc gcg aat gat ctg tcg gcg cag gtg gag gaa cgc ccc 307
Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln Val Glu Glu Arg Pro
55 60 65

gac gaa gat tcc ccc gaa ccc gat atg ttc gct ttt tct ggg gct gca 355
Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala Phe Ser Gly Ala Ala
70 75 80 85

aac tct agt ggc aat ctg att ccg gaa gaa aca gtt gat acg ctg cgc 403
Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr Val Asp Thr Leu Arg
90 95 100

gat cgt ttc gca ggc agc atc acg gga atc agc gtt ggc gga atg ggt 451
Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser Val Gly Gly Met Gly
105 110 115

acg caa ggc act ctc atc ggc gac acc gca gat ctt aaa tcc gat ctc 499
Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp Leu Lys Ser Asp Leu
120 125 130

ctc ggc gtc aac gag gat tat atg tgg atg aat ggc gtc gaa atg aac 547
Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn Gly Val Glu Met Asn
135 140 145

tac ggc cgc gcc atc acg caa gac gat gtt gcc gct cag cgc ccc gtt 595
Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala Ala Gln Arg Pro Val
150 155 160 165

gcg gtc atc gcc cca gac acc ttt aat acg ctt ttc gac gca aac ccc 643
Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu Phe Asp Ala Asn Pro

```
                    170                 175                 180

aac ctc gct ctg ggg tcc gaa gta gct ttt gaa ctc aac ggt caa gag   691
Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu Leu Asn Gly Gln Glu
                185                 190                 195

aca ttt ttg cgg gtt atc ggt gtg tat aaa gaa gcc gca gca ggt gga   739
Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu Ala Ala Ala Gly Gly
        200                 205                 210

ctt gtg gga agc aat cca acc gtc cac acc tac acc cca tat acg gtg   787
Leu Val Gly Ser Asn Pro Thr Val His Thr Tyr Thr Pro Tyr Thr Val
    215                 220                 225

gcc aat gac atc acc cac acg gaa gat gga ttg aac acg tta agt atc   835
Ala Asn Asp Ile Thr His Thr Glu Asp Gly Leu Asn Thr Leu Ser Ile
230                 235                 240                 245

cgt gca gct cag ggc gta gac cag gat tca ctt aag ggt tca ctg caa   883
Arg Ala Ala Gln Gly Val Asp Gln Asp Ser Leu Lys Gly Ser Leu Gln
                250                 255                 260

acc tac ttc gac gcg ctg tac gcc aac aat gac tcg cac cac gtt gcc   931
Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn Asp Ser His His Val Ala
            265                 270                 275

atg ttg gac ttc cgt aaa cag atc gaa gag ttc aac acc att ctc ggc   979
Met Leu Asp Phe Arg Lys Gln Ile Glu Glu Phe Asn Thr Ile Leu Gly
        280                 285                 290

gca atg agt ttg ggt atc tca gcc atc ggc gga att tcc ttg ctt gtc   1027
Ala Met Ser Leu Gly Ile Ser Ala Ile Gly Gly Ile Ser Leu Leu Val
    295                 300                 305

ggt ggc atc gga gtg atg aac att atg ttg gtg tct gtc acc gag cga   1075
Gly Gly Ile Gly Val Met Asn Ile Met Leu Val Ser Val Thr Glu Arg
310                 315                 320                 325

acc cgc gaa atc ggt gtc cga aaa gcc ctc ggc gct cgt cga cgt gac   1123
Thr Arg Glu Ile Gly Val Arg Lys Ala Leu Gly Ala Arg Arg Arg Asp
                330                 335                 340

att cgc ctg caa ttc gtc gtt gaa gcc atg atc att tgt ttc atc ggt   1171
Ile Arg Leu Gln Phe Val Val Glu Ala Met Ile Ile Cys Phe Ile Gly
            345                 350                 355

ggc atc ctc ggc gtg ctt ttg ggc ggc att ttg gga ttg atc atg tcc   1219
Gly Ile Leu Gly Val Leu Leu Gly Gly Ile Leu Gly Leu Ile Met Ser
        360                 365                 370

agc gct att ggc tac att tcc ttg cca cca ctg agt gga atc gtg atc   1267
Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro Leu Ser Gly Ile Val Ile
    375                 380                 385

gcc ttg gta ttt tcc atg gct atc ggc ctg ttt ttc ggc tac tac ccc   1315
Ala Leu Val Phe Ser Met Ala Ile Gly Leu Phe Phe Gly Tyr Tyr Pro
390                 395                 400                 405

gcc aac aag gca gca aag ctc gat cca att gac gcc ttg cgt tat gag   1363
Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile Asp Ala Leu Arg Tyr Glu
                410                 415                 420
```

taaaagcctc gtttttaagg tag 1386

<210> 70
<211> 421
<212> PRT
<213> Corynebacterium glutamicum

<400> 70

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Met Ser Leu Ala Glu Ser Ile Leu Leu Ala Leu Thr Ser Leu Arg Ser
  1               5                  10                  15

Asn Lys Met Arg Ala Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile
             20                  25                  30

Ala Ser Val Ile Gly Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln
         35                  40                  45

Thr Leu Asn Ser Leu Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln
     50                  55                  60

Val Glu Glu Arg Pro Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala
 65                  70                  75                  80

Phe Ser Gly Ala Ala Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr
                 85                  90                  95

Val Asp Thr Leu Arg Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser
            100                 105                 110

Val Gly Gly Met Gly Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp
        115                 120                 125

Leu Lys Ser Asp Leu Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn
    130                 135                 140

Gly Val Glu Met Asn Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala
145                 150                 155                 160

Ala Gln Arg Pro Val Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu
                165                 170                 175

Phe Asp Ala Asn Pro Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu
            180                 185                 190

Leu Asn Gly Gln Glu Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu
        195                 200                 205

Ala Ala Ala Gly Gly Leu Val Gly Ser Asn Pro Thr Val His Thr Tyr
    210                 215                 220

Thr Pro Tyr Thr Val Ala Asn Asp Ile Thr His Thr Glu Asp Gly Leu
225                 230                 235                 240

Asn Thr Leu Ser Ile Arg Ala Ala Gln Gly Val Asp Gln Asp Ser Leu
                245                 250                 255

Lys Gly Ser Leu Gln Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn Asp
            260                 265                 270
```

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Ser His His Val Ala Met Leu Asp Phe Arg Lys Gln Ile Glu Glu Phe
275 280 285

Asn Thr Ile Leu Gly Ala Met Ser Leu Gly Ile Ser Ala Ile Gly Gly
290 295 300

Ile Ser Leu Leu Val Gly Gly Ile Gly Val Met Asn Ile Met Leu Val
305 310 315 320

Ser Val Thr Glu Arg Thr Arg Glu Ile Gly Val Arg Lys Ala Leu Gly
325 330 335

Ala Arg Arg Arg Asp Ile Arg Leu Gln Phe Val Val Glu Ala Met Ile
340 345 350

Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile Leu
355 360 365

Gly Leu Ile Met Ser Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro Leu
370 375 380

Ser Gly Ile Val Ile Ala Leu Val Phe Ser Met Ala Ile Gly Leu Phe
385 390 395 400

Phe Gly Tyr Tyr Pro Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile Asp
405 410 415

Ala Leu Arg Tyr Glu
420

<210> 71
<211> 760
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(760)
<223> FRXA00525

<400> 71
ccatcgtgtt tattactcac aaccctgagc ttgctgatga atctgatcgg gtggtcacca 60

tggttgacgg gcgcatcatt gggtctgagg tgaaacactc atg agc ctt gca gaa 115
Met Ser Leu Ala Glu
1 5

tca att ctt ttg gcg ctc acc agc ctg aga agc aac aag atg cgt gca 163
Ser Ile Leu Leu Ala Leu Thr Ser Leu Arg Ser Asn Lys Met Arg Ala
10 15 20

ttg ttg acg ctg tta gga gtc atc att ggt atc gca tca gtc atc gga 211
Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile Ala Ser Val Ile Gly
25 30 35

att ttg acc att ggt aaa gcc ctg cag gat caa act ttg aat agt ttg 259
Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln Thr Leu Asn Ser Leu
40 45 50

gaa agc ttg ggc gcg aat gat ctg tcg gcg cag gtg gag gaa cgc ccc 307

```
Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln Val Glu Glu Arg Pro
     55                  60                  65

gac gaa gat tcc ccc gaa ccc gat atg ttc gct ttt tct ggg gct gca   355
Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala Phe Ser Gly Ala Ala
 70                  75                  80                  85

aac tct agt ggc aat ctg att ccg gaa gaa aca gtt gat acg ctg cgc   403
Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr Val Asp Thr Leu Arg
                 90                  95                 100

gat cgt ttc gca ggc agc atc acg gga atc agc gtt ggc gga atg ggt   451
Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser Val Gly Gly Met Gly
            105                 110                 115

acg caa ggc act ctc atc ggc gac acc gca gat ctt aaa tcc gat ctc   499
Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp Leu Lys Ser Asp Leu
        120                 125                 130

ctc ggc gtc aac gag gat tat atg tgg atg aat ggc gtc gaa atg aac   547
Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn Gly Val Glu Met Asn
    135                 140                 145

tac ggc cgc gcc atc acg caa gac gat gtt gcc gct cag cgc ccc gtt   595
Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala Ala Gln Arg Pro Val
150                 155                 160                 165

gcg gtc atc gcc cca gac acc ttt aat acg ctt ttc gac gca aac ccc   643
Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu Phe Asp Ala Asn Pro
                170                 175                 180

aac ctc gct ctg ggg tcc gaa gta gct ttt gaa ctc aac ggt caa gag   691
Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu Leu Asn Gly Gln Glu
            185                 190                 195

aca ttt ttg cgg gtt atc ggt gtg tat aaa gaa gcc gca gca ggt gga   739
Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu Ala Ala Ala Gly Gly
        200                 205                 210

ctt gtg gga agc aat cca acc                                      760
Leu Val Gly Ser Asn Pro Thr
    215                 220
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<210> 72
<211> 220
<212> PRT
<213> Corynebacterium glutamicum

<400> 72

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Met Ser Leu Ala Glu Ser Ile Leu Leu Ala Leu Thr Ser Leu Arg Ser
  1               5                  10                  15

Asn Lys Met Arg Ala Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile
             20                  25                  30

Ala Ser Val Ile Gly Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln
         35                  40                  45

Thr Leu Asn Ser Leu Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln
     50                  55                  60
```

```
Val Glu Glu Arg Pro Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala
 65                  70                  75                  80

Phe Ser Gly Ala Ala Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr
                85                  90                  95

Val Asp Thr Leu Arg Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser
            100                 105                 110

Val Gly Gly Met Gly Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp
        115                 120                 125

Leu Lys Ser Asp Leu Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn
    130                 135                 140

Gly Val Glu Met Asn Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala
145                 150                 155                 160

Ala Gln Arg Pro Val Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu
                165                 170                 175

Phe Asp Ala Asn Pro Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu
            180                 185                 190

Leu Asn Gly Gln Glu Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu
        195                 200                 205

Ala Ala Ala Gly Gly Leu Val Gly Ser Asn Pro Thr
    210                 215                 220


<210> 73
<211> 617
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(594)
<223> FRXA00556

<400> 73
tac acc cca tat acg gtg gcc aat gac atc acc cac acg aaa gat gga   48
Tyr Thr Pro Tyr Thr Val Ala Asn Asp Ile Thr His Thr Lys Asp Gly
  1               5                  10                  15

ttg aac acg tta agt atc cgt gca gct cag ggc gta gac cag gat tca   96
Leu Asn Thr Leu Ser Ile Arg Ala Ala Gln Gly Val Asp Gln Asp Ser
             20                  25                  30

ctt aag ggt tca ctg caa acc tac ttc gac gcg ctg tac gcc aac aat  144
Leu Lys Gly Ser Leu Gln Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn
         35                  40                  45

gac tcg cac cac gtt gcc atg ttg gac ttc cgt aaa cag atc gaa gag  192
Asp Ser His His Val Ala Met Leu Asp Phe Arg Lys Gln Ile Glu Glu
     50                  55                  60

ttc aac acc att ctc ggc gca atg agt ttg ggt atc tca gcc atc ggc  240
Phe Asn Thr Ile Leu Gly Ala Met Ser Leu Gly Ile Ser Ala Ile Gly
```

```
 65                  70                  75                  80

gga att tcc ttg ctt gtc ggt ggc atc gga gtg atg aac att atg ttg   288
Gly Ile Ser Leu Leu Val Gly Gly Ile Gly Val Met Asn Ile Met Leu
                 85                  90                  95

gtg tct gtc acc gag cga acc cgc gaa atc ggt gtc cga aaa gcc ctc   336
Val Ser Val Thr Glu Arg Thr Arg Glu Ile Gly Val Arg Lys Ala Leu
            100                 105                 110

ggc gct cgt cga cgt gac att cgc ctg caa ttc gtc gtt gaa gcc atg   384
Gly Ala Arg Arg Arg Asp Ile Arg Leu Gln Phe Val Val Glu Ala Met
        115                 120                 125

atc att tgt ttc atc ggt ggc atc ctc ggc gtg ctt ttg ggc ggc att   432
Ile Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile
    130                 135                 140

ttg gga ttg atc atg tcc agc gct att ggc tac att tcc ttg cca cca   480
Leu Gly Leu Ile Met Ser Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro
145                 150                 155                 160

ctg agt gga atc gtg atc gcc ttg gta ttt tcc atg gct atc ggc ctg   528
Leu Ser Gly Ile Val Ile Ala Leu Val Phe Ser Met Ala Ile Gly Leu
                165                 170                 175

ttt ttc ggc tac tac ccc gcc aac aag gca gca aag ctc gat cca att   576
Phe Phe Gly Tyr Tyr Pro Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile
            180                 185                 190

gac gcc ttg cgt tat gag taaaagcctc gtttttaagg tag                 617
Asp Ala Leu Arg Tyr Glu
        195
```

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<210> 74
<211> 198
<212> PRT
<213> Corynebacterium glutamicum

<400> 74

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Tyr Thr Pro Tyr Thr Val Ala Asn Asp Ile Thr His Thr Lys Asp Gly
  1               5                  10                  15

Leu Asn Thr Leu Ser Ile Arg Ala Ala Gln Gly Val Asp Gln Asp Ser
             20                  25                  30

Leu Lys Gly Ser Leu Gln Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn
         35                  40                  45

Asp Ser His His Val Ala Met Leu Asp Phe Arg Lys Gln Ile Glu Glu
     50                  55                  60

Phe Asn Thr Ile Leu Gly Ala Met Ser Leu Gly Ile Ser Ala Ile Gly
 65                  70                  75                  80

Gly Ile Ser Leu Leu Val Gly Gly Ile Gly Val Met Asn Ile Met Leu
                 85                  90                  95

Val Ser Val Thr Glu Arg Thr Arg Glu Ile Gly Val Arg Lys Ala Leu
            100                 105                 110
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Gly Ala Arg Arg Arg Asp Ile Arg Leu Gln Phe Val Val Glu Ala Met
        115                 120                 125

Ile Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile
    130                 135                 140

Leu Gly Leu Ile Met Ser Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro
145                 150                 155                 160

Leu Ser Gly Ile Val Ile Ala Leu Val Phe Ser Met Ala Ile Gly Leu
                165                 170                 175

Phe Phe Gly Tyr Tyr Pro Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile
            180                 185                 190

Asp Ala Leu Arg Tyr Glu
        195
```

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<210> 75
<211> 939
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(916)
<223> RXA02750

<400> 75
gttccatgga cgatgtattt ctagcagtta cagctgaacg gaaacgatca tgattacagt 60

tctgacacgc agacacttgc gctgcttttt ccgcgaccgc atg gca gtg ctg ttt 115
                                              Met Ala Val Leu Phe
                                                1               5

tcc atc atg ggt gcg ctc atc ctt ttg gtc ctg tac gtg ctg ttt tta 163
Ser Ile Met Gly Ala Leu Ile Leu Leu Val Leu Tyr Val Leu Phe Leu
                10                  15                  20

gga aaa ctg caa att gac ggt ctc atg gtg gat cta cct gac tca gcc 211
Gly Lys Leu Gln Ile Asp Gly Leu Met Val Asp Leu Pro Asp Ser Ala
            25                  30                  35

cga gac gat gtt gaa gga ttc gtc ttc aat tgg gtg ttt tcc gga att 259
Arg Asp Asp Val Glu Gly Phe Val Phe Asn Trp Val Phe Ser Gly Ile
        40                  45                  50

ctc atc acg tcc gca atc act gtt ccg caa gca gca ctt gga gtg ctg 307
Leu Ile Thr Ser Ala Ile Thr Val Pro Gln Ala Ala Leu Gly Val Leu
    55                  60                  65

gtt gaa gat cgc acc cgc gga ggc atc aaa gat ttc ctc gtg gca ccc 355
Val Glu Asp Arg Thr Arg Gly Gly Ile Lys Asp Phe Leu Val Ala Pro
70                  75                  80                  85

gta tcc aga acg acg ctg acg gtg tcc tat atc ttc gca gca gtc att 403
Val Ser Arg Thr Thr Leu Thr Val Ser Tyr Ile Phe Ala Ala Val Ile
                90                  95                  100
```
```

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gtc gcc atg acg att ttg atc ttt gaa atc gtg gtg gga agt att ggt   451
Val Ala Met Thr Ile Leu Ile Phe Glu Ile Val Val Gly Ser Ile Gly
            105                 110                 115

tta gct att ttg ggg cac ttc agc atg agc att gct cgc gtg ctc gaa   499
Leu Ala Ile Leu Gly His Phe Ser Met Ser Ile Ala Arg Val Leu Glu
        120                 125                 130

ttg gta gtc gcc ttg ctt ctg ctc acc ctg gtg ttt tcc gca att gca   547
Leu Val Val Ala Leu Leu Leu Leu Thr Leu Val Phe Ser Ala Ile Ala
    135                 140                 145

gca ttt ctg atc acc ttg gtg aaa tct caa ggc gga atg tct gcg ctt   595
Ala Phe Leu Ile Thr Leu Val Lys Ser Gln Gly Gly Met Ser Ala Leu
150                 155                 160                 165

tca agc ctg gta ggc acc ctg gcg ggc ttt tta tct gct gct tat att   643
Ser Ser Leu Val Gly Thr Leu Ala Gly Phe Leu Ser Ala Ala Tyr Ile
                170                 175                 180

cca ccc atc gca ttg cct gaa gca gtg aca aac gtg ttg aac ttc ctc   691
Pro Pro Ile Ala Leu Pro Glu Ala Val Thr Asn Val Leu Asn Phe Leu
            185                 190                 195

ccg ttt acc cca gct gga atg ttg atc aga caa att gtg gtt gcc cca   739
Pro Phe Thr Pro Ala Gly Met Leu Ile Arg Gln Ile Val Val Ala Pro
        200                 205                 210

gca ttg gac gcg att tca ctt cca ccc gaa gcc ttc gat atc ttc caa   787
Ala Leu Asp Ala Ile Ser Leu Pro Pro Glu Ala Phe Asp Ile Phe Gln
    215                 220                 225

ttc gga tac gga ctc aaa ctg gaa atg ttt ggg gaa ccc gtt tct aca   835
Phe Gly Tyr Gly Leu Lys Leu Glu Met Phe Gly Glu Pro Val Ser Thr
230                 235                 240                 245

tgg gtg gca gta gga att gtt gcc tca tgg gga gtg gtg ttt gga ctc   883
Trp Val Ala Val Gly Ile Val Ala Ser Trp Gly Val Val Phe Gly Leu
                250                 255                 260

att gcc gcg ttc aaa atg aaa agc gtg gtg cga taaatcctgc taaagaatgc 936
Ile Ala Ala Phe Lys Met Lys Ser Val Val Arg
            265                 270

ttc                                                               939
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<210> 76
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 76

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Met Ala Val Leu Phe Ser Ile Met Gly Ala Leu Ile Leu Leu Val Leu
  1               5                  10                  15

Tyr Val Leu Phe Leu Gly Lys Leu Gln Ile Asp Gly Leu Met Val Asp
             20                  25                  30

Leu Pro Asp Ser Ala Arg Asp Asp Val Glu Gly Phe Val Phe Asn Trp
         35                  40                  45
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Val Phe Ser Gly Ile Leu Ile Thr Ser Ala Ile Thr Val Pro Gln Ala
50 55 60

Ala Leu Gly Val Leu Val Glu Asp Arg Thr Arg Gly Gly Ile Lys Asp
65 70 75 80

Phe Leu Val Ala Pro Val Ser Arg Thr Thr Leu Thr Val Ser Tyr Ile
85 90 95

Phe Ala Ala Val Ile Val Ala Met Thr Ile Leu Ile Phe Glu Ile Val
100 105 110

Val Gly Ser Ile Gly Leu Ala Ile Leu Gly His Phe Ser Met Ser Ile
115 120 125

Ala Arg Val Leu Glu Leu Val Val Ala Leu Leu Leu Leu Thr Leu Val
130 135 140

Phe Ser Ala Ile Ala Ala Phe Leu Ile Thr Leu Val Lys Ser Gln Gly
145 150 155 160

Gly Met Ser Ala Leu Ser Ser Leu Val Gly Thr Leu Ala Gly Phe Leu
165 170 175

Ser Ala Ala Tyr Ile Pro Pro Ile Ala Leu Pro Glu Ala Val Thr Asn
180 185 190

Val Leu Asn Phe Leu Pro Phe Thr Pro Ala Gly Met Leu Ile Arg Gln
195 200 205

Ile Val Val Ala Pro Ala Leu Asp Ala Ile Ser Leu Pro Pro Glu Ala
210 215 220

Phe Asp Ile Phe Gln Phe Gly Tyr Gly Leu Lys Leu Glu Met Phe Gly
225 230 235 240

Glu Pro Val Ser Thr Trp Val Ala Val Gly Ile Val Ala Ser Trp Gly
245 250 255

Val Val Phe Gly Leu Ile Ala Ala Phe Lys Met Lys Ser Val Val Arg
260 265 270

<210> 77
<211> 1815
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1792)
<223> RXN02096

<400> 77
cgcttcgacg acctcaccca cagcgatatc cgcaggaatc tcatcgcggt ttttgatgag 60

ccgttcttgt actcctcctc cataccgcga gaacatctcg atg ggt ttg gat gtc 115

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                                                    Met Gly Leu Asp Val
                                                      1               5

agt gat gag cag atc gaa cac gca gcc agg ctt gcc cag gct cat gat   163
Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu Ala Gln Ala His Asp
                  10                  15                  20

ttt atc gat cgc ctt cca aac aaa tac gag gaa gtc att ggc gaa cgc   211
Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu Val Ile Gly Glu Arg
              25                  30                  35

ggc ctg acg ctt tct ggt ggt caa cgc caa cgc atc gcc ctc gca cgg   259
Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Leu Ala Arg
          40                  45                  50

gct ttc ctg gcg cat ccc aaa gtg ttg gtg ctt gat gat gcc acc tct   307
Ala Phe Leu Ala His Pro Lys Val Leu Val Leu Asp Asp Ala Thr Ser
      55                  60                  65

gcc att gat gcc tcc act gag gac cgc att ttc cag gcc ttg cgc gaa   355
Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe Gln Ala Leu Arg Glu
  70                  75                  80                  85

gaa ctg cac gat gtc acc att ttg atc atc gcg cac cgc cac tcc act   403
Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala His Arg His Ser Thr
                  90                  95                 100

ttg gag ctc ggc gat cgg gtt ggt ctg gtc gaa gat gga cgg gta aca   451
Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu Asp Gly Arg Val Thr
              105                 110                 115

gca ctg gga ccg ttg agt gag atg cgt gat cac gct cgt ttc tcg cat   499
Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His Ala Arg Phe Ser His
          120                 125                 130

ctg atg gct ctt gat ttc cag gat tct cac gat ccg gaa ttc acc ctc   547
Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp Pro Glu Phe Thr Leu
      135                 140                 145

gac aac ggt tca cta ccc agc caa gag caa ttg tgg ccg gag gtc tcc   595
Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu Trp Pro Glu Val Ser
  150                 155                 160                 165

aca gaa aag cag tac aag att ctt gcg cct gcc cct ggt cga ggc cgt   643
Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala Pro Gly Arg Gly Arg
                  170                 175                 180

ggc atg tcc atg cca gca acc cct gag ctg ctc gcc cag att gag gcg   691
Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu Ala Gln Ile Glu Ala
              185                 190                 195

ctg cca gca gca acg gaa gaa aca cga gtt gat gcc ggg agg cta cgc   739
Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp Ala Gly Arg Leu Arg
          200                 205                 210

acc agt acc tcc ggt ttc aaa ttg ctc agt tta ttc aag cag gtc cgt   787
Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu Phe Lys Gln Val Arg
      215                 220                 225

tgg ctc gtc gtc gcg gtc atc gcg ttg ttg ctg gtg ggc gta gcc gcc   835
Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu Val Gly Val Ala Ala
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230                 235                 240                 245

gat cta gca ttt cca aca ctg atg cgc gca gcc atc gac aac ggt gtg   883
Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala Ile Asp Asn Gly Val
                250                 255                 260

caa gca caa agc acc tcc acg ttg tgg tgg atc gcc atc gca ggc agc   931
Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile Ala Ile Ala Gly Ser
            265                 270                 275

gta gta gtc ctt ctg tcc tgg gcc gcc gcc gcg atc aac acg att atc   979
Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala Ile Asn Thr Ile Ile
        280                 285                 290

acg gca cgc acc ggt gaa cgg ctg ctt tac ggc ttg cgt ctg cgc tca   1027
Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly Leu Arg Leu Arg Ser
    295                 300                 305

ttt gtg cat cta ttg cgc ctg tcc atg agc tat ttc gaa cgc acc atg   1075
Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr Phe Glu Arg Thr Met
310                 315                 320                 325

tcc ggc cgc atc atg acg cgc atg acc acc gac atc gac aac ctc tcg   1123
Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp Ile Asp Asn Leu Ser
                330                 335                 340

tcc ttc ctc caa tca ggt ctg gcg caa aca gtt gtc tct gtg ggc acg   1171
Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val Val Ser Val Gly Thr
            345                 350                 355

ctc atc ggt gtg gtc acc atg ctc gcc atc acc gac gca caa cta gca   1219
Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr Asp Ala Gln Leu Ala
        360                 365                 370

ctc gtt gcg ctg tcc gtg gtg ccg atc atc atc gtg ctc act ctc att   1267
Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile Val Leu Thr Leu Ile
    375                 380                 385

ttc cga cgc atc agc tcc agg ctg tac acc gct tca cgc gag caa gcc   1315
Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala Ser Arg Glu Gln Ala
390                 395                 400                 405

agc cag gtc aac gcg gta ttc cac gag tcc atc gcc ggt tta cgc acc   1363
Ser Gln Val Asn Ala Val Phe His Glu Ser Ile Ala Gly Leu Arg Thr
                410                 415                 420

gcg cag atg cac cgc atg gaa gac caa gtc ttt gac aat tat gcg ggc   1411
Ala Gln Met His Arg Met Glu Asp Gln Val Phe Asp Asn Tyr Ala Gly
            425                 430                 435

gaa gca gag gaa ttc cga cgc ctg cgt gtg aaa tcc cag acg gcc atc   1459
Glu Ala Glu Glu Phe Arg Arg Leu Arg Val Lys Ser Gln Thr Ala Ile
        440                 445                 450

gcc atc tac ttc ccc ggc ctt ggc gcg ctc tct gaa atc gcc cag gca   1507
Ala Ile Tyr Phe Pro Gly Leu Gly Ala Leu Ser Glu Ile Ala Gln Ala
    455                 460                 465

ctc gtc ctc ggt ttc ggc gca ctg caa gta acg cgc ggc gac atc tcc   1555
Leu Val Leu Gly Phe Gly Ala Leu Gln Val Thr Arg Gly Asp Ile Ser
470                 475                 480                 485
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acc ggc gta ctc gtg gca ttc gtg ctg tac atg ggc ctg atg ttc ggc   1603
Thr Gly Val Leu Val Ala Phe Val Leu Tyr Met Gly Leu Met Phe Gly
                490                 495                 500

ccc atc caa caa cta agc caa atc ttc gac tcc tac caa caa gcc gcc   1651
Pro Ile Gln Gln Leu Ser Gln Ile Phe Asp Ser Tyr Gln Gln Ala Ala
            505                 510                 515

gtc ggc ttc cgt cgc atc acc gaa ctg ctc gca acg cag ccc agc gtc   1699
Val Gly Phe Arg Arg Ile Thr Glu Leu Leu Ala Thr Gln Pro Ser Val
        520                 525                 530

cag atc tgg gca cca aca ggc acg cta ggc agg ctg cca cgc agc ctt   1747
Gln Ile Trp Ala Pro Thr Gly Thr Leu Gly Arg Leu Pro Arg Ser Leu
    535                 540                 545

tat tgc ttg acg acg tca cct tcg gct att cag acg atc cga tcc       1792
Tyr Cys Leu Thr Thr Ser Pro Ser Ala Ile Gln Thr Ile Arg Ser
550                 555                 560

tagacaacgt caccgtccag atc                                        1815
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<210> 78
<211> 564
<212> PRT
<213> Corynebacterium glutamicum

<400> 78

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Met Gly Leu Asp Val Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu
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Ala Gln Ala His Asp Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu
            20                  25                  30

Val Ile Gly Glu Arg Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg
        35                  40                  45

Ile Ala Leu Ala Arg Ala Phe Leu Ala His Pro Lys Val Leu Val Leu
    50                  55                  60

Asp Asp Ala Thr Ser Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe
65                  70                  75                  80

Gln Ala Leu Arg Glu Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala
                85                  90                  95

His Arg His Ser Thr Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu
            100                 105                 110

Asp Gly Arg Val Thr Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His
        115                 120                 125

Ala Arg Phe Ser His Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp
    130                 135                 140

Pro Glu Phe Thr Leu Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu
145                 150                 155                 160

Trp Pro Glu Val Ser Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala
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                    165                 170                 175

Pro Gly Arg Gly Arg Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu
            180                 185                 190

Ala Gln Ile Glu Ala Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp
        195                 200                 205

Ala Gly Arg Leu Arg Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu
    210                 215                 220

Phe Lys Gln Val Arg Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu
225                 230                 235                 240

Val Gly Val Ala Ala Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala
                245                 250                 255

Ile Asp Asn Gly Val Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile
            260                 265                 270

Ala Ile Ala Gly Ser Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala
        275                 280                 285

Ile Asn Thr Ile Ile Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly
    290                 295                 300

Leu Arg Leu Arg Ser Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr
305                 310                 315                 320

Phe Glu Arg Thr Met Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp
                325                 330                 335

Ile Asp Asn Leu Ser Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val
            340                 345                 350

Val Ser Val Gly Thr Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr
        355                 360                 365

Asp Ala Gln Leu Ala Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile
    370                 375                 380

Val Leu Thr Leu Ile Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala
385                 390                 395                 400

Ser Arg Glu Gln Ala Ser Gln Val Asn Ala Val Phe His Glu Ser Ile
                405                 410                 415

Ala Gly Leu Arg Thr Ala Gln Met His Arg Met Glu Asp Gln Val Phe
            420                 425                 430

Asp Asn Tyr Ala Gly Glu Ala Glu Glu Phe Arg Arg Leu Arg Val Lys
        435                 440                 445

Ser Gln Thr Ala Ile Ala Ile Tyr Phe Pro Gly Leu Gly Ala Leu Ser
    450                 455                 460

Glu Ile Ala Gln Ala Leu Val Leu Gly Phe Gly Ala Leu Gln Val Thr
465                 470                 475                 480

Arg Gly Asp Ile Ser Thr Gly Val Leu Val Ala Phe Val Leu Tyr Met
                485                 490                 495
```

```
Gly Leu Met Phe Gly Pro Ile Gln Gln Leu Ser Gln Ile Phe Asp Ser
            500                 505                 510

Tyr Gln Gln Ala Ala Val Gly Phe Arg Arg Ile Thr Glu Leu Leu Ala
        515                 520                 525

Thr Gln Pro Ser Val Gln Ile Trp Ala Pro Thr Gly Thr Leu Gly Arg
    530                 535                 540

Leu Pro Arg Ser Leu Tyr Cys Leu Thr Thr Ser Pro Ser Ala Ile Gln
545                 550                 555                 560

Thr Ile Arg Ser
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<210> 79
<211> 1417
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1417)
<223> FRXA02096

<400> 79

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ccgttcttgt actcctcctc ataccgcga gaacatctcg atg ggt ttg gat gtc   115
                                          Met Gly Leu Asp Val
                                            1               5

agt gat gag cag atc gaa cac gca gcc agg ctt gcc cag gct cat gat   163
Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu Ala Gln Ala His Asp
                10                  15                  20

ttt atc gat cgc ctt cca aac aaa tac gag gaa gtc att ggc gaa cgc   211
Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu Val Ile Gly Glu Arg
            25                  30                  35

ggc ctg acg ctt tct ggt ggt caa cgc caa cgc atc gcc ctc gca cgg   259
Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Leu Ala Arg
        40                  45                  50

gct ttc ctg gcg cat ccc aaa gtg ttg gtg ctt gat gat gcc acc tct   307
Ala Phe Leu Ala His Pro Lys Val Leu Val Leu Asp Asp Ala Thr Ser
    55                  60                  65

gcc att gat gcc tcc act gag gac cgc att ttc cag gcc ttg cgc gaa   355
Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe Gln Ala Leu Arg Glu
70                  75                  80                  85

gaa ctg cac gat gtc acc att ttg atc atc gcg cac cgc cac tcc act   403
Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala His Arg His Ser Thr
                90                  95                  100

ttg gag ctc ggc gat cgg gtt ggt ctg gtc gaa gat gga cgg gta aca   451
Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu Asp Gly Arg Val Thr
            105                 110                 115
```

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gca ctg gga ccg ttg agt gag atg cgt gat cac gct cgt ttc tcg cat   499
Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His Ala Arg Phe Ser His
        120                 125                 130

ctg atg gct ctt gat ttc cag gat tct cac gat ccg gaa ttc acc ctc   547
Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp Pro Glu Phe Thr Leu
    135                 140                 145

gac aac ggt tca cta ccc agc caa gag caa ttg tgg ccg gag gtc tcc   595
Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu Trp Pro Glu Val Ser
150                 155                 160                 165

aca gaa aag cag tac aag att ctt gcg cct gcc cct ggt cga ggc cgt   643
Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala Pro Gly Arg Gly Arg
                170                 175                 180

ggc atg tcc atg cca gca acc cct gag ctg ctc gcc cag att gag gcg   691
Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu Ala Gln Ile Glu Ala
            185                 190                 195

ctg cca gca gca acg gaa gaa aca cga gtt gat gcc ggg agg cta cgc   739
Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp Ala Gly Arg Leu Arg
        200                 205                 210

acc agt acc tcc ggt ttc aaa ttg ctc agt tta ttc aag cag gtc cgt   787
Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu Phe Lys Gln Val Arg
    215                 220                 225

tgg ctc gtc gtc gcg gtc atc gcg ttg ttg ctg gtg ggc gta gcc gcc   835
Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu Val Gly Val Ala Ala
230                 235                 240                 245

gat cta gca ttt cca aca ctg atg cgc gca gcc atc gac aac ggt gtg   883
Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala Ile Asp Asn Gly Val
                250                 255                 260

caa gca caa agc acc tcc acg ttg tgg tgg atc gcc atc gca ggc agc   931
Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile Ala Ile Ala Gly Ser
            265                 270                 275

gta gta gtc ctt ctg tcc tgg gcc gcc gcc gcg atc aac acg att atc   979
Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala Ile Asn Thr Ile Ile
        280                 285                 290

acg gca cgc acc ggt gaa cgg ctg ctt tac ggc ttg cgt ctg cgc tca   1027
Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly Leu Arg Leu Arg Ser
    295                 300                 305

ttt gtg cat cta ttg cgc ctg tcc atg agc tat ttc gaa cgc acc atg   1075
Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr Phe Glu Arg Thr Met
310                 315                 320                 325

tcc ggc cgc atc atg acg cgc atg acc acc gac atc gac aac ctc tcg   1123
Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp Ile Asp Asn Leu Ser
                330                 335                 340

tcc ttc ctc caa tca ggt ctg gcg caa aca gtt gtc tct gtg ggc acg   1171
Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val Val Ser Val Gly Thr
            345                 350                 355
```

```
ctc atc ggt gtg gtc acc atg ctc gcc atc acc gac gca caa cta gca   1219
Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr Asp Ala Gln Leu Ala
        360                 365                 370

ctc gtt gcg ctg tcc gtg gtg ccg atc atc atc gtg ctc act ctc att   1267
Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile Val Leu Thr Leu Ile
    375                 380                 385

ttc cga cgc atc agc tcc agg ctg tac acc gct tca cgc gag caa gcc   1315
Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala Ser Arg Glu Gln Ala
390                 395                 400                 405

agc cag gtc aac gcg gta ttc cac gag tcc atc gcc ggt tta cgc acc   1363
Ser Gln Val Asn Ala Val Phe His Glu Ser Ile Ala Gly Leu Arg Thr
                410                 415                 420

gcg cag atg cac cgc atg gaa gac caa gtc ttt gac aat tat gcg ggc   1411
Ala Gln Met His Arg Met Glu Asp Gln Val Phe Asp Asn Tyr Ala Gly
            425                 430                 435

gaa gca                                                          1417
Glu Ala
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<210> 80
<211> 439
<212> PRT
<213> Corynebacterium glutamicum

<400> 80

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Met Gly Leu Asp Val Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu
  1               5                  10                  15

Ala Gln Ala His Asp Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu
             20                  25                  30

Val Ile Gly Glu Arg Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg
         35                  40                  45

Ile Ala Leu Ala Arg Ala Phe Leu Ala His Pro Lys Val Leu Val Leu
     50                  55                  60

Asp Asp Ala Thr Ser Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe
 65                  70                  75                  80

Gln Ala Leu Arg Glu Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala
                 85                  90                  95

His Arg His Ser Thr Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu
            100                 105                 110

Asp Gly Arg Val Thr Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His
        115                 120                 125

Ala Arg Phe Ser His Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp
    130                 135                 140

Pro Glu Phe Thr Leu Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu
145                 150                 155                 160
```

Trp Pro Glu Val Ser Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala
165 170 175

Pro Gly Arg Gly Arg Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu
180 185 190

Ala Gln Ile Glu Ala Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp
195 200 205

Ala Gly Arg Leu Arg Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu
210 215 220

Phe Lys Gln Val Arg Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu
225 230 235 240

Val Gly Val Ala Ala Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala
245 250 255

Ile Asp Asn Gly Val Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile
260 265 270

Ala Ile Ala Gly Ser Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala
275 280 285

Ile Asn Thr Ile Ile Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly
290 295 300

Leu Arg Leu Arg Ser Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr
305 310 315 320

Phe Glu Arg Thr Met Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp
325 330 335

Ile Asp Asn Leu Ser Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val
340 345 350

Val Ser Val Gly Thr Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr
355 360 365

Asp Ala Gln Leu Ala Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile
370 375 380

Val Leu Thr Leu Ile Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala
385 390 395 400

Ser Arg Glu Gln Ala Ser Gln Val Asn Ala Val Phe His Glu Ser Ile
405 410 415

Ala Gly Leu Arg Thr Ala Gln Met His Arg Met Glu Asp Gln Val Phe
420 425 430

Asp Asn Tyr Ala Gly Glu Ala
435

<210> 81
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(820)
<223> RXA02562

<400> 81
cgggtgcgct gagggtgagg ttggggcgac gaggcgtgca tggactttag gttaggttat 60

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tgagcagatt tatttgggct tttgtctagg gtggggagct atg ttc ttg aca aag   115
                                            Met Phe Leu Thr Lys
                                              1               5

gtt tcg ctg ctt gat cat ccg gag tca ttg ccg ggg tat tta tcg agc   163
Val Ser Leu Leu Asp His Pro Glu Ser Leu Pro Gly Tyr Leu Ser Ser
                 10                  15                  20

ctg gcg atc gtg gaa tat ctg cat gaa cag ccg ttg gag ttt cgt gca   211
Leu Ala Ile Val Glu Tyr Leu His Glu Gln Pro Leu Glu Phe Arg Ala
             25                  30                  35

ccg att act gtg att act ggt gaa aat ggg gtg ggt aaa tcc acg ttg   259
Pro Ile Thr Val Ile Thr Gly Glu Asn Gly Val Gly Lys Ser Thr Leu
         40                  45                  50

gtt gag gct ttg gcg gtg ggg atg cgc ctt aat ccg tct ggt ggc tct   307
Val Glu Ala Leu Ala Val Gly Met Arg Leu Asn Pro Ser Gly Gly Ser
     55                  60                  65

agg cat gca aac ttt ggc agg gaa ggc gat att gtg tcg tcg ctt cat   355
Arg His Ala Asn Phe Gly Arg Glu Gly Asp Ile Val Ser Ser Leu His
 70                  75                  80                  85

cag tcg ttg aag ttg gtg cgg aga gaa aac cct cgg gat gcg ttc ttt   403
Gln Ser Leu Lys Leu Val Arg Arg Glu Asn Pro Arg Asp Ala Phe Phe
                 90                  95                 100

ttt cgg ggt gag acg atg tat aac gtg gct tcc tat tat gag gag tta   451
Phe Arg Gly Glu Thr Met Tyr Asn Val Ala Ser Tyr Tyr Glu Glu Leu
            105                 110                 115

atg ggg gaa aag aac atg cat gat ctt cac aag atg agc cat ggc gaa   499
Met Gly Glu Lys Asn Met His Asp Leu His Lys Met Ser His Gly Glu
        120                 125                 130

tcg gta ttt gcg gtg att gat cgg cgt ttt aac aat caa gga ttt ttt   547
Ser Val Phe Ala Val Ile Asp Arg Arg Phe Asn Asn Gln Gly Phe Phe
    135                 140                 145

gtt ttg gac gag cct gag gca ggc ctt tcc atg ctg agg cag ttg gag   595
Val Leu Asp Glu Pro Glu Ala Gly Leu Ser Met Leu Arg Gln Leu Glu
150                 155                 160                 165

ttg ttg gga aag ttg ggc aac ctt gct cga ggt ggt gcg cag atc atc   643
Leu Leu Gly Lys Leu Gly Asn Leu Ala Arg Gly Gly Ala Gln Ile Ile
                170                 175                 180

atg gct acg cac tct cca ata ttg ttg gct att ccg ggg gca gag atc   691
Met Ala Thr His Ser Pro Ile Leu Leu Ala Ile Pro Gly Ala Glu Ile
            185                 190                 195

ctt gaa att aca tct tcg ggt gtt gca aag gtg aat ttt gag gat gcg   739
Leu Glu Ile Thr Ser Ser Gly Val Ala Lys Val Asn Phe Glu Asp Ala
```

```
        200                 205                 210

gag gct gtt cgt gcg gct cgg gaa ttt gtg gca gat ccg cga ggt acg   787
Glu Ala Val Arg Ala Ala Arg Glu Phe Val Ala Asp Pro Arg Gly Thr
    215                 220                 225

gcg gcg ttt ctg act gcg gag gag gat cac caa tgatgccgta tatcaccgat 840
Ala Ala Phe Leu Thr Ala Glu Glu Asp His Gln
230                 235                 240

att                                                               843
```

<210> 82
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 82

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Met Phe Leu Thr Lys Val Ser Leu Leu Asp His Pro Glu Ser Leu Pro
  1               5                  10                  15

Gly Tyr Leu Ser Ser Leu Ala Ile Val Glu Tyr Leu His Glu Gln Pro
             20                  25                  30

Leu Glu Phe Arg Ala Pro Ile Thr Val Ile Thr Gly Glu Asn Gly Val
         35                  40                  45

Gly Lys Ser Thr Leu Val Glu Ala Leu Ala Val Gly Met Arg Leu Asn
     50                  55                  60

Pro Ser Gly Gly Ser Arg His Ala Asn Phe Gly Arg Glu Gly Asp Ile
 65                  70                  75                  80

Val Ser Ser Leu His Gln Ser Leu Lys Leu Val Arg Arg Glu Asn Pro
                 85                  90                  95

Arg Asp Ala Phe Phe Phe Arg Gly Glu Thr Met Tyr Asn Val Ala Ser
            100                 105                 110

Tyr Tyr Glu Glu Leu Met Gly Glu Lys Asn Met His Asp Leu His Lys
        115                 120                 125

Met Ser His Gly Glu Ser Val Phe Ala Val Ile Asp Arg Arg Phe Asn
    130                 135                 140

Asn Gln Gly Phe Phe Val Leu Asp Glu Pro Glu Ala Gly Leu Ser Met
145                 150                 155                 160

Leu Arg Gln Leu Glu Leu Leu Gly Lys Leu Gly Asn Leu Ala Arg Gly
                165                 170                 175

Gly Ala Gln Ile Ile Met Ala Thr His Ser Pro Ile Leu Leu Ala Ile
            180                 185                 190

Pro Gly Ala Glu Ile Leu Glu Ile Thr Ser Ser Gly Val Ala Lys Val
        195                 200                 205

Asn Phe Glu Asp Ala Glu Ala Val Arg Ala Ala Arg Glu Phe Val Ala
    210                 215                 220
```

Asp Pro Arg Gly Thr Ala Ala Phe Leu Thr Ala Glu Glu Asp His Gln
225 230 235 240

<210> 83
<211> 1029
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1006)
<223> RXA00950

<400> 83
tctccgtacg ccccacgaag acacctcgaa gttcccacgc gaaatgtttc acgtgaaaca 60

tctgctgatt tttgtctcca agtggagttg aatgagagtt atg aac act ccg gca 115
Met Asn Thr Pro Ala
1 5

gtt cag gtt caa aat cta agt ttg agt ttt ggg tcg ttc aca gct gtc 163
Val Gln Val Gln Asn Leu Ser Leu Ser Phe Gly Ser Phe Thr Ala Val
10 15 20

aac ggc ctc agc ctc acg gtg gag cag ggg agc att cac ggc ttc ctc 211
Asn Gly Leu Ser Leu Thr Val Glu Gln Gly Ser Ile His Gly Phe Leu
25 30 35

ggc ccc aac ggt gca gga aag tca aca acc atc agg gca ctc att gga 259
Gly Pro Asn Gly Ala Gly Lys Ser Thr Thr Ile Arg Ala Leu Ile Gly
40 45 50

gtg cta aaa ccc caa aca ggt tca gtc gct att ctc ggc caa gat cct 307
Val Leu Lys Pro Gln Thr Gly Ser Val Ala Ile Leu Gly Gln Asp Pro
55 60 65

gtt gct cac ccc gat gtc ctt cga aga gtt ggc tac gtt cca gga gat 355
Val Ala His Pro Asp Val Leu Arg Arg Val Gly Tyr Val Pro Gly Asp
70 75 80 85

gcc aca ctg tgg gac aac ctc act ggg gcg gaa gtt ttc agg gcg ctc 403
Ala Thr Leu Trp Asp Asn Leu Thr Gly Ala Glu Val Phe Arg Ala Leu
90 95 100

gaa tca ctc cgc aag act cca tcc aac cga gct cta gaa aac gag ctc 451
Glu Ser Leu Arg Lys Thr Pro Ser Asn Arg Ala Leu Glu Asn Glu Leu
105 110 115

att gac gcc ttc caa ttg gat ccc tcg aag aag atc cgc gaa tac tcg 499
Ile Asp Ala Phe Gln Leu Asp Pro Ser Lys Lys Ile Arg Glu Tyr Ser
120 125 130

aca ggt aac aga agg aaa gtc agt ctc atc gcg gcg ctc agt cat gag 547
Thr Gly Asn Arg Arg Lys Val Ser Leu Ile Ala Ala Leu Ser His Glu
135 140 145

ccc gag ctc ctc atc gtt gac gag ccc acc gca ggc ttg gat ccc atc 595

```
Pro Glu Leu Leu Ile Val Asp Glu Pro Thr Ala Gly Leu Asp Pro Ile
150                 155                 160                 165

atg gag caa gtc ttt gtc acc tat gtc cgc aag gca cga acc aac ggc   643
Met Glu Gln Val Phe Val Thr Tyr Val Arg Lys Ala Arg Thr Asn Gly
                170                 175                 180

gcg tcc gtg tta ctc agc agc cac att ctc agt gag gtg gag cag ctg   691
Ala Ser Val Leu Leu Ser Ser His Ile Leu Ser Glu Val Glu Gln Leu
            185                 190                 195

tgt gat tac gtc acg gtc ctt aaa gag ggg cga gca gtt gca tct aat   739
Cys Asp Tyr Val Thr Val Leu Lys Glu Gly Arg Ala Val Ala Ser Asn
        200                 205                 210

gag gtg agc tat ctg agg aag atc tcc gct cac cgc att act gcc acg   787
Glu Val Ser Tyr Leu Arg Lys Ile Ser Ala His Arg Ile Thr Ala Thr
    215                 220                 225

att ccg gcg gta cct caa cac ctt gct ggc agg gga gaa gtg gat ttc   835
Ile Pro Ala Val Pro Gln His Leu Ala Gly Arg Gly Glu Val Asp Phe
230                 235                 240                 245

gat gct ggc cat ctc agc atc acc tgc gat gcc tcc gag gtt ccc gat   883
Asp Ala Gly His Leu Ser Ile Thr Cys Asp Ala Ser Glu Val Pro Asp
                250                 255                 260

att ttg cgc atc atc atc gac gct ggc ggc cag gac atc atc agc acc   931
Ile Leu Arg Ile Ile Ile Asp Ala Gly Gly Gln Asp Ile Ile Ser Thr
            265                 270                 275

gcg gcg tcg ctg gag gag atc ttc ttg cgt cac tat gga gaa acc gtg   979
Ala Ala Ser Leu Glu Glu Ile Phe Leu Arg His Tyr Gly Glu Thr Val
        280                 285                 290

agt ggt tca gaa agc aag gca tca caa tgatccgtct taatctacgt        1026
Ser Gly Ser Glu Ser Lys Ala Ser Gln
    295                 300

ctt                                                              1029


<210> 84
<211> 302
<212> PRT
<213> Corynebacterium glutamicum

<400> 84
Met Asn Thr Pro Ala Val Gln Val Gln Asn Leu Ser Leu Ser Phe Gly
  1               5                  10                  15

Ser Phe Thr Ala Val Asn Gly Leu Ser Leu Thr Val Glu Gln Gly Ser
             20                  25                  30

Ile His Gly Phe Leu Gly Pro Asn Gly Ala Gly Lys Ser Thr Thr Ile
         35                  40                  45

Arg Ala Leu Ile Gly Val Leu Lys Pro Gln Thr Gly Ser Val Ala Ile
     50                  55                  60

Leu Gly Gln Asp Pro Val Ala His Pro Asp Val Leu Arg Arg Val Gly
```

65 70 75 80

Tyr Val Pro Gly Asp Ala Thr Leu Trp Asp Asn Leu Thr Gly Ala Glu
85 90 95

Val Phe Arg Ala Leu Glu Ser Leu Arg Lys Thr Pro Ser Asn Arg Ala
100 105 110

Leu Glu Asn Glu Leu Ile Asp Ala Phe Gln Leu Asp Pro Ser Lys Lys
115 120 125

Ile Arg Glu Tyr Ser Thr Gly Asn Arg Arg Lys Val Ser Leu Ile Ala
130 135 140

Ala Leu Ser His Glu Pro Glu Leu Leu Ile Val Asp Glu Pro Thr Ala
145 150 155 160

Gly Leu Asp Pro Ile Met Glu Gln Val Phe Val Thr Tyr Val Arg Lys
165 170 175

Ala Arg Thr Asn Gly Ala Ser Val Leu Leu Ser Ser His Ile Leu Ser
180 185 190

Glu Val Glu Gln Leu Cys Asp Tyr Val Thr Val Leu Lys Glu Gly Arg
195 200 205

Ala Val Ala Ser Asn Glu Val Ser Tyr Leu Arg Lys Ile Ser Ala His
210 215 220

Arg Ile Thr Ala Thr Ile Pro Ala Val Pro Gln His Leu Ala Gly Arg
225 230 235 240

Gly Glu Val Asp Phe Asp Ala Gly His Leu Ser Ile Thr Cys Asp Ala
245 250 255

Ser Glu Val Pro Asp Ile Leu Arg Ile Ile Ile Asp Ala Gly Gly Gln
260 265 270

Asp Ile Ile Ser Thr Ala Ala Ser Leu Glu Glu Ile Phe Leu Arg His
275 280 285

Tyr Gly Glu Thr Val Ser Gly Ser Glu Ser Lys Ala Ser Gln
290 295 300

<210> 85
<211> 1764
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1741)
<223> RXA02119

<400> 85
ttcggtccgc tctggcaaaa atggctggct gccacctcgg cgcagcagct taagggctgg 60

gcttaaattg cttgtcgacg cctagtgcca caatggagac atg acc gaa aca ctt 115
Met Thr Glu Thr Leu
1 5

```
gtg gtg aat ggc ctt gca ggc ggc tat ggg cac cgc aca tta ttt aac   163
Val Val Asn Gly Leu Ala Gly Gly Tyr Gly His Arg Thr Leu Phe Asn
                10                  15                  20

gat gtg aat ctc acc gta gct gcc ggc gat gtc gtg ggc gtt gtc ggc   211
Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val Val Gly Val Val Gly
            25                  30                  35

gtc aat ggc gct ggt aaa tcc aca ttt cta aaa att ctg gcg ggc gtg   259
Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys Ile Leu Ala Gly Val
        40                  45                  50

gaa aag cca ctg gct gga act atc gcg ctt tcg cca gcc gat gct ttt   307
Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser Pro Ala Asp Ala Phe
    55                  60                  65

gtg ggc tac ttg cca cag gaa cac acc cgc acg tct gga gag acg atc   355
Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr Ser Gly Glu Thr Ile
70                  75                  80                  85

gca gtt tac att gct cgt cga acc ggc tgc caa gct gca aca act gcc   403
Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln Ala Ala Thr Thr Ala
                90                  95                  100

atg gat gac acc gcc gaa gcg ttt ggt gcg gat cca gac aac gct gcc   451
Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp Pro Asp Asn Ala Ala
            105                 110                 115

ttg gcc gat gca tac gcc gag gcg ctg gat cgg tgg atg gcc agt ggc   499
Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg Trp Met Ala Ser Gly
        120                 125                 130

gca gcc gat ttg gat gaa cgc atc ccc atc gtg ctc gct gat ttg ggc   547
Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val Leu Ala Asp Leu Gly
    135                 140                 145

ttt gag ctt ccc acc tcg acg ctg atg gaa gga ctt tca ggc ggg cag   595
Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly Leu Ser Gly Gly Gln
150                 155                 160                 165

gca gcc cgg gtc ggg ctg gcg gcg tta ctg ttg tca cgt ttt gac att   643
Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu Ser Arg Phe Asp Ile
                170                 175                 180

gtg ctt ctc gac gag ccc acc aac gat ttg gat ctc gac ggt ctt gag   691
Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Leu Asp Gly Leu Glu
            185                 190                 195

caa ctg gag aat ttt gtt cag ggg ctt cgc ggg gga gtc gta ctg gtc   739
Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly Gly Val Val Leu Val
        200                 205                 210

agc cat gat cgt gag ttt ctt tcc agg tgt gtg acc act gtg ctg gaa   787
Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val Thr Thr Val Leu Glu
    215                 220                 225

ctc gat ctg cac caa aat tcc cac cat gtt tat ggc ggt gga tat gat   835
Leu Asp Leu His Gln Asn Ser His His Val Tyr Gly Gly Gly Tyr Asp
230                 235                 240                 245
```

```
tcc tac ctt gag gaa cgc gca gtg cta cgc cag cac gcc cgt gac caa   883
Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln His Ala Arg Asp Gln
                    250                 255                 260

tat gag gaa ttt gcg gaa aag aag aag gac ctt gtg gca cgt gct cga   931
Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu Val Ala Arg Ala Arg
                265                 270                 275

acg cag cgt gaa tgg tct agt cac ggt gtc cgc aat gct att aaa cgt   979
Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg Asn Ala Ile Lys Arg
            280                 285                 290

gca cct gac aac gac aaa ctt cgg aag aaa gcc gct gcg gaa tcc agt   1027
Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala Ala Ala Glu Ser Ser
        295                 300                 305

gaa aag cag gct caa aaa gtc cgc cag atg gaa agc cgc atc gct cgg   1075
Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu Ser Arg Ile Ala Arg
310                 315                 320                 325

tta gaa gaa gtt gaa gag cca cgt aaa gaa tgg aaa ctg cag ttc agc   1123
Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp Lys Leu Gln Phe Ser
                    330                 335                 340

gtc ggt aag gcg tcg cgg tca agt tct gtt gtt tcc acg ttg aat gat   1171
Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val Ser Thr Leu Asn Asp
                345                 350                 355

gca agc ttc acc caa ggc gat ttc acc ttg gga cca gta tcc atc caa   1219
Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly Pro Val Ser Ile Gln
            360                 365                 370

gta aat gct ggc gat cgc att ggc atc aca gga ccc aac ggt gct ggt   1267
Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly Pro Asn Gly Ala Gly
        375                 380                 385

aaa tcc aca ttg ctg cgc gga cta ttg gga aac caa gaa ccc acc agc   1315
Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn Gln Glu Pro Thr Ser
390                 395                 400                 405

ggt act gcc acg atg ggc acg agc gtg gcg atc gga gaa atc gat cag   1363
Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile Gly Glu Ile Asp Gln
                    410                 415                 420

gca cga gcg tta ctt gat cca cag ttg cca ctg att tct gcg ttt gaa   1411
Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu Ile Ser Ala Phe Glu
                425                 430                 435

aag cat gtt cca gac tta ccg atc agt gag gtg cgc aca ctg ctc gcg   1459
Lys His Val Pro Asp Leu Pro Ile Ser Glu Val Arg Thr Leu Leu Ala
            440                 445                 450

aaa ttt ggg ctg aat gat aat cat gtg gaa cgg gac gtc gaa aag cta   1507
Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg Asp Val Glu Lys Leu
        455                 460                 465

tct cct ggc gag cgc acg cgc gcc gga ctt gcg ctg cta cag gtg cgg   1555
Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala Leu Leu Gln Val Arg
470                 475                 480                 485

ggc gtc aac gtg ctt gtt ctt gat gag ccc acc aac cac ctt gac ctg   1603
```

```
Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr Asn His Leu Asp Leu
                490                 495                 500

gag gcc atc gag caa ttg gag caa gcg ttg gcc tcg tat gat ggt gtg   1651
Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala Ser Tyr Asp Gly Val
            505                 510                 515

ttg ctg ctg gtc acg cac gat cgt cgc atg ttg gac gct gtg cag acc   1699
Leu Leu Leu Val Thr His Asp Arg Arg Met Leu Asp Ala Val Gln Thr
        520                 525                 530

aat cgt cgt tgg cat gtc gag gct ggc gaa gtt agg gag cta           1741
Asn Arg Arg Trp His Val Glu Ala Gly Glu Val Arg Glu Leu
    535                 540                 545

taaccgtttc cgtattgatg cca                                        1764
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<210> 86
<211> 547
<212> PRT
<213> Corynebacterium glutamicum

<400> 86

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Met Thr Glu Thr Leu Val Val Asn Gly Leu Ala Gly Gly Tyr Gly His
  1               5                  10                  15

Arg Thr Leu Phe Asn Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val
             20                  25                  30

Val Gly Val Val Gly Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys
         35                  40                  45

Ile Leu Ala Gly Val Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser
     50                  55                  60

Pro Ala Asp Ala Phe Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr
 65                  70                  75                  80

Ser Gly Glu Thr Ile Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln
                 85                  90                  95

Ala Ala Thr Thr Ala Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp
            100                 105                 110

Pro Asp Asn Ala Ala Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg
        115                 120                 125

Trp Met Ala Ser Gly Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val
    130                 135                 140

Leu Ala Asp Leu Gly Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly
145                 150                 155                 160

Leu Ser Gly Gly Gln Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu
                165                 170                 175

Ser Arg Phe Asp Ile Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp
            180                 185                 190

Leu Asp Gly Leu Glu Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly
```

195 200 205

Gly Val Val Leu Val Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val
210 215 220

Thr Thr Val Leu Glu Leu Asp Leu His Gln Asn Ser His His Val Tyr
225 230 235 240

Gly Gly Gly Tyr Asp Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln
245 250 255

His Ala Arg Asp Gln Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu
260 265 270

Val Ala Arg Ala Arg Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg
275 280 285

Asn Ala Ile Lys Arg Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala
290 295 300

Ala Ala Glu Ser Ser Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu
305 310 315 320

Ser Arg Ile Ala Arg Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp
325 330 335

Lys Leu Gln Phe Ser Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val
340 345 350

Ser Thr Leu Asn Asp Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly
355 360 365

Pro Val Ser Ile Gln Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly
370 375 380

Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn
385 390 395 400

Gln Glu Pro Thr Ser Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile
405 410 415

Gly Glu Ile Asp Gln Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu
420 425 430

Ile Ser Ala Phe Glu Lys His Val Pro Asp Leu Pro Ile Ser Glu Val
435 440 445

Arg Thr Leu Leu Ala Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg
450 455 460

Asp Val Glu Lys Leu Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala
465 470 475 480

Leu Leu Gln Val Arg Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr
485 490 495

Asn His Leu Asp Leu Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala
500 505 510

Ser Tyr Asp Gly Val Leu Leu Leu Val Thr His Asp Arg Arg Met Leu
515 520 525

09-15-05 15:39:39

Asp Ala Val Gln Thr Asn Arg Arg Trp His Val Glu Ala Gly Glu Val
530 535 540

Arg Glu Leu
545

<210> 87
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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(958)
<223> RXA01185

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catagccgcc gacacgtgaa tcgaaagaag ttcatctccg atg act gat cct gaa 115
Met Thr Asp Pro Glu
1 5

aac tcg caa gga acc cca cag att tgt ccg act gat ccg act acg caa 163
Asn Ser Gln Gly Thr Pro Gln Ile Cys Pro Thr Asp Pro Thr Thr Gln
10 15 20

gca tta gca gtt cgg ggc tta acc aag tcc tat ggt gat gca aca gta 211
Ala Leu Ala Val Arg Gly Leu Thr Lys Ser Tyr Gly Asp Ala Thr Val
25 30 35

gtg aac aat atc aat ctg gac atc ccc aaa gga gcc att tac ggc atc 259
Val Asn Asn Ile Asn Leu Asp Ile Pro Lys Gly Ala Ile Tyr Gly Ile
40 45 50

gtt gga cct aat ggt gca ggt aaa acc acc atg ctg tcc atg gca acg 307
Val Gly Pro Asn Gly Ala Gly Lys Thr Thr Met Leu Ser Met Ala Thr
55 60 65

ggt tta ctg agg ccg aat aaa ggc acc gcg tgg att tcg ggt ttc aat 355
Gly Leu Leu Arg Pro Asn Lys Gly Thr Ala Trp Ile Ser Gly Phe Asn
70 75 80 85

gtg tgg gaa gag cca aac gat gca aaa cga agc atg gga ttg ttg gca 403
Val Trp Glu Glu Pro Asn Asp Ala Lys Arg Ser Met Gly Leu Leu Ala
90 95 100

gat ggc ttg ccc atc ttt gat cgc ttg act ggc aaa gaa ctg ctc aca 451
Asp Gly Leu Pro Ile Phe Asp Arg Leu Thr Gly Lys Glu Leu Leu Thr
105 110 115

tat gtc ggg gca ttg cgt gag ttg gat gaa ggc att gtt gat caa cgt 499
Tyr Val Gly Ala Leu Arg Glu Leu Asp Glu Gly Ile Val Asp Gln Arg
120 125 130

agt gag gaa ttg ctg gag gcc ctc ggg ctt aaa gaa gca gcg ggc aag 547
Ser Glu Glu Leu Leu Glu Ala Leu Gly Leu Lys Glu Ala Ala Gly Lys
135 140 145

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aga gtc gtc gac tat tcc gcc ggc atg acg aag aag att ctt ttg gcc   595
Arg Val Val Asp Tyr Ser Ala Gly Met Thr Lys Lys Ile Leu Leu Ala
150                 155                 160                 165

cag gcc ctc att cac aat ccg aaa gtg ctc atc ctt gat gaa cct ttg   643
Gln Ala Leu Ile His Asn Pro Lys Val Leu Ile Leu Asp Glu Pro Leu
                170                 175                 180

gaa gcg gtt gat ccg gtg tct ggt cgt ttg att cag cag att ttg aag   691
Glu Ala Val Asp Pro Val Ser Gly Arg Leu Ile Gln Gln Ile Leu Lys
            185                 190                 195

aac ttt gcg caa acg ggt gga acc gtc gtt ttg agt tcg cat gtc atg   739
Asn Phe Ala Gln Thr Gly Gly Thr Val Val Leu Ser Ser His Val Met
        200                 205                 210

gaa ttg gtt gag ggg ttg tgc gat cac gtt gcc atc atc aac agg gga   787
Glu Leu Val Glu Gly Leu Cys Asp His Val Ala Ile Ile Asn Arg Gly
    215                 220                 225

gtg gtg gag att gcc gga cat gtg aat gag gtt cgt cgg ggc aga tct   835
Val Val Glu Ile Ala Gly His Val Asn Glu Val Arg Arg Gly Arg Ser
230                 235                 240                 245

tac cgg atg tct tcg tta atg cgg ttg aag gcg ctg ctc ttc aag agg   883
Tyr Arg Met Ser Ser Leu Met Arg Leu Lys Ala Leu Leu Phe Lys Arg
                250                 255                 260

ggt cac tat ctt ggt tgg gtg cgt ccg aag gcc ata gcg aag gcc aaa   931
Gly His Tyr Leu Gly Trp Val Arg Pro Lys Ala Ile Ala Lys Ala Lys
            265                 270                 275

atc aga acg agg atc ggg ctg agt aaa tgactaaaac acttctgaaa         978
Ile Arg Thr Arg Ile Gly Leu Ser Lys
        280                 285

cta                                                               981
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US-10-624-099-88

<200> 88
<211> 286
<212> PRT
<213> Corynebacterium glutamicum

<400> 88

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Met Thr Asp Pro Glu Asn Ser Gln Gly Thr Pro Gln Ile Cys Pro Thr
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Asp Pro Thr Thr Gln Ala Leu Ala Val Arg Gly Leu Thr Lys Ser Tyr
             20                  25                  30

Gly Asp Ala Thr Val Val Asn Asn Ile Asn Leu Asp Ile Pro Lys Gly
         35                  40                  45

Ala Ile Tyr Gly Ile Val Gly Pro Asn Gly Ala Gly Lys Thr Thr Met
     50                  55                  60

Leu Ser Met Ala Thr Gly Leu Leu Arg Pro Asn Lys Gly Thr Ala Trp
 65                  70                  75                  80

Ile Ser Gly Phe Asn Val Trp Glu Glu Pro Asn Asp Ala Lys Arg Ser
```

```
                  85                  90                  95

Met Gly Leu Leu Ala Asp Gly Leu Pro Ile Phe Asp Arg Leu Thr Gly
            100                 105                 110

Lys Glu Leu Leu Thr Tyr Val Gly Ala Leu Arg Glu Leu Asp Glu Gly
        115                 120                 125

Ile Val Asp Gln Arg Ser Glu Glu Leu Leu Glu Ala Leu Gly Leu Lys
    130                 135                 140

Glu Ala Ala Gly Lys Arg Val Val Asp Tyr Ser Ala Gly Met Thr Lys
145                 150                 155                 160

Lys Ile Leu Leu Ala Gln Ala Leu Ile His Asn Pro Lys Val Leu Ile
                165                 170                 175

Leu Asp Glu Pro Leu Glu Ala Val Asp Pro Val Ser Gly Arg Leu Ile
            180                 185                 190

Gln Gln Ile Leu Lys Asn Phe Ala Gln Thr Gly Gly Thr Val Val Leu
        195                 200                 205

Ser Ser His Val Met Glu Leu Val Glu Gly Leu Cys Asp His Val Ala
    210                 215                 220

Ile Ile Asn Arg Gly Val Val Glu Ile Ala Gly His Val Asn Glu Val
225                 230                 235                 240

Arg Arg Gly Arg Ser Tyr Arg Met Ser Ser Leu Met Arg Leu Lys Ala
                245                 250                 255

Leu Leu Phe Lys Arg Gly His Tyr Leu Gly Trp Val Arg Pro Lys Ala
            260                 265                 270

Ile Ala Lys Ala Lys Ile Arg Thr Arg Ile Gly Leu Ser Lys
        275                 280                 285
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<210> 89
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1180)
<223> RXN00412

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cttttgtccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg 115
                                              Val Ser His Thr Ala
                                                1               5

tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163
Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln
                  10                  15                  20

ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat 211

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Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn
            25                  30                  35

aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa   259
Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu
        40                  45                  50

ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc ggc aag tcc   307
Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser
    55                  60                  65

act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg   355
Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser
70                  75                  80                  85

ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg   403
Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu
                90                  95                  100

cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg   451
Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu
            105                 110                 115

ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt   499
Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val
        120                 125                 130

gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc   547
Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu
    135                 140                 145

gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg   595
Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu
150                 155                 160                 165

tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc   643
Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr
                170                 175                 180

aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca   691
Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro
            185                 190                 195

gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa   739
Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu
        200                 205                 210

ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt   787
Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg
    215                 220                 225

tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa   835
Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu
230                 235                 240                 245

tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct   883
Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala
                250                 255                 260

caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa   931
Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu
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            265                 270                 275

tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg   979
Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu
        280                 285                 290

act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa   1027
Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln
    295                 300                 305

ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc   1075
Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg
310                 315                 320                 325

caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg   1123
Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala
                330                 335                 340

att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag   1171
Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu
            345                 350                 355

atc acc cga tgaacgagat gatcctcgca gct                            1203
Ile Thr Arg
        360
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<210> 90
<211> 360
<212> PRT
<213> Corynebacterium glutamicum

<400> 90

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Val Ser His Thr Ala Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln
  1               5                  10                  15

Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys
             20                  25                  30

Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val
         35                  40                  45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser
     50                  55                  60

Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser
 65                  70                  75                  80

Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met
                 85                  90                  95

Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe
            100                 105                 110

Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu
        115                 120                 125

Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg
    130                 135                 140

Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn
```

145 150 155 160

Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala
165 170 175

Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr
180 185 190

Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg
195 200 205

Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu
210 215 220

Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser
225 230 235 240

Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro
245 250 255

Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr
260 265 270

Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu
275 280 285

Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala
290 295 300

Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val
305 310 315 320

Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr
325 330 335

Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr
340 345 350

Thr Thr Ile Lys Glu Ile Thr Arg
355 360

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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<223> FRXA00412

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cttttgtccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg 115
Val Ser His Thr Ala
1 5

tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163
Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln

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                    10                  15                  20

ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat   211
Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn
            25                  30                  35

aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa   259
Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu
        40                  45                  50

ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc ggc aag tcc   307
Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser
    55                  60                  65

act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg   355
Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser
70                  75                  80                  85

ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg   403
Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu
                90                  95                  100

cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg   451
Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu
            105                 110                 115

ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt   499
Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val
        120                 125                 130

gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc   547
Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu
    135                 140                 145

gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg   595
Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu
150                 155                 160                 165

tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc   643
Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr
                170                 175                 180

aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca   691
Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro
            185                 190                 195

gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa   739
Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu
        200                 205                 210

ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt   787
Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg
    215                 220                 225

tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa   835
Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu
230                 235                 240                 245

tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct   883
Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala
                250                 255                 260
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```
caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa   931
Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu
            265                 270                 275

tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg   979
Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu
        280                 285                 290

act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa   1027
Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln
    295                 300                 305

ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc   1075
Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg
310                 315                 320                 325

caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg   1123
Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala
                330                 335                 340

att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag   1171
Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu
            345                 350                 355

atc acc cga tgaacgagat gatcctcgca gct                            1203
Ile Thr Arg
        360
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<210> 92
<211> 360
<212> PRT
<213> Corynebacterium glutamicum

<400> 92

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Val Ser His Thr Ala Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln
  1               5                  10                  15

Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys
             20                  25                  30

Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val
         35                  40                  45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser
     50                  55                  60

Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser
 65                  70                  75                  80

Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met
                 85                  90                  95

Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe
            100                 105                 110

Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu
        115                 120                 125

Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg
```

```
    130                 135                 140

Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn
145                 150                 155                 160

Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala
                165                 170                 175

Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr
            180                 185                 190

Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg
        195                 200                 205

Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu
    210                 215                 220

Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser
225                 230                 235                 240

Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro
                245                 250                 255

Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr
            260                 265                 270

Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu
        275                 280                 285

Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala
    290                 295                 300

Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val
305                 310                 315                 320

Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr
                325                 330                 335

Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr
            340                 345                 350

Thr Thr Ile Lys Glu Ile Thr Arg
        355                 360
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<210> 93
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(2317)
<223> RXN02925

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catcatctcg accccgaccg ggttgagcgg aaggaacctc atg agc act ccc cac 115
                                    Met Ser Thr Pro His
                                      1               5

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cac cac ggt gat cac ccc gct ccg gaa aca gac cac acc cac cac ccg   163
His His Gly Asp His Pro Ala Pro Glu Thr Asp His Thr His His Pro
                 10                  15                  20

aat cat gcc ggt cac gag cac cat gcg gat gcc gcc acc cac ggc cag   211
Asn His Ala Gly His Glu His His Ala Asp Ala Ala Thr His Gly Gln
             25                  30                  35

gcc atg ccg cac gat cat ccg cat tcc act gtc gat gaa gaa cat cag   259
Ala Met Pro His Asp His Pro His Ser Thr Val Asp Glu Glu His Gln
         40                  45                  50

gtc cac agt cac ggt gaa cac gcc ggc cac agc gcc gcg atg ttc cgg   307
Val His Ser His Gly Glu His Ala Gly His Ser Ala Ala Met Phe Arg
     55                  60                  65

gac cgc ttc tgg tgg tcg ctg atc ctg tcg gtt ccg gtg gtg ttc ttc   355
Asp Arg Phe Trp Trp Ser Leu Ile Leu Ser Val Pro Val Val Phe Phe
 70                  75                  80                  85

agc ccg atg ttc gcc gac ctg ctg gga tat aat att ccg gag att ccg   403
Ser Pro Met Phe Ala Asp Leu Leu Gly Tyr Asn Ile Pro Glu Ile Pro
                 90                  95                 100

gga gcc tac tgg att cct ccg gtc ctg ggc acg atc atc ttc ctc tac   451
Gly Ala Tyr Trp Ile Pro Pro Val Leu Gly Thr Ile Ile Phe Leu Tyr
             105                 110                 115

ggc ggc acc ccc ttc ctc aag ggc gca atg acc gag ctg aaa tcc cgc   499
Gly Gly Thr Pro Phe Leu Lys Gly Ala Met Thr Glu Leu Lys Ser Arg
         120                 125                 130

caa ccg ggc atg atg ctc ctg atc gcc atg gcg atc acc gtg gcg ttt   547
Gln Pro Gly Met Met Leu Leu Ile Ala Met Ala Ile Thr Val Ala Phe
     135                 140                 145

atc gcc tcc tgg gtc acc acc ctg ggg ctg ggc ggg ttc cac cta gat   595
Ile Ala Ser Trp Val Thr Thr Leu Gly Leu Gly Gly Phe His Leu Asp
150                 155                 160                 165

ttc tgg tgg gaa ctg gcc ctg ctg gtg acc atc atg ctg ttg ggc cac   643
Phe Trp Trp Glu Leu Ala Leu Leu Val Thr Ile Met Leu Leu Gly His
                170                 175                 180

tgg ctg gag atg cgc gct ctt ggt gca gcc tcc tcc gcg ctt gac gcg   691
Trp Leu Glu Met Arg Ala Leu Gly Ala Ala Ser Ser Ala Leu Asp Ala
            185                 190                 195

ctg gca gcg ctc ctg ccc gat gag gcc gag aag gtc gtc gac ggg acc   739
Leu Ala Ala Leu Leu Pro Asp Glu Ala Glu Lys Val Val Asp Gly Thr
        200                 205                 210

acc cgc acc gta gcg atc tca gag ctg gcc gtc gac gat gtc gtg ctg   787
Thr Arg Thr Val Ala Ile Ser Glu Leu Ala Val Asp Asp Val Val Leu
    215                 220                 225

gtc cga gca ggt gcc cgc gtc ccg gcc gac ggg acc atc atc gac gga   835
Val Arg Ala Gly Ala Arg Val Pro Ala Asp Gly Thr Ile Ile Asp Gly
230                 235                 240                 245
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CN 1313494 A 20010919

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gcg gcc gaa ttc gat gag gcc atg atc acc ggc gaa tcc cga ccc gtc   883
Ala Ala Glu Phe Asp Glu Ala Met Ile Thr Gly Glu Ser Arg Pro Val
                250                 255                 260

tac cgg gat acc ggt gag acc gtg gtg gcc ggc acc gtg gcc acc gac   931
Tyr Arg Asp Thr Gly Glu Thr Val Val Ala Gly Thr Val Ala Thr Asp
            265                 270                 275

aac acc gtc cgt atc cgg gtg gag gcc acc ggt ggg gac acc gcc ctg   979
Asn Thr Val Arg Ile Arg Val Glu Ala Thr Gly Gly Asp Thr Ala Leu
        280                 285                 290

gca ggc atc cag cgc atg gtc gcc gac gcc cag gcc tcc tcc tcc cgg   1027
Ala Gly Ile Gln Arg Met Val Ala Asp Ala Gln Ala Ser Ser Ser Arg
    295                 300                 305

gcc cag gcc ctg gcc gat cga gcc gca gcc tta ctg ttc tgg ttc gcc   1075
Ala Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu Leu Phe Trp Phe Ala
310                 315                 320                 325

ctg atc acg gcc ctg atc acc gcc gtg gtc tgg acc atc atc ggc agc   1123
Leu Ile Thr Ala Leu Ile Thr Ala Val Val Trp Thr Ile Ile Gly Ser
                330                 335                 340

ccc gac gat gcc gtg gtc cgc gcg gtg acc gtg ctg atc atc gcc tgc   1171
Pro Asp Asp Ala Val Val Arg Ala Val Thr Val Leu Ile Ile Ala Cys
            345                 350                 355

ccg cac gcc ctg ggc ctg gcc atc ccg ctg gtc atc gcg atc tcc tcc   1219
Pro His Ala Leu Gly Leu Ala Ile Pro Leu Val Ile Ala Ile Ser Ser
        360                 365                 370

gag cgc gcc gcg aaa tcc ggg gtg ctc atc aag gac cgc atg gca ctc   1267
Glu Arg Ala Ala Lys Ser Gly Val Leu Ile Lys Asp Arg Met Ala Leu
    375                 380                 385

gag cac atg cgc acc atc gac gtc gtc ttg ttc gat aag acc ggc acc   1315
Glu His Met Arg Thr Ile Asp Val Val Leu Phe Asp Lys Thr Gly Thr
390                 395                 400                 405

ctg acc gaa ggc gca cac gcc gtc acc ggc gtg gct ccg gcc acg ggt   1363
Leu Thr Glu Gly Ala His Ala Val Thr Gly Val Ala Pro Ala Thr Gly
                410                 415                 420

atc gcc gag ggt gag ctg ctg gcc ctg gcc gcc gcc gct gag gcc gat   1411
Ile Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala Ala Ala Glu Ala Asp
            425                 430                 435

agt gag cac ccc gtg gcc cgc gcg atc gtg act gcc gcg gcc gca cac   1459
Ser Glu His Pro Val Ala Arg Ala Ile Val Thr Ala Ala Ala Ala His
        440                 445                 450

ccg gag gcc tcg cag cgt cag ctg cgc gca acc ggt ttc acc gcc gcc   1507
Pro Glu Ala Ser Gln Arg Gln Leu Arg Ala Thr Gly Phe Thr Ala Ala
    455                 460                 465

tcc ggc cgc ggg atc cgg gcc acc gtc gac ggt gcc gaa atc ctc gtg   1555
Ser Gly Arg Gly Ile Arg Ala Thr Val Asp Gly Ala Glu Ile Leu Val
470                 475                 480                 485

ggc ggg ccg aac atg cta cgc gag ttc aat ctg acc acc ccg ggt gag   1603
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US 2005/0153394 A1

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Gly Gly Pro Asn Met Leu Arg Glu Phe Asn Leu Thr Thr Pro Gly Glu
                490                 495                 500

ctc gcc gac atc acc ggt tcc tgg gca cag cga ggt gcc gga gtg cta   1651
Leu Ala Asp Ile Thr Gly Ser Trp Ala Gln Arg Gly Ala Gly Val Leu
            505                 510                 515

cat gtc gtc cgc gac ggt gag atc atc ggt gcg gtg gca gtg gag gac   1699
His Val Val Arg Asp Gly Glu Ile Ile Gly Ala Val Ala Val Glu Asp
        520                 525                 530

aaa atc cgc ccc gaa tcc cgc gcg gcg gta cgc gcc ctg cag gcc cgc   1747
Lys Ile Arg Pro Glu Ser Arg Ala Ala Val Arg Ala Leu Gln Ala Arg
    535                 540                 545

ggg gtg aag gtg gcg atg atc acc ggt gac gcc acc cag gtc gcc cag   1795
Gly Val Lys Val Ala Met Ile Thr Gly Asp Ala Thr Gln Val Ala Gln
550                 555                 560                 565

gca gtg ggc aag gat ctg ggg atc gat gag gtc ttc gcc gag gtt ctg   1843
Ala Val Gly Lys Asp Leu Gly Ile Asp Glu Val Phe Ala Glu Val Leu
                570                 575                 580

ccg cag gac aag gac acc aag gtc acc cag ctg cag gag cgc ggt ctg   1891
Pro Gln Asp Lys Asp Thr Lys Val Thr Gln Leu Gln Glu Arg Gly Leu
            585                 590                 595

agc gtg gcc atg gtc ggc gac ggt gtc aat gac gcc ccg gcc ctg gcc   1939
Ser Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Ala
        600                 605                 610

cgg gcc gag gtc ggt att gcg att ggc gcg ggt aca gat gtg gcg atg   1987
Arg Ala Glu Val Gly Ile Ala Ile Gly Ala Gly Thr Asp Val Ala Met
    615                 620                 625

gag tcc gcc ggg gtg gtc ctg gcc agt gat gat ccc cgg gcc gtg ctg   2035
Glu Ser Ala Gly Val Val Leu Ala Ser Asp Asp Pro Arg Ala Val Leu
630                 635                 640                 645

tcg atg atc gag ctc tcc cat gcc agc tac cgc aag atg gtc cag aac   2083
Ser Met Ile Glu Leu Ser His Ala Ser Tyr Arg Lys Met Val Gln Asn
                650                 655                 660

ctg gtc tgg gcg acc ggg tac aac atc gtg gcc gtt ccg ctg gcc gcc   2131
Leu Val Trp Ala Thr Gly Tyr Asn Ile Val Ala Val Pro Leu Ala Ala
            665                 670                 675

ggt gtg ctc gcc cct atc ggt gtg ctg ctt ccc ccg gcg gcg gcc gcc   2179
Gly Val Leu Ala Pro Ile Gly Val Leu Leu Pro Pro Ala Ala Ala Ala
        680                 685                 690

atc ttg atg tcc ctg tcc acg atc atc gtc gcc ctc aac gcc cag ctg   2227
Ile Leu Met Ser Leu Ser Thr Ile Ile Val Ala Leu Asn Ala Gln Leu
    695                 700                 705

cta cgc cgg atc gac ctg gac ccg gct cac cta gct ccg acc gac ggg   2275
Leu Arg Arg Ile Asp Leu Asp Pro Ala His Leu Ala Pro Thr Asp Gly
710                 715                 720                 725

aag gag gag aag gct gct gtg agc tct gca gcc ccc gtc cgc           2317
Lys Glu Glu Lys Ala Ala Val Ser Ser Ala Ala Pro Val Arg
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730 735

tgactttcaa tgcttcatgg act 2340

<210> 94
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<212> PRT
<213> Corynebacterium glutamicum

<400> 94

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Met Ser Thr Pro His His His Gly Asp His Pro Ala Pro Glu Thr Asp
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His Thr His His Pro Asn His Ala Gly His Glu His His Ala Asp Ala
             20                  25                  30

Ala Thr His Gly Gln Ala Met Pro His Asp His Pro His Ser Thr Val
         35                  40                  45

Asp Glu Glu His Gln Val His Ser His Gly Glu His Ala Gly His Ser
     50                  55                  60

Ala Ala Met Phe Arg Asp Arg Phe Trp Trp Ser Leu Ile Leu Ser Val
 65                  70                  75                  80

Pro Val Val Phe Phe Ser Pro Met Phe Ala Asp Leu Leu Gly Tyr Asn
                 85                  90                  95

Ile Pro Glu Ile Pro Gly Ala Tyr Trp Ile Pro Pro Val Leu Gly Thr
            100                 105                 110

Ile Ile Phe Leu Tyr Gly Gly Thr Pro Phe Leu Lys Gly Ala Met Thr
        115                 120                 125

Glu Leu Lys Ser Arg Gln Pro Gly Met Met Leu Leu Ile Ala Met Ala
    130                 135                 140

Ile Thr Val Ala Phe Ile Ala Ser Trp Val Thr Thr Leu Gly Leu Gly
145                 150                 155                 160

Gly Phe His Leu Asp Phe Trp Trp Glu Leu Ala Leu Leu Val Thr Ile
                165                 170                 175

Met Leu Leu Gly His Trp Leu Glu Met Arg Ala Leu Gly Ala Ala Ser
            180                 185                 190

Ser Ala Leu Asp Ala Leu Ala Ala Leu Leu Pro Asp Glu Ala Glu Lys
        195                 200                 205

Val Val Asp Gly Thr Thr Arg Thr Val Ala Ile Ser Glu Leu Ala Val
    210                 215                 220

Asp Asp Val Val Leu Val Arg Ala Gly Ala Arg Val Pro Ala Asp Gly
225                 230                 235                 240

Thr Ile Ile Asp Gly Ala Ala Glu Phe Asp Glu Ala Met Ile Thr Gly
                245                 250                 255

Glu Ser Arg Pro Val Tyr Arg Asp Thr Gly Glu Thr Val Val Ala Gly
            260                 265                 270
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Thr Val Ala Thr Asp Asn Thr Val Arg Ile Arg Val Glu Ala Thr Gly
275 280 285

Gly Asp Thr Ala Leu Ala Gly Ile Gln Arg Met Val Ala Asp Ala Gln
290 295 300

Ala Ser Ser Ser Arg Ala Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu
305 310 315 320

Leu Phe Trp Phe Ala Leu Ile Thr Ala Leu Ile Thr Ala Val Val Trp
325 330 335

Thr Ile Ile Gly Ser Pro Asp Asp Ala Val Val Arg Ala Val Thr Val
340 345 350

Leu Ile Ile Ala Cys Pro His Ala Leu Gly Leu Ala Ile Pro Leu Val
355 360 365

Ile Ala Ile Ser Ser Glu Arg Ala Ala Lys Ser Gly Val Leu Ile Lys
370 375 380

Asp Arg Met Ala Leu Glu His Met Arg Thr Ile Asp Val Val Leu Phe
385 390 395 400

Asp Lys Thr Gly Thr Leu Thr Glu Gly Ala His Ala Val Thr Gly Val
405 410 415

Ala Pro Ala Thr Gly Ile Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala
420 425 430

Ala Ala Glu Ala Asp Ser Glu His Pro Val Ala Arg Ala Ile Val Thr
435 440 445

Ala Ala Ala Ala His Pro Glu Ala Ser Gln Arg Gln Leu Arg Ala Thr
450 455 460

Gly Phe Thr Ala Ala Ser Gly Arg Gly Ile Arg Ala Thr Val Asp Gly
465 470 475 480

Ala Glu Ile Leu Val Gly Gly Pro Asn Met Leu Arg Glu Phe Asn Leu
485 490 495

Thr Thr Pro Gly Glu Leu Ala Asp Ile Thr Gly Ser Trp Ala Gln Arg
500 505 510

Gly Ala Gly Val Leu His Val Val Arg Asp Gly Glu Ile Ile Gly Ala
515 520 525

Val Ala Val Glu Asp Lys Ile Arg Pro Glu Ser Arg Ala Ala Val Arg
530 535 540

Ala Leu Gln Ala Arg Gly Val Lys Val Ala Met Ile Thr Gly Asp Ala
545 550 555 560

Thr Gln Val Ala Gln Ala Val Gly Lys Asp Leu Gly Ile Asp Glu Val
565 570 575

Phe Ala Glu Val Leu Pro Gln Asp Lys Asp Thr Lys Val Thr Gln Leu
580 585 590

```
Gln Glu Arg Gly Leu Ser Val Ala Met Val Gly Asp Gly Val Asn Asp
        595                 600                 605

Ala Pro Ala Leu Ala Arg Ala Glu Val Gly Ile Ala Ile Gly Ala Gly
    610                 615                 620

Thr Asp Val Ala Met Glu Ser Ala Gly Val Val Leu Ala Ser Asp Asp
625                 630                 635                 640

Pro Arg Ala Val Leu Ser Met Ile Glu Leu Ser His Ala Ser Tyr Arg
                645                 650                 655

Lys Met Val Gln Asn Leu Val Trp Ala Thr Gly Tyr Asn Ile Val Ala
            660                 665                 670

Val Pro Leu Ala Ala Gly Val Leu Ala Pro Ile Gly Val Leu Leu Pro
        675                 680                 685

Pro Ala Ala Ala Ala Ile Leu Met Ser Leu Ser Thr Ile Ile Val Ala
    690                 695                 700

Leu Asn Ala Gln Leu Leu Arg Arg Ile Asp Leu Asp Pro Ala His Leu
705                 710                 715                 720

Ala Pro Thr Asp Gly Lys Glu Glu Lys Ala Ala Val Ser Ser Ala Ala
                725                 730                 735

Pro Val Arg
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09/15/2005 15:39:29 #

<210> 95
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<212> DNA
<213> Corynebacterium glutamicum

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<222> (50)..(1285)
<223> RXN00939

<400> 95

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gaattccacc ctggacaaag atcatcccac cgtgtcgaag acgcccaggatg aca agg  58
                                                        Met Thr Arg
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caa aaa acc cag ccg ttc ctg gag aaa ttc tcg aag tac tac acc ccc  106
Gln Lys Thr Gln Pro Phe Leu Glu Lys Phe Ser Lys Tyr Tyr Thr Pro
      5                  10                  15

ggc gtc atg atc gcc gcc ctg gcc gtc ggc ctg atc acc ctg aac gtt  154
Gly Val Met Ile Ala Ala Leu Ala Val Gly Leu Ile Thr Leu Asn Val
 20                  25                  30                  35

gaa ctg gcc ctg acc ctg ctg gtc atc gcc tgc ccg ggt gcc ctg gtc  202
Glu Leu Ala Leu Thr Leu Leu Val Ile Ala Cys Pro Gly Ala Leu Val
                 40                  45                  50

atc tcg atc ccg gtc tcg atc gtc gcc ggt atc ggc cgc tcc gcc aag  250
Ile Ser Ile Pro Val Ser Ile Val Ala Gly Ile Gly Arg Ser Ala Lys
             55                  60                  65
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```
gac ggc gtc ctg atc aag ggc ggg gaa tac ctg gag acc tcc gcg aag   298
Asp Gly Val Leu Ile Lys Gly Gly Glu Tyr Leu Glu Thr Ser Ala Lys
          70                  75                  80

gtc gac acc gta gtc gtc gac aag acc ggc acc ctg acc aac ggc cgc   346
Val Asp Thr Val Val Val Asp Lys Thr Gly Thr Leu Thr Asn Gly Arg
      85                  90                  95

ccc gag ctg acc aac gtc gac gtc ctt gac ccc gcc tac tcg gac gat   394
Pro Glu Leu Thr Asn Val Asp Val Leu Asp Pro Ala Tyr Ser Asp Asp
100                 105                 110                 115

gag gtg ctc acc ctg gcc gcc cgc gcg gaa acc gcc tcc gag cac ccc   442
Glu Val Leu Thr Leu Ala Ala Arg Ala Glu Thr Ala Ser Glu His Pro
                120                 125                 130

ctg gcc gag gcc atc atc cgc ggc gcg gag aac agg ggc ttg acc gtg   490
Leu Ala Glu Ala Ile Ile Arg Gly Ala Glu Asn Arg Gly Leu Thr Val
            135                 140                 145

gcg atg gta gaa aag gcc gaa ccg gtc gcc ggc cgc ggc atc cgc gct   538
Ala Met Val Glu Lys Ala Glu Pro Val Ala Gly Arg Gly Ile Arg Ala
        150                 155                 160

gac gtg gac ggt gcc acc gtg gcc gtg ggc tca gcc gac ctg ctc gat   586
Asp Val Asp Gly Ala Thr Val Ala Val Gly Ser Ala Asp Leu Leu Asp
    165                 170                 175

cac acc ccg gat aac acc cgc att ctc gag ctc aac gaa cag ggc agg   634
His Thr Pro Asp Asn Thr Arg Ile Leu Glu Leu Asn Glu Gln Gly Arg
180                 185                 190                 195

acc gcc atg tac gtc ggc atc aac ggc aag gcc gtg ggc atc gtc gct   682
Thr Ala Met Tyr Val Gly Ile Asn Gly Lys Ala Val Gly Ile Val Ala
                200                 205                 210

gtg gcc gac acc atc cga gat gat gcc ccg gcc gcg atc agg tcc ctg   730
Val Ala Asp Thr Ile Arg Asp Asp Ala Pro Ala Ala Ile Arg Ser Leu
            215                 220                 225

cac aat aag gga atc cgc gtg gtc atg gcc acc ggt gat gcc gaa cgc   778
His Asn Lys Gly Ile Arg Val Val Met Ala Thr Gly Asp Ala Glu Arg
        230                 235                 240

gtc gcc cgc aac gtc gcc gcc gag ctc ggt gtc gat gag gtg agg gca   826
Val Ala Arg Asn Val Ala Ala Glu Leu Gly Val Asp Glu Val Arg Ala
    245                 250                 255

gaa ctg atg cct gag gac aag ctc gag atc gtc aag gag ctg cag gcg   874
Glu Leu Met Pro Glu Asp Lys Leu Glu Ile Val Lys Glu Leu Gln Ala
260                 265                 270                 275

cag ggc cgg gtc gtg gcc atg gtt ggc gac ggt gtc aat gac acc ccg   922
Gln Gly Arg Val Val Ala Met Val Gly Asp Gly Val Asn Asp Thr Pro
                280                 285                 290

gca ctg gcc acc gcg gac atc ggt gtg gcg atg ggt gcg gcc ggt tcg   970
Ala Leu Ala Thr Ala Asp Ile Gly Val Ala Met Gly Ala Ala Gly Ser
            295                 300                 305
```

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cct gcc gcc atc gag acc gcc gat atc gcc ctg atg gcc gac aag ctg   1018
Pro Ala Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala Asp Lys Leu
        310                 315                 320

ccg cgg ctg ccc tac gcc ctg ggt ctg gcc cag cgc acg gtg cgc acc   1066
Pro Arg Leu Pro Tyr Ala Leu Gly Leu Ala Gln Arg Thr Val Arg Thr
    325                 330                 335

atg cgg gtc aac atc ggc atc gcc ctg ctc act gtc acg atc ctg ctg   1114
Met Arg Val Asn Ile Gly Ile Ala Leu Leu Thr Val Thr Ile Leu Leu
340                 345                 350                 355

gcc ggt gtc ctg ctc ggt gga gtg acc atg tcg att ggc atg ctc gtc   1162
Ala Gly Val Leu Leu Gly Gly Val Thr Met Ser Ile Gly Met Leu Val
                360                 365                 370

cac gag gcc tcc gtc ctg ctg gtc atc gcg att gcg atg ctc ctg ctg   1210
His Glu Ala Ser Val Leu Leu Val Ile Ala Ile Ala Met Leu Leu Leu
            375                 380                 385

cgc ccc acc ctg aag gaa gac aag gac aag gca gac gtc agt act gct   1258
Arg Pro Thr Leu Lys Glu Asp Lys Asp Lys Ala Asp Val Ser Thr Ala
        390                 395                 400

gac gcc gcg aag gag acg ctg agc gcc taacgacaca atcgccacag         1305
Asp Ala Ala Lys Glu Thr Leu Ser Ala
    405                 410

cca                                                               1308


<210> 96
<211> 412
<212> PRT
<213> Corynebacterium glutamicum

<400> 96
Met Thr Arg Gln Lys Thr Gln Pro Phe Leu Glu Lys Phe Ser Lys Tyr
  1               5                  10                  15

Tyr Thr Pro Gly Val Met Ile Ala Ala Leu Ala Val Gly Leu Ile Thr
             20                  25                  30

Leu Asn Val Glu Leu Ala Leu Thr Leu Leu Val Ile Ala Cys Pro Gly
         35                  40                  45

Ala Leu Val Ile Ser Ile Pro Val Ser Ile Val Ala Gly Ile Gly Arg
     50                  55                  60

Ser Ala Lys Asp Gly Val Leu Ile Lys Gly Gly Glu Tyr Leu Glu Thr
 65                  70                  75                  80

Ser Ala Lys Val Asp Thr Val Val Val Asp Lys Thr Gly Thr Leu Thr
                 85                  90                  95

Asn Gly Arg Pro Glu Leu Thr Asn Val Asp Val Leu Asp Pro Ala Tyr
            100                 105                 110

Ser Asp Asp Glu Val Leu Thr Leu Ala Ala Arg Ala Glu Thr Ala Ser
        115                 120                 125
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Glu His Pro Leu Ala Glu Ala Ile Ile Arg Gly Ala Glu Asn Arg Gly
130 135 140

Leu Thr Val Ala Met Val Glu Lys Ala Glu Pro Val Ala Gly Arg Gly
145 150 155 160

Ile Arg Ala Asp Val Asp Gly Ala Thr Val Ala Val Gly Ser Ala Asp
165 170 175

Leu Leu Asp His Thr Pro Asp Asn Thr Arg Ile Leu Glu Leu Asn Glu
180 185 190

Gln Gly Arg Thr Ala Met Tyr Val Gly Ile Asn Gly Lys Ala Val Gly
195 200 205

Ile Val Ala Val Ala Asp Thr Ile Arg Asp Asp Ala Pro Ala Ala Ile
210 215 220

Arg Ser Leu His Asn Lys Gly Ile Arg Val Val Met Ala Thr Gly Asp
225 230 235 240

Ala Glu Arg Val Ala Arg Asn Val Ala Ala Glu Leu Gly Val Asp Glu
245 250 255

Val Arg Ala Glu Leu Met Pro Glu Asp Lys Leu Glu Ile Val Lys Glu
260 265 270

Leu Gln Ala Gln Gly Arg Val Val Ala Met Val Gly Asp Gly Val Asn
275 280 285

Asp Thr Pro Ala Leu Ala Thr Ala Asp Ile Gly Val Ala Met Gly Ala
290 295 300

Ala Gly Ser Pro Ala Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala
305 310 315 320

Asp Lys Leu Pro Arg Leu Pro Tyr Ala Leu Gly Leu Ala Gln Arg Thr
325 330 335

Val Arg Thr Met Arg Val Asn Ile Gly Ile Ala Leu Leu Thr Val Thr
340 345 350

Ile Leu Leu Ala Gly Val Leu Leu Gly Gly Val Thr Met Ser Ile Gly
355 360 365

Met Leu Val His Glu Ala Ser Val Leu Leu Val Ile Ala Ile Ala Met
370 375 380

Leu Leu Leu Arg Pro Thr Leu Lys Glu Asp Lys Asp Lys Ala Asp Val
385 390 395 400

Ser Thr Ala Asp Ala Ala Lys Glu Thr Leu Ser Ala
405 410

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<212> DNA
<213> Corynebacterium glutamicum

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<222> (1)..(168)
<223> FRXA00939

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ggt gtc ctg ctc ggt gga gtg acc atg tcg att ggc atg ctc gtc cac 48
Gly Val Leu Leu Gly Gly Val Thr Met Ser Ile Gly Met Leu Val His
1 5 10 15

gag gcc tcc gtc ctg ctg gtc atc gcg att gcg atg ctc ctg ctg cgc 96
Glu Ala Ser Val Leu Leu Val Ile Ala Ile Ala Met Leu Leu Leu Arg
20 25 30

ccc acc ctg aag gaa gac aag gac aag gca gac gtc agt act gct gac 144
Pro Thr Leu Lys Glu Asp Lys Asp Lys Ala Asp Val Ser Thr Ala Asp
35 40 45

gcc gcg aag gag acg ctg agc gcc taacgacaca atcgccacag cca 191
Ala Ala Lys Glu Thr Leu Ser Ala
50 55

<210> 98
<211> 56
<212> PRT
<213> Corynebacterium glutamicum

<400> 98
Gly Val Leu Leu Gly Gly Val Thr Met Ser Ile Gly Met Leu Val His
1 5 10 15

Glu Ala Ser Val Leu Leu Val Ile Ala Ile Ala Met Leu Leu Leu Arg
20 25 30

Pro Thr Leu Lys Glu Asp Lys Asp Lys Ala Asp Val Ser Thr Ala Asp
35 40 45

Ala Ala Lys Glu Thr Leu Ser Ala
50 55

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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(2365)
<223> RXN01323

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cagtgagtca tgtaaacata ctcgcagaag gagcgatccc atg gct cag aca ccc 115
Met Ala Gln Thr Pro
1 5

gcc aaa atc ccg gcg gca ctg aat ttc att gac gtc gac ctc ggc gtt 163
Ala Lys Ile Pro Ala Ala Leu Asn Phe Ile Asp Val Asp Leu Gly Val
10 15 20

```
acc ggc atg acc tgc act tct tgc tcc gcc cgc gtc gag cgc aaa ctg   211
Thr Gly Met Thr Cys Thr Ser Cys Ser Ala Arg Val Glu Arg Lys Leu
             25                  30                  35

aac aag ctc gac ggc gtt gaa gca acc gtc aac tac gcg acg gaa tcc   259
Asn Lys Leu Asp Gly Val Glu Ala Thr Val Asn Tyr Ala Thr Glu Ser
         40                  45                  50

gca cag gtc agc tac gac ccc tca aag gtc agc cct gaa cag ctg att   307
Ala Gln Val Ser Tyr Asp Pro Ser Lys Val Ser Pro Glu Gln Leu Ile
     55                  60                  65

aag act gtt gag gac acc ggc tac ggt gct ttc acg atg gct tcc gca   355
Lys Thr Val Glu Asp Thr Gly Tyr Gly Ala Phe Thr Met Ala Ser Ala
 70                  75                  80                  85

gct gcc gaa tca gaa gag gac aac gct cca gct gac agc ggc cag tcc   403
Ala Ala Glu Ser Glu Glu Asp Asn Ala Pro Ala Asp Ser Gly Gln Ser
                 90                  95                 100

cgc atc gac gca gct cgc gac cac gaa gca gcc gac ctg aaa cac cgc   451
Arg Ile Asp Ala Ala Arg Asp His Glu Ala Ala Asp Leu Lys His Arg
            105                 110                 115

gtg atc gtc tct gca ctg ttg tca gtt cct gtg gtt ttg gtc agc atg   499
Val Ile Val Ser Ala Leu Leu Ser Val Pro Val Val Leu Val Ser Met
        120                 125                 130

atc ccg gcg ctg caa ttc aac aac tgg cag tgg gcc gta ctc act ttg   547
Ile Pro Ala Leu Gln Phe Asn Asn Trp Gln Trp Ala Val Leu Thr Leu
    135                 140                 145

gtc acc ccg att ttc ttc tgg ggc ggt tca ccg ttc cac aag gca acg   595
Val Thr Pro Ile Phe Phe Trp Gly Gly Ser Pro Phe His Lys Ala Thr
150                 155                 160                 165

tgg gca aac ctg aag cgc ggt tcc ttc acc atg aac acc ctg gtt tca   643
Trp Ala Asn Leu Lys Arg Gly Ser Phe Thr Met Asn Thr Leu Val Ser
                170                 175                 180

ctc ggc acg tcc gct gct gac ctg tgg tcc ctg tgg gct ttg ttc att   691
Leu Gly Thr Ser Ala Ala Asp Leu Trp Ser Leu Trp Ala Leu Phe Ile
            185                 190                 195

gaa aat gct ggt cac cct ggc atg aag atg gag atg cac ctg ctg ccg   739
Glu Asn Ala Gly His Pro Gly Met Lys Met Glu Met His Leu Leu Pro
        200                 205                 210

tcg gcc tcc acg atg gat gag att tac ctc gaa acc gtc gcg gtc gtt   787
Ser Ala Ser Thr Met Asp Glu Ile Tyr Leu Glu Thr Val Ala Val Val
    215                 220                 225

att acg ttc ctg ctg ctt gga cgc tgg ttt gag aca aaa gct aag ggc   835
Ile Thr Phe Leu Leu Leu Gly Arg Trp Phe Glu Thr Lys Ala Lys Gly
230                 235                 240                 245

caa tct tcg gaa gct ctg cgc aag ctg ctg gac atg ggc gcc aaa gat   883
Gln Ser Ser Glu Ala Leu Arg Lys Leu Leu Asp Met Gly Ala Lys Asp
                250                 255                 260
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gca gtc gtc tta cgt gac ggc gcc gaa gtc cgc gtt cct gtg aat cag   931
Ala Val Val Leu Arg Asp Gly Ala Glu Val Arg Val Pro Val Asn Gln
            265                 270                 275

ctt aaa ctc ggc gac gtt ttc atc acc cgc ccc ggc gag aaa atc gcc   979
Leu Lys Leu Gly Asp Val Phe Ile Thr Arg Pro Gly Glu Lys Ile Ala
        280                 285                 290

acc gac ggt gaa gtc gac gaa ggt tcc tcc gca gtc gac gaa tcc atg   1027
Thr Asp Gly Glu Val Asp Glu Gly Ser Ser Ala Val Asp Glu Ser Met
    295                 300                 305

ctc acc ggc gaa tcc atc ccc gtt gaa gtc acc aag ggc tcc aaa gtt   1075
Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr Lys Gly Ser Lys Val
310                 315                 320                 325

acc ggc gca acg ctg aac act tcc ggc cgc ctc atg gtg aaa gta acc   1123
Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu Met Val Lys Val Thr
                330                 335                 340

cgc atc ggc gcc gac acc acc ctg tcg caa atg gct aaa ctg gtc acg   1171
Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met Ala Lys Leu Val Thr
            345                 350                 355

gac gca cag tcc aaa aag gcc cct gtc cag cgt ctt gtt gac caa atc   1219
Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg Leu Val Asp Gln Ile
        360                 365                 370

tcg cag gtt ttc gtt ccc gtt gtc atc gta att gct att gcg acg ctg   1267
Ser Gln Val Phe Val Pro Val Val Ile Val Ile Ala Ile Ala Thr Leu
    375                 380                 385

atc gcg cac ctc gtc ttc acc gac gcc ggc ctc gcc cca gca ttc acc   1315
Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu Ala Pro Ala Phe Thr
390                 395                 400                 405

gca gca gtc gcc gtc ctc att atc gcc tgc cct tgt gcc ctc ggc ctg   1363
Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro Cys Ala Leu Gly Leu
                410                 415                 420

gca acc cca acc gca ctt ctg gtc gga acc ggc cgc ggc gcg caa ctt   1411
Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly Arg Gly Ala Gln Leu
            425                 430                 435

ggt ctg ttg atc aag ggc cct gaa atc ctc gaa tcc acc aaa aaa gtc   1459
Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu Ser Thr Lys Lys Val
        440                 445                 450

gac acc atc gtc ctc gac aaa acc ggc acc gtc acc acc ggc acc atg   1507
Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val Thr Thr Gly Thr Met
    455                 460                 465

tcc gtc acc gac gtc acc gcc atc aac tac agc gaa acc gaa atc ctc   1555
Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser Glu Thr Glu Ile Leu
470                 475                 480                 485

gaa ttc gct gca gcc gtc gag tcc gcc tcc gaa cac ccc atc gcc cag   1603
Glu Phe Ala Ala Ala Val Glu Ser Ala Ser Glu His Pro Ile Ala Gln
                490                 495                 500

gca atc gcc aag gcc gcc gaa cac gag caa gtc acc gac ttc caa aac   1651
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US 2005/0153394 A1

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Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val Thr Asp Phe Gln Asn
            505                 510                 515

acc gca ggt cag gaa gtc acc ggt gta gtc cgc gga cac gag gtc cgc   1699
Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg Gly His Glu Val Arg
        520                 525                 530

gtg ggc agg cct tca agc acg ctt atc gac gcc ctc ctc cac ccc ttc   1747
Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala Leu Leu His Pro Phe
    535                 540                 545

caa cac gcc caa aaa atc ggc gga acc ccc gta gtc gtc acg att gac   1795
Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val Val Val Thr Ile Asp
550                 555                 560                 565

ggc gta gat tcc gga ata atc acg gtc cgc gac acc gtc aaa gac acc   1843
Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp Thr Val Lys Asp Thr
                570                 575                 580

tcc gcc gaa gca atc cgc gga ctc aag gaa ctg gga ctc acc cca atc   1891
Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu Gly Leu Thr Pro Ile
            585                 590                 595

cta ctc acc gga gac aat gaa ggc gca gct aaa tcc gta gcc gct gaa   1939
Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys Ser Val Ala Ala Glu
        600                 605                 610

gtc ggc atc gac caa gtc atc gcc aac gtc ctc ccc cac gaa aaa gtc   1987
Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu Pro His Glu Lys Val
    615                 620                 625

caa aac gta gaa gcc ctc caa gca caa ggc aaa aac gtt gcg atg gtc   2035
Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys Asn Val Ala Met Val
630                 635                 640                 645

ggc gac ggc gtc aac gat gcc gca gct ctt gcc caa gct gac ctc gga   2083
Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala Gln Ala Asp Leu Gly
                650                 655                 660

ctc gcc atg gga gcc ggc acc gac gta gcc atc gaa gcc tcc gac atc   2131
Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile Glu Ala Ser Asp Ile
            665                 670                 675

acc ctc atg aac aac gac ctc cga tcc gca gtc gac gcc atc cga ctg   2179
Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val Asp Ala Ile Arg Leu
        680                 685                 690

tcc cgt aaa acc ctc ggc acc atc aag gga aac ctt ttc tgg gct ttc   2227
Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn Leu Phe Trp Ala Phe
    695                 700                 705

gcc tac aat gtt gca cta atc cca gta gcg gcg atc gga ctc ctc aac   2275
Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala Ile Gly Leu Leu Asn
710                 715                 720                 725

cca atg ctt gcc ggc att gcg atg gcc ttc agt tca gtt ttc gtc gtc   2323
Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser Ser Val Phe Val Val
                730                 735                 740

tcc aat tcc ttg cgt ctg cga gga ttc aaa gca agg agc aac           2365
Ser Asn Ser Leu Arg Leu Arg Gly Phe Lys Ala Arg Ser Asn
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99639130.1:PRO:30-SEP-99

745 750 755

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Val Glu Arg Lys Leu Asn Lys Leu Asp Gly Val Glu Ala Thr Val Asn
         35                  40                  45

Tyr Ala Thr Glu Ser Ala Gln Val Ser Tyr Asp Pro Ser Lys Val Ser
     50                  55                  60

Pro Glu Gln Leu Ile Lys Thr Val Glu Asp Thr Gly Tyr Gly Ala Phe
 65                  70                  75                  80

Thr Met Ala Ser Ala Ala Ala Glu Ser Glu Glu Asp Asn Ala Pro Ala
                 85                  90                  95

Asp Ser Gly Gln Ser Arg Ile Asp Ala Ala Arg Asp His Glu Ala Ala
            100                 105                 110

Asp Leu Lys His Arg Val Ile Val Ser Ala Leu Leu Ser Val Pro Val
        115                 120                 125

Val Leu Val Ser Met Ile Pro Ala Leu Gln Phe Asn Asn Trp Gln Trp
    130                 135                 140

Ala Val Leu Thr Leu Val Thr Pro Ile Phe Phe Trp Gly Gly Ser Pro
145                 150                 155                 160

Phe His Lys Ala Thr Trp Ala Asn Leu Lys Arg Gly Ser Phe Thr Met
                165                 170                 175

Asn Thr Leu Val Ser Leu Gly Thr Ser Ala Ala Asp Leu Trp Ser Leu
            180                 185                 190

Trp Ala Leu Phe Ile Glu Asn Ala Gly His Pro Gly Met Lys Met Glu
        195                 200                 205

Met His Leu Leu Pro Ser Ala Ser Thr Met Asp Glu Ile Tyr Leu Glu
    210                 215                 220

Thr Val Ala Val Val Ile Thr Phe Leu Leu Leu Gly Arg Trp Phe Glu
225                 230                 235                 240

Thr Lys Ala Lys Gly Gln Ser Ser Glu Ala Leu Arg Lys Leu Leu Asp
                245                 250                 255

Met Gly Ala Lys Asp Ala Val Val Leu Arg Asp Gly Ala Glu Val Arg
            260                 265                 270
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Val Pro Val Asn Gln Leu Lys Leu Gly Asp Val Phe Ile Thr Arg Pro
275 280 285

Gly Glu Lys Ile Ala Thr Asp Gly Glu Val Asp Glu Gly Ser Ser Ala
290 295 300

Val Asp Glu Ser Met Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr
305 310 315 320

Lys Gly Ser Lys Val Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu
325 330 335

Met Val Lys Val Thr Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met
340 345 350

Ala Lys Leu Val Thr Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg
355 360 365

Leu Val Asp Gln Ile Ser Gln Val Phe Val Pro Val Val Ile Val Ile
370 375 380

Ala Ile Ala Thr Leu Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu
385 390 395 400

Ala Pro Ala Phe Thr Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro
405 410 415

Cys Ala Leu Gly Leu Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly
420 425 430

Arg Gly Ala Gln Leu Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu
435 440 445

Ser Thr Lys Lys Val Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val
450 455 460

Thr Thr Gly Thr Met Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser
465 470 475 480

Glu Thr Glu Ile Leu Glu Phe Ala Ala Ala Val Glu Ser Ala Ser Glu
485 490 495

His Pro Ile Ala Gln Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val
500 505 510

Thr Asp Phe Gln Asn Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg
515 520 525

Gly His Glu Val Arg Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala
530 535 540

Leu Leu His Pro Phe Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val
545 550 555 560

Val Val Thr Ile Asp Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp
565 570 575

Thr Val Lys Asp Thr Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu
580 585 590

Gly Leu Thr Pro Ile Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys
595 600 605

Ser Val Ala Ala Glu Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu
610 615 620

Pro His Glu Lys Val Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys
625 630 635 640

Asn Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala
645 650 655

Gln Ala Asp Leu Gly Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile
660 665 670

Glu Ala Ser Asp Ile Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val
675 680 685

Asp Ala Ile Arg Leu Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn
690 695 700

Leu Phe Trp Ala Phe Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala
705 710 715 720

Ile Gly Leu Leu Asn Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser
725 730 735

Ser Val Phe Val Val Ser Asn Ser Leu Arg Leu Arg Gly Phe Lys Ala
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Arg Ser Asn
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<223> FRXA01323

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Met Ala Gln Thr Pro
1 5

gcc aaa atc ccg gcg gca ctg aat ttc att gac gtc gac ctc ggc gtt 163
Ala Lys Ile Pro Ala Ala Leu Asn Phe Ile Asp Val Asp Leu Gly Val
10 15 20

acc ggc atg acc tgc act tct tgc tcc gcc cgc gtc gag cgc aaa ctg 211
Thr Gly Met Thr Cys Thr Ser Cys Ser Ala Arg Val Glu Arg Lys Leu
25 30 35

aac aag ctc gac ggc gtt gaa gca acc gtc aac tac gcg acg gaa tcc 259
Asn Lys Leu Asp Gly Val Glu Ala Thr Val Asn Tyr Ala Thr Glu Ser

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          40                  45                  50

gca cag gtc agc tac gac ccc tca aag gtc agc cct gaa cag ctg att   307
Ala Gln Val Ser Tyr Asp Pro Ser Lys Val Ser Pro Glu Gln Leu Ile
     55                  60                  65

aag act gtt gag gac acc ggc tac ggt gct ttc acg atg gct tcc gca   355
Lys Thr Val Glu Asp Thr Gly Tyr Gly Ala Phe Thr Met Ala Ser Ala
 70                  75                  80                  85

gct gcc gaa tca gaa gag gac aac gct cca gct gac agc ggc cag tcc   403
Ala Ala Glu Ser Glu Glu Asp Asn Ala Pro Ala Asp Ser Gly Gln Ser
                 90                  95                 100

cgc atc gac gca gct cgc gac cac gaa gca gcc gac ctg aaa cac cgc   451
Arg Ile Asp Ala Ala Arg Asp His Glu Ala Ala Asp Leu Lys His Arg
            105                 110                 115

gtg atc gtc tct gca ctg ttg tca gtt cct gtg gtt ttg gtc agc atg   499
Val Ile Val Ser Ala Leu Leu Ser Val Pro Val Val Leu Val Ser Met
        120                 125                 130

atc ccg gcg ctg caa ttc aac aac tgg cag tgg gcc gta ctc act ttg   547
Ile Pro Ala Leu Gln Phe Asn Asn Trp Gln Trp Ala Val Leu Thr Leu
    135                 140                 145

gtc acc ccg att ttc ttc tgg ggc ggt tca ccg ttc cac aag gca acg   595
Val Thr Pro Ile Phe Phe Trp Gly Gly Ser Pro Phe His Lys Ala Thr
150                 155                 160                 165

tgg gca aac ctg aag cgc ggt tcc ttc acc atg aac acc ctg gtt tca   643
Trp Ala Asn Leu Lys Arg Gly Ser Phe Thr Met Asn Thr Leu Val Ser
                170                 175                 180

ctc ggc acg tcc gct gct gac ctg tgg tcc ctg tgg gct ttg ttc att   691
Leu Gly Thr Ser Ala Ala Asp Leu Trp Ser Leu Trp Ala Leu Phe Ile
            185                 190                 195

gaa aat gct ggt cac cct ggc atg aag atg gag atg cac ctg ctg ccg   739
Glu Asn Ala Gly His Pro Gly Met Lys Met Glu Met His Leu Leu Pro
        200                 205                 210

tcg gcc tcc acg atg gat gag att tac ctc gaa acc gtc gcg gtc gtt   787
Ser Ala Ser Thr Met Asp Glu Ile Tyr Leu Glu Thr Val Ala Val Val
    215                 220                 225

att acg ttc ctg ctg ctt gga cgc tgg ttt gag aca aaa gct aag ggc   835
Ile Thr Phe Leu Leu Leu Gly Arg Trp Phe Glu Thr Lys Ala Lys Gly
230                 235                 240                 245

caa tct tcg gaa gct ctg cgc aag ctg ctg gac atg ggc gcc aaa gat   883
Gln Ser Ser Glu Ala Leu Arg Lys Leu Leu Asp Met Gly Ala Lys Asp
                250                 255                 260

gca gtc gtc tta cgt gac ggc gcc gaa gtc cgc gtt cct gtg aat cag   931
Ala Val Val Leu Arg Asp Gly Ala Glu Val Arg Val Pro Val Asn Gln
            265                 270                 275

ctt aaa ctc ggc gac gtt ttc atc acc cgc ccc ggc gag aaa atc gcc   979
Leu Lys Leu Gly Asp Val Phe Ile Thr Arg Pro Gly Glu Lys Ile Ala
        280                 285                 290
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acc gac ggt gaa gtc gac gaa ggt tcc tcc gca gtc gac gaa tcc atg   1027
Thr Asp Gly Glu Val Asp Glu Gly Ser Ser Ala Val Asp Glu Ser Met
    295                 300                 305

ctc acc ggc gaa tcc atc ccc gtt gaa gtc acc aag ggc tcc aaa gtt   1075
Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr Lys Gly Ser Lys Val
310                 315                 320                 325

acc ggc gca acg ctg aac act tcc ggc cgc ctc atg gtg aaa gta acc   1123
Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu Met Val Lys Val Thr
                330                 335                 340

cgc atc ggc gcc gac acc acc ctg tcg caa atg gct aaa ctg gtc acg   1171
Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met Ala Lys Leu Val Thr
            345                 350                 355

gac gca cag tcc aaa aag gcc cct gtc cag cgt ctt gtt gac caa atc   1219
Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg Leu Val Asp Gln Ile
        360                 365                 370

tcg cag gtt ttc gtt ccc gtt gtc atc gta att gct att gcg acg ctg   1267
Ser Gln Val Phe Val Pro Val Val Ile Val Ile Ala Ile Ala Thr Leu
    375                 380                 385

atc gcg cac ctc gtc ttc acc gac gcc ggc ctc gcc cca gca ttc acc   1315
Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu Ala Pro Ala Phe Thr
390                 395                 400                 405

gca gca gtc gcc gtc ctc att atc gcc tgc cct tgt gcc ctc ggc ctg   1363
Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro Cys Ala Leu Gly Leu
                410                 415                 420

gca acc cca acc gca ctt ctg gtc gga acc ggc cgc ggc gcg caa ctt   1411
Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly Arg Gly Ala Gln Leu
            425                 430                 435

ggt ctg ttg atc aag ggc cct gaa atc ctc gaa tcc acc aaa aaa gtc   1459
Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu Ser Thr Lys Lys Val
        440                 445                 450

gac acc atc gtc ctc gac aaa acc ggc acc gtc acc acc ggc acc atg   1507
Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val Thr Thr Gly Thr Met
    455                 460                 465

tcc gtc acc gac gtc acc gcc atc aac tac agc gaa acc gaa atc ctc   1555
Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser Glu Thr Glu Ile Leu
470                 475                 480                 485

gaa ttc gct gca gcc gtc gag tcc gcc tcc gaa cac ccc atc gcc cag   1603
Glu Phe Ala Ala Ala Val Glu Ser Ala Ser Glu His Pro Ile Ala Gln
                490                 495                 500

gca atc gcc aag gcc gcc gaa cac gag caa gtc acc gac ttc caa aac   1651
Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val Thr Asp Phe Gln Asn
            505                 510                 515

acc gca ggt cag gaa gtc acc ggt gta gtc cgc gga cac gag gtc cgc   1699
Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg Gly His Glu Val Arg
        520                 525                 530
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gtg ggc agg cct tca agc acg ctt atc gac gcc ctc ctc cac ccc ttc   1747
Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala Leu Leu His Pro Phe
    535                 540                 545

caa cac gcc caa aaa atc ggc gga acc ccc gta gtc gtc acg att gac   1795
Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val Val Val Thr Ile Asp
550                 555                 560                 565

ggc gta gat tcc gga ata atc acg gtc cgc gac acc gtc aaa gac acc   1843
Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp Thr Val Lys Asp Thr
                570                 575                 580

tcc gcc gaa gca atc cgc gga ctc aag gaa ctg gga ctc acc cca atc   1891
Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu Gly Leu Thr Pro Ile
            585                 590                 595

cta ctc acc gga gac aat gaa ggc gca gct aaa tcc gta gcc gct gaa   1939
Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys Ser Val Ala Ala Glu
        600                 605                 610

gtc ggc atc gac caa gtc atc gcc aac gtc ctc ccc cac gaa aaa gtc   1987
Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu Pro His Glu Lys Val
    615                 620                 625

caa aac gta gaa gcc ctc caa gca caa ggc aaa aac gtt gcg atg gtc   2035
Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys Asn Val Ala Met Val
630                 635                 640                 645

ggc gac ggc gtc aac gat gcc gca gct ctt gcc caa gct gac ctc gga   2083
Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala Gln Ala Asp Leu Gly
                650                 655                 660

ctc gcc atg gga gcc ggc acc gac gta gcc atc gaa gcc tcc gac atc   2131
Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile Glu Ala Ser Asp Ile
            665                 670                 675

acc ctc atg aac aac gac ctc cga tcc gca gtc gac gcc atc cga ctg   2179
Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val Asp Ala Ile Arg Leu
        680                 685                 690

tcc cgt aaa acc ctc ggc acc atc aag gga aac ctt ttc tgg gct ttc   2227
Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn Leu Phe Trp Ala Phe
    695                 700                 705

gcc tac aat gtt gca cta atc cca gta gcg gcg atc gga ctc ctc aac   2275
Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala Ile Gly Leu Leu Asn
710                 715                 720                 725

cca atg ctt gcc ggc att gcg atg gcc ttc agt tca gtt ttc gtc gtc   2323
Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser Ser Val Phe Val Val
                730                 735                 740

tcc aat tcc ttg cgt ctg cga gga ttc aaa gca agg agc aac           2365
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            745                 750                 755

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Val Glu Arg Lys Leu Asn Lys Leu Asp Gly Val Glu Ala Thr Val Asn
        35                  40                  45

Tyr Ala Thr Glu Ser Ala Gln Val Ser Tyr Asp Pro Ser Lys Val Ser
    50                  55                  60

Pro Glu Gln Leu Ile Lys Thr Val Glu Asp Thr Gly Tyr Gly Ala Phe
65                  70                  75                  80

Thr Met Ala Ser Ala Ala Ala Glu Ser Glu Glu Asp Asn Ala Pro Ala
                85                  90                  95

Asp Ser Gly Gln Ser Arg Ile Asp Ala Ala Arg Asp His Glu Ala Ala
            100                 105                 110

Asp Leu Lys His Arg Val Ile Val Ser Ala Leu Leu Ser Val Pro Val
        115                 120                 125

Val Leu Val Ser Met Ile Pro Ala Leu Gln Phe Asn Asn Trp Gln Trp
    130                 135                 140

Ala Val Leu Thr Leu Val Thr Pro Ile Phe Phe Trp Gly Gly Ser Pro
145                 150                 155                 160

Phe His Lys Ala Thr Trp Ala Asn Leu Lys Arg Gly Ser Phe Thr Met
                165                 170                 175

Asn Thr Leu Val Ser Leu Gly Thr Ser Ala Ala Asp Leu Trp Ser Leu
            180                 185                 190

Trp Ala Leu Phe Ile Glu Asn Ala Gly His Pro Gly Met Lys Met Glu
        195                 200                 205

Met His Leu Leu Pro Ser Ala Ser Thr Met Asp Glu Ile Tyr Leu Glu
    210                 215                 220

Thr Val Ala Val Val Ile Thr Phe Leu Leu Leu Gly Arg Trp Phe Glu
225                 230                 235                 240

Thr Lys Ala Lys Gly Gln Ser Ser Glu Ala Leu Arg Lys Leu Leu Asp
                245                 250                 255

Met Gly Ala Lys Asp Ala Val Val Leu Arg Asp Gly Ala Glu Val Arg
            260                 265                 270

Val Pro Val Asn Gln Leu Lys Leu Gly Asp Val Phe Ile Thr Arg Pro
        275                 280                 285

Gly Glu Lys Ile Ala Thr Asp Gly Glu Val Asp Glu Gly Ser Ser Ala
    290                 295                 300
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Val Asp Glu Ser Met Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr
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Lys Gly Ser Lys Val Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu
325 330 335

Met Val Lys Val Thr Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met
340 345 350

Ala Lys Leu Val Thr Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg
355 360 365

Leu Val Asp Gln Ile Ser Gln Val Phe Val Pro Val Val Ile Val Ile
370 375 380

Ala Ile Ala Thr Leu Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu
385 390 395 400

Ala Pro Ala Phe Thr Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro
405 410 415

Cys Ala Leu Gly Leu Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly
420 425 430

Arg Gly Ala Gln Leu Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu
435 440 445

Ser Thr Lys Lys Val Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val
450 455 460

Thr Thr Gly Thr Met Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser
465 470 475 480

Glu Thr Glu Ile Leu Glu Phe Ala Ala Ala Val Glu Ser Ala Ser Glu
485 490 495

His Pro Ile Ala Gln Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val
500 505 510

Thr Asp Phe Gln Asn Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg
515 520 525

Gly His Glu Val Arg Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala
530 535 540

Leu Leu His Pro Phe Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val
545 550 555 560

Val Val Thr Ile Asp Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp
565 570 575

Thr Val Lys Asp Thr Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu
580 585 590

Gly Leu Thr Pro Ile Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys
595 600 605

Ser Val Ala Ala Glu Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu
610 615 620

Pro His Glu Lys Val Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys

625 630 635 640

Asn Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala
645 650 655

Gln Ala Asp Leu Gly Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile
660 665 670

Glu Ala Ser Asp Ile Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val
675 680 685

Asp Ala Ile Arg Leu Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn
690 695 700

Leu Phe Trp Ala Phe Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala
705 710 715 720

Ile Gly Leu Leu Asn Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser
725 730 735

Ser Val Phe Val Val Ser Asn Ser Leu Arg Leu Arg Gly Phe Lys Ala
740 745 750

Arg Ser Asn
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<223> RXN00702

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Met Ser Ala Pro Phe
1 5

agc gcg cgc act gcg tgg tcg acg gac ccc gtg ctg gaa ctg gaa agc 163
Ser Ala Arg Thr Ala Trp Ser Thr Asp Pro Val Leu Glu Leu Glu Ser
10 15 20

gtc gct gcc tcg tat tat gac gat gag cgc acg ctg gcg gcg ccg cag 211
Val Ala Ala Ser Tyr Tyr Asp Asp Glu Arg Thr Leu Ala Ala Pro Gln
25 30 35

atc agc gac gtg aat ctg acg ctt ttt gaa ggc gaa atc ctg ctg gtt 259
Ile Ser Asp Val Asn Leu Thr Leu Phe Glu Gly Glu Ile Leu Leu Val
40 45 50

gtg ggg cgc acc ggc tcc ggc aaa tcg acg ctg ctg aac gcg atg tcc 307
Val Gly Arg Thr Gly Ser Gly Lys Ser Thr Leu Leu Asn Ala Met Ser
55 60 65

ggc gcg atg ccg cat gcg acc ggc ggc cga ctt gat ggg cgc gtg cgc 355

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Gly Ala Met Pro His Ala Thr Gly Gly Arg Leu Asp Gly Arg Val Arg
 70                  75                  80                  85

gtg gtc ggc cgg gat acg cgt gat ttc cca cca cgc atg ctt tcc gac   403
Val Val Gly Arg Asp Thr Arg Asp Phe Pro Pro Arg Met Leu Ser Asp
                90                  95                 100

gtg gtc ggc gtc gtt ggg caa gat ccg gcg gca agt ttt atc acc aac   451
Val Val Gly Val Val Gly Gln Asp Pro Ala Ala Ser Phe Ile Thr Asn
            105                 110                 115

acg gtt gaa gaa gaa ctt gcc tac agc atg gag caa tta ggg ctc cca   499
Thr Val Glu Glu Glu Leu Ala Tyr Ser Met Glu Gln Leu Gly Leu Pro
        120                 125                 130

cct gcg gtc atg cgc aag cgc gta gag gaa acc ctt gat ctt tta ggc   547
Pro Ala Val Met Arg Lys Arg Val Glu Glu Thr Leu Asp Leu Leu Gly
    135                 140                 145

atc gcg gag ctg cga tac gtg cca ttg gcg gaa cta tct ggt ggt gag   595
Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu Leu Ser Gly Gly Glu
150                 155                 160                 165

cag cag cgc gtg gcg att ggc gcg gtg ctg acc act cgc ccc gcg ctg   643
Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr Thr Arg Pro Ala Leu
                170                 175                 180

att atc ttg gat gaa cca acc agc gct ttg gac cct aat ggt gcc gag   691
Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro Asn Gly Ala Glu
            185                 190                 195

gat gtg ctg gca acc gta acc aag ctg gct cat gac ttg gcg atg acc   739
Asp Val Leu Ala Thr Val Thr Lys Leu Ala His Asp Leu Ala Met Thr
        200                 205                 210

gta gtg ctt gct gaa cac cgc atc gag cgc gta ctg cag tac gtg gac   787
Val Val Leu Ala Glu His Arg Ile Glu Arg Val Leu Gln Tyr Val Asp
    215                 220                 225

cgc gtg gcg cat gtg ggc gct gat ggg cac gtc act gtt ggg acg ccg   835
Arg Val Ala His Val Gly Ala Asp Gly His Val Thr Val Gly Thr Pro
230                 235                 240                 245

gaa gaa atc atg gct gat tct gat gtg gca cca ccc att gtg gaa tta   883
Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro Pro Ile Val Glu Leu
                250                 255                 260

gga cgc tgg gct ggc tgg gct ccc cta ccg cta tcg atc cgc gat gca   931
Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu Ser Ile Arg Asp Ala
            265                 270                 275

cgc gca cac tcc gct gac atg cgc aaa cgc ctg tat cag cgt ggt tta   979
Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu Tyr Gln Arg Gly Leu
        280                 285                 290

gtg gtg aac aaa tta cac aac cac gct gtc cag cca ctt ttg atc gcc   1027
Val Val Asn Lys Leu His Asn His Ala Val Gln Pro Leu Leu Ile Ala
    295                 300                 305

gaa gat atc atg gtt gat ttc ccc gaa atc cgt gcc gtt gac ggc gtg   1075
Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg Ala Val Asp Gly Val
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310 315 320 325

aac ttg aat ctc aac tcc ggt gaa att acc gtg ctc atg ggc cga aac 1123
Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val Leu Met Gly Arg Asn
330 335 340

ggc tgc gga aaa tca tcc ctg ctg tgg gct tta caa ggt tca ggg act 1171
Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu Gln Gly Ser Gly Thr
345 350 355

aga aat cag ggc tcg gtg cag gtg ctt gat gag gcc gcg gga ttt tcg 1219
Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu Ala Ala Gly Phe Ser
360 365 370

tgg aca gac ccc aaa act tta aag ccc gcc aag cgg cgc aat ctt gtg 1267
Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys Arg Arg Asn Leu Val
375 380 385

tcc atg gtt ccg caa aca ccg acc gat att ttg tat gaa tca acc gtg 1315
Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu Tyr Glu Ser Thr Val
390 395 400 405

cat gca gag ctc gca cgc tct gat aaa gat gcc gca gca ccc gcc ggc 1363
His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala Ala Ala Pro Ala Gly
410 415 420

acc acg cgg gaa atc ctg gat tca ctg gtc ccg aat atc ccg gac cat 1411
Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro Asn Ile Pro Asp His
425 430 435

ctc cac cca cgt gat cta tca gaa ggc caa aag ctc tcc ctc gcg ctg 1459
Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys Leu Ser Leu Ala Leu
440 445 450

tcc atc caa ctc gcc gca aaa ccc cgc gtg gta ttt ttc gac gaa ccc 1507
Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val Phe Phe Asp Glu Pro
455 460 465

acc cgc ggc cta gac tac gac ggc aag aaa tcc ctc gcc cgc tcc ttc 1555
Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser Leu Ala Arg Ser Phe
470 475 480 485

caa caa ctc gca gac gac ggc cac gcc att ttg gtg gtc acc cac gac 1603
Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu Val Val Thr His Asp
490 495 500

gtg gaa ttc tct gca ctg tgc gcc gac cga gtg ttg ttt atg gcc tct 1651
Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val Leu Phe Met Ala Ser
505 510 515

gga aag atc atc tcc gat ggc aca gcc gta gaa atc ctc ccc gca tca 1699
Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile Leu Pro Ala Ser
520 525 530

ccg gct tac gcc cca caa gtc gca aaa atc acc gcc ggc atc caa gag 1747
Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala Gly Ile Gln Glu
535 540 545

gaa tca cac tgg ctc aca gtc tcg gcc gtg aaa gct gcg cta ggg cat 1795
Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala Ala Leu Gly His
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ggt gaa atc tca tgatcaacgc catcacactc aag 1830
Gly Glu Ile Ser

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<211> 569
<212> PRT
<213> Corynebacterium glutamicum

<400> 104
Met Ser Ala Pro Phe Ser Ala Arg Thr Ala Trp Ser Thr Asp Pro Val
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Leu Ala Ala Pro Gln Ile Ser Asp Val Asn Leu Thr Leu Phe Glu Gly
35 40 45

Glu Ile Leu Leu Val Val Gly Arg Thr Gly Ser Gly Lys Ser Thr Leu
50 55 60

Leu Asn Ala Met Ser Gly Ala Met Pro His Ala Thr Gly Gly Arg Leu
65 70 75 80

Asp Gly Arg Val Arg Val Val Gly Arg Asp Thr Arg Asp Phe Pro Pro
85 90 95

Arg Met Leu Ser Asp Val Val Gly Val Val Gly Gln Asp Pro Ala Ala
100 105 110

Ser Phe Ile Thr Asn Thr Val Glu Glu Glu Leu Ala Tyr Ser Met Glu
115 120 125

Gln Leu Gly Leu Pro Pro Ala Val Met Arg Lys Arg Val Glu Glu Thr
130 135 140

Leu Asp Leu Leu Gly Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu
145 150 155 160

Leu Ser Gly Gly Glu Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr
165 170 175

Thr Arg Pro Ala Leu Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp
180 185 190

Pro Asn Gly Ala Glu Asp Val Leu Ala Thr Val Thr Lys Leu Ala His
195 200 205

Asp Leu Ala Met Thr Val Val Leu Ala Glu His Arg Ile Glu Arg Val
210 215 220

Leu Gln Tyr Val Asp Arg Val Ala His Val Gly Ala Asp Gly His Val
225 230 235 240

Thr Val Gly Thr Pro Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro
245 250 255

Pro Ile Val Glu Leu Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu

260 265 270

Ser Ile Arg Asp Ala Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu
275 280 285

Tyr Gln Arg Gly Leu Val Val Asn Lys Leu His Asn His Ala Val Gln
290 295 300

Pro Leu Leu Ile Ala Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg
305 310 315 320

Ala Val Asp Gly Val Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val
325 330 335

Leu Met Gly Arg Asn Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu
340 345 350

Gln Gly Ser Gly Thr Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu
355 360 365

Ala Ala Gly Phe Ser Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys
370 375 380

Arg Arg Asn Leu Val Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu
385 390 395 400

Tyr Glu Ser Thr Val His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala
405 410 415

Ala Ala Pro Ala Gly Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro
420 425 430

Asn Ile Pro Asp His Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys
435 440 445

Leu Ser Leu Ala Leu Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val
450 455 460

Phe Phe Asp Glu Pro Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser
465 470 475 480

Leu Ala Arg Ser Phe Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu
485 490 495

Val Val Thr His Asp Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val
500 505 510

Leu Phe Met Ala Ser Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu
515 520 525

Ile Leu Pro Ala Ser Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr
530 535 540

Ala Gly Ile Gln Glu Glu Ser His Trp Leu Thr Val Ser Ala Val Lys
545 550 555 560

Ala Ala Leu Gly His Gly Glu Ile Ser
565

<210> 105

<211> 1343
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1320)
<223> FRXA00702

<400> 105

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Leu Gly Leu Pro Pro Ala Val Met Arg Lys Arg Val Glu Glu Thr Leu
  1               5                  10                  15

gat ctt tta ggc atc gcg gag ctg cga tac gtg cca ttg gcg gaa cta   96
Asp Leu Leu Gly Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu Leu
             20                  25                  30

tct ggt ggt gag cag cag cgc gtg gcg att ggc gcg gtg ctg acc act   144
Ser Gly Gly Glu Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr Thr
         35                  40                  45

cgc ccc gcg ctg att atc ttg gat gaa cca acc agc gct ttg gac cct   192
Arg Pro Ala Leu Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro
     50                  55                  60

aat ggt gcc gag gat gtg ctg gca acc gta acc aag ctg gct cat gac   240
Asn Gly Ala Glu Asp Val Leu Ala Thr Val Thr Lys Leu Ala His Asp
 65                  70                  75                  80

ttg gcg atg acc gta gtg ctt gct gaa cac cgc atc gag cgc gta ctg   288
Leu Ala Met Thr Val Val Leu Ala Glu His Arg Ile Glu Arg Val Leu
                 85                  90                  95

cag tac gtg gac cgc gtg gcg cat gtg ggc gct gat ggg cac gtc act   336
Gln Tyr Val Asp Arg Val Ala His Val Gly Ala Asp Gly His Val Thr
            100                 105                 110

gtt ggg acg ccg gaa gaa atc atg gct gat tct gat gtg gca cca ccc   384
Val Gly Thr Pro Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro Pro
        115                 120                 125

att gtg gaa tta gga cgc tgg gct ggc tgg gct ccc cta ccg cta tcg   432
Ile Val Glu Leu Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu Ser
    130                 135                 140

atc cgc gat gca cgc gca cac tcc gct gac atg cgc aaa cgc ctg tat   480
Ile Arg Asp Ala Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu Tyr
145                 150                 155                 160

cag cgt ggt tta gtg gtg aac aaa tta cac aac cac gct gtc cag cca   528
Gln Arg Gly Leu Val Val Asn Lys Leu His Asn His Ala Val Gln Pro
                165                 170                 175

ctt ttg atc gcc gaa gat atc atg gtt gat ttc ccc gaa atc cgt gcc   576
Leu Leu Ile Ala Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg Ala
            180                 185                 190

gtt gac ggc gtg aac ttg aat ctc aac tcc ggt gaa att acc gtg ctc   624
Val Asp Gly Val Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val Leu
        195                 200                 205
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atg ggc cga aac ggc tgc gga aaa tca tcc ctg ctg tgg gct tta caa   672
Met Gly Arg Asn Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu Gln
    210                 215                 220

ggt tca ggg act aga aat cag ggc tcg gtg cag gtg ctt gat gag gcc   720
Gly Ser Gly Thr Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu Ala
225                 230                 235                 240

gcg gga ttt tcg tgg aca gac ccc aaa act tta aag ccc gcc aag cgg   768
Ala Gly Phe Ser Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys Arg
                245                 250                 255

cgc aat ctt gtg tcc atg gtt ccg caa aca ccg acc gat att ttg tat   816
Arg Asn Leu Val Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu Tyr
            260                 265                 270

gaa tca acc gtg cat gca gag ctc gca cgc tct gat aaa gat gcc gca   864
Glu Ser Thr Val His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala Ala
        275                 280                 285

gca ccc gcc ggc acc acg cgg gaa atc ctg gat tca ctg gtc ccg aat   912
Ala Pro Ala Gly Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro Asn
    290                 295                 300

atc ccg gac cat ctc cac cca cgt gat cta tca gaa ggc caa aag ctc   960
Ile Pro Asp His Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys Leu
305                 310                 315                 320

tcc ctc gcg ctg tcc atc caa ctc gcc gca aaa ccc cgc gtg gta ttt  1008
Ser Leu Ala Leu Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val Phe
                325                 330                 335

ttc gac gaa ccc acc cgc ggc cta gac tac gac ggc aag aaa tcc ctc  1056
Phe Asp Glu Pro Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser Leu
            340                 345                 350

gcc cgc tcc ttc caa caa ctc gca gac gac ggc cac gcc att ttg gtg  1104
Ala Arg Ser Phe Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu Val
        355                 360                 365

gtc acc cac gac gtg gaa ttc tct gca ctg tgc gcc gac cga gtg ttg  1152
Val Thr His Asp Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val Leu
    370                 375                 380

ttt atg gcc tct gga aag atc atc tcc gat ggc aca gcc gta gaa atc  1200
Phe Met Ala Ser Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile
385                 390                 395                 400

ctc ccc gca tca ccg gct tac gcc cca caa gtc gca aaa atc acc gcc  1248
Leu Pro Ala Ser Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala
                405                 410                 415

ggc atc caa gag gaa tca cac tgg ctc aca gtc tcg gcc gtg aaa gct  1296
Gly Ile Gln Glu Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala
            420                 425                 430

gcg cta ggg cat ggt gaa atc tca tgatcaacgc catcacactc aag        1343
Ala Leu Gly His Gly Glu Ile Ser
        435                 440
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CN 1313542 A 20010919

<210> 106
<211> 440
<212> PRT
<213> Corynebacterium glutamicum

<400> 106

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Asp Leu Leu Gly Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu Leu
             20                  25                  30

Ser Gly Gly Glu Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr Thr
         35                  40                  45

Arg Pro Ala Leu Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro
     50                  55                  60

Asn Gly Ala Glu Asp Val Leu Ala Thr Val Thr Lys Leu Ala His Asp
 65                  70                  75                  80

Leu Ala Met Thr Val Val Leu Ala Glu His Arg Ile Glu Arg Val Leu
                 85                  90                  95

Gln Tyr Val Asp Arg Val Ala His Val Gly Ala Asp Gly His Val Thr
            100                 105                 110

Val Gly Thr Pro Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro Pro
        115                 120                 125

Ile Val Glu Leu Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu Ser
    130                 135                 140

Ile Arg Asp Ala Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu Tyr
145                 150                 155                 160

Gln Arg Gly Leu Val Val Asn Lys Leu His Asn His Ala Val Gln Pro
                165                 170                 175

Leu Leu Ile Ala Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg Ala
            180                 185                 190

Val Asp Gly Val Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val Leu
        195                 200                 205

Met Gly Arg Asn Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu Gln
    210                 215                 220

Gly Ser Gly Thr Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu Ala
225                 230                 235                 240

Ala Gly Phe Ser Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys Arg
                245                 250                 255

Arg Asn Leu Val Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu Tyr
            260                 265                 270

Glu Ser Thr Val His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala Ala
        275                 280                 285
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Ala Pro Ala Gly Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro Asn
    290                 295                 300

Ile Pro Asp His Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys Leu
305                 310                 315                 320

Ser Leu Ala Leu Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val Phe
                325                 330                 335

Phe Asp Glu Pro Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser Leu
            340                 345                 350

Ala Arg Ser Phe Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu Val
        355                 360                 365

Val Thr His Asp Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val Leu
    370                 375                 380

Phe Met Ala Ser Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile
385                 390                 395                 400

Leu Pro Ala Ser Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala
                405                 410                 415

Gly Ile Gln Glu Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala
            420                 425                 430

Ala Leu Gly His Gly Glu Ile Ser
        435                 440
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US20050153417A1

<210> 107
<211> 576
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXN00828

<400> 107

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tgcttccgcg aaaagtgggc agctggaact ctctgacacg gtg cgc ggc ggc ctt   115
                                              Val Arg Gly Gly Leu
                                                1               5

aac acg ccc ccg cac aag tgg cgt tca gct gat cta gct gca cgt att   163
Asn Thr Pro Pro His Lys Trp Arg Ser Ala Asp Leu Ala Ala Arg Ile
                10                  15                  20

ggc act gtc ttt cag gat cca gag cac caa ttt gtg gcg cgc act gtg   211
Gly Thr Val Phe Gln Asp Pro Glu His Gln Phe Val Ala Arg Thr Val
            25                  30                  35

cgt gat gag cta gaa att ggg ccg aaa atc atg aaa gtc gat gca agc   259
Arg Asp Glu Leu Glu Ile Gly Pro Lys Ile Met Lys Val Asp Ala Ser
        40                  45                  50

gag cgc atc gag gag ctg ctt gat cgt ttg cgc ctc cgc cac ttg gaa   307
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Glu Arg Ile Glu Glu Leu Leu Asp Arg Leu Arg Leu Arg His Leu Glu
     55                  60                  65

aac gcc aat ccg ttt acc ttg agt ggt gga gaa aag cgc cgc cta tct   355
Asn Ala Asn Pro Phe Thr Leu Ser Gly Gly Glu Lys Arg Arg Leu Ser
 70                  75                  80                  85

gtg gcg aca gcc ttg gtg gca gca ccg aaa ctt ctc att ttg gat gag   403
Val Ala Thr Ala Leu Val Ala Ala Pro Lys Leu Leu Ile Leu Asp Glu
                 90                  95                 100

cct acg ttt ggc caa gat ccc gag acc ttc aca gag ctg gtg acg atg   451
Pro Thr Phe Gly Gln Asp Pro Glu Thr Phe Thr Glu Leu Val Thr Met
            105                 110                 115

ttg cgt gaa tta aca gac aac gga atc agc att gtg tcg gta acc cat   499
Leu Arg Glu Leu Thr Asp Asn Gly Ile Ser Ile Val Ser Val Thr His
        120                 125                 130

gat cct gat ttc atc gca gcg ctg ggc gat cac cac att gag gtg agc   547
Asp Pro Asp Phe Ile Ala Ala Leu Gly Asp His His Ile Glu Val Ser
    135                 140                 145

gcg aag tgaacctgct gatcaaaatt aat                                 576
Ala Lys
150
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<210> 108
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 108

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Leu Ala Ala Arg Ile Gly Thr Val Phe Gln Asp Pro Glu His Gln Phe
             20                  25                  30

Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly Pro Lys Ile Met
         35                  40                  45

Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu Asp Arg Leu Arg
     50                  55                  60

Leu Arg His Leu Glu Asn Ala Asn Pro Phe Thr Leu Ser Gly Gly Glu
 65                  70                  75                  80

Lys Arg Arg Leu Ser Val Ala Thr Ala Leu Val Ala Ala Pro Lys Leu
                 85                  90                  95

Leu Ile Leu Asp Glu Pro Thr Phe Gly Gln Asp Pro Glu Thr Phe Thr
            100                 105                 110

Glu Leu Val Thr Met Leu Arg Glu Leu Thr Asp Asn Gly Ile Ser Ile
        115                 120                 125

Val Ser Val Thr His Asp Pro Asp Phe Ile Ala Ala Leu Gly Asp His
    130                 135                 140
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His Ile Glu Val Ser Ala Lys
145                 150


<210> 109
<211> 392
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (1)..(369)
<223> FRXA00828

<400> 109
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Glu His Gln Phe Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly
  1               5                  10                  15

ccg aaa atc atg aaa gtt gat gca agc gag cgc atc gag gag ttg ctt   96
Pro Lys Ile Met Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu
             20                  25                  30

gat cgg ttg cgc ctc cgc cac tta gaa aat gct aat ccg ttt acc ttg   144
Asp Arg Leu Arg Leu Arg His Leu Glu Asn Ala Asn Pro Phe Thr Leu
         35                  40                  45

agt ggt gga gaa aag cgc cgc cta tct gtg gcg aca gcc ttg gtg gca   192
Ser Gly Gly Glu Lys Arg Arg Leu Ser Val Ala Thr Ala Leu Val Ala
     50                  55                  60

gca ccg aaa ctt ctc att ttg gat gag cct acg ttt ggc caa gat ccc   240
Ala Pro Lys Leu Leu Ile Leu Asp Glu Pro Thr Phe Gly Gln Asp Pro
 65                  70                  75                  80

gag acc ttc aca gag ctg gtg acg atg ttg cgt gaa tta aca gac aac   288
Glu Thr Phe Thr Glu Leu Val Thr Met Leu Arg Glu Leu Thr Asp Asn
                 85                  90                  95

gga atc agc att gtg tca gta acc cat gat cct gat ttc atc gca gcg   336
Gly Ile Ser Ile Val Ser Val Thr His Asp Pro Asp Phe Ile Ala Ala
            100                 105                 110

ctg ggc gat cac cac att gag gtg agc gcg aag tgaacctgct gatcaaaatt 389
Leu Gly Asp His His Ile Glu Val Ser Ala Lys
        115                 120

aat                                                               392


<210> 110
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 110
Glu His Gln Phe Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly
  1               5                  10                  15

Pro Lys Ile Met Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu
             20                  25                  30
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Asp Arg Leu Arg Leu Arg His Leu Glu Asn Ala Asn Pro Phe Thr Leu
35 40 45

Ser Gly Gly Glu Lys Arg Arg Leu Ser Val Ala Thr Ala Leu Val Ala
50 55 60

Ala Pro Lys Leu Leu Ile Leu Asp Glu Pro Thr Phe Gly Gln Asp Pro
65 70 75 80

Glu Thr Phe Thr Glu Leu Val Thr Met Leu Arg Glu Leu Thr Asp Asn
85 90 95

Gly Ile Ser Ile Val Ser Val Thr His Asp Pro Asp Phe Ile Ala Ala
100 105 110

Leu Gly Asp His His Ile Glu Val Ser Ala Lys
115 120

<210> 111
<211> 703
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(703)
<223> RXN03020

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acgctccgca ctcatgaacg cataagaaaa ggaacctcac atg act ctc cac gtt 115
Met Thr Leu His Val
1 5

tca aat ctc aat ctg acc gtc gcc gac gga tcc acc tca cgc acc ctg 163
Ser Asn Leu Asn Leu Thr Val Ala Asp Gly Ser Thr Ser Arg Thr Leu
10 15 20

ctc aac aac ata cac ttt tgg atg tcc aac cag gcg aag tcg tcg gta 211
Leu Asn Asn Ile His Phe Trp Met Ser Asn Gln Ala Lys Ser Ser Val
25 30 35

tca ccg gcc cat ccg gct ccg gaa aat cca ccc tac tcg ccg tcc tcg 259
Ser Pro Ala His Pro Ala Pro Glu Asn Pro Pro Tyr Ser Pro Ser Ser
40 45 50

gct gcc tcc aaa gcg ccc gat tcc ggc acc gcg acg ctc ggc gac atc 307
Ala Ala Ser Lys Ala Pro Asp Ser Gly Thr Ala Thr Leu Gly Asp Ile
55 60 65

gac ctg ctc aac ccc caa aac cga gct gct tta cga cgc aac cac cta 355
Asp Leu Leu Asn Pro Gln Asn Arg Ala Ala Leu Arg Arg Asn His Leu
70 75 80 85

gga att gtc ttc caa cag cca aac ctg ctc ccc tcg ttg act gtc ctc 403
Gly Ile Val Phe Gln Gln Pro Asn Leu Leu Pro Ser Leu Thr Val Leu
90 95 100

US08435756

```
gac caa ctg ctg ctc att ccc cgg ctc ggc agg atc ctc ccg ccc agc   451
Asp Gln Leu Leu Leu Ile Pro Arg Leu Gly Arg Ile Leu Pro Pro Ser
            105                 110                 115

cgc agc gca cgc acc caa cac aaa gac aaa gcc ctt tca ctt ctg aac   499
Arg Ser Ala Arg Thr Gln His Lys Asp Lys Ala Leu Ser Leu Leu Asn
        120                 125                 130

tcc atc gga ctc ggc gac tta gca aaa cgc aag gtc agc gaa cta tcc   547
Ser Ile Gly Leu Gly Asp Leu Ala Lys Arg Lys Val Ser Glu Leu Ser
    135                 140                 145

ggt gga caa caa gcc cgc gtt aac ttg gcc cgc gcg ctg atg aac tcc   595
Gly Gly Gln Gln Ala Arg Val Asn Leu Ala Arg Ala Leu Met Asn Ser
150                 155                 160                 165

ccc aag ctc ctg ctt gtc gat gaa ccc acc gcc gcc ctc gat caa cat   643
Pro Lys Leu Leu Leu Val Asp Glu Pro Thr Ala Ala Leu Asp Gln His
                170                 175                 180

tcc gcc agc gaa gtc acc gaa cta atc gtc tcg atg gcc cac caa tac   691
Ser Ala Ser Glu Val Thr Glu Leu Ile Val Ser Met Ala His Gln Tyr
            185                 190                 195

aac gcc ccc aca                                                  703
Asn Ala Pro Thr
        200
```

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<210> 112
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 112

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Met Thr Leu His Val Ser Asn Leu Asn Leu Thr Val Ala Asp Gly Ser
  1               5                  10                  15

Thr Ser Arg Thr Leu Leu Asn Asn Ile His Phe Trp Met Ser Asn Gln
             20                  25                  30

Ala Lys Ser Ser Val Ser Pro Ala His Pro Ala Pro Glu Asn Pro Pro
         35                  40                  45

Tyr Ser Pro Ser Ser Ala Ala Ser Lys Ala Pro Asp Ser Gly Thr Ala
     50                  55                  60

Thr Leu Gly Asp Ile Asp Leu Leu Asn Pro Gln Asn Arg Ala Ala Leu
 65                  70                  75                  80

Arg Arg Asn His Leu Gly Ile Val Phe Gln Gln Pro Asn Leu Leu Pro
                 85                  90                  95

Ser Leu Thr Val Leu Asp Gln Leu Leu Leu Ile Pro Arg Leu Gly Arg
            100                 105                 110

Ile Leu Pro Pro Ser Arg Ser Ala Arg Thr Gln His Lys Asp Lys Ala
        115                 120                 125

Leu Ser Leu Leu Asn Ser Ile Gly Leu Gly Asp Leu Ala Lys Arg Lys
    130                 135                 140
```

```
Val Ser Glu Leu Ser Gly Gly Gln Gln Ala Arg Val Asn Leu Ala Arg
145                 150                 155                 160

Ala Leu Met Asn Ser Pro Lys Leu Leu Leu Val Asp Glu Pro Thr Ala
                165                 170                 175

Ala Leu Asp Gln His Ser Ala Ser Glu Val Thr Glu Leu Ile Val Ser
            180                 185                 190

Met Ala His Gln Tyr Asn Ala Pro Thr
        195                 200


<210> 113
<211> 614
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(591)
<223> RXN00726

<400> 113
aac gcg ggt cgc ttg tat gtc gat ggc gat ctc att ggc tac cga gag   48
Asn Ala Gly Arg Leu Tyr Val Asp Gly Asp Leu Ile Gly Tyr Arg Glu
  1               5                  10                  15

cgc gat ggc gtg ctg tac gaa atc tct gag aag gac gcc gcc aag cag   96
Arg Asp Gly Val Leu Tyr Glu Ile Ser Glu Lys Asp Ala Ala Lys Gln
             20                  25                  30

cgc tcc gat atc ggc atg gtg ttc cag aac ttc aac ctc ttc ccc cac  144
Arg Ser Asp Ile Gly Met Val Phe Gln Asn Phe Asn Leu Phe Pro His
         35                  40                  45

cgc acg gtg atc gag aac atc atc gaa gct ccc atc cac gtg aag aag  192
Arg Thr Val Ile Glu Asn Ile Ile Glu Ala Pro Ile His Val Lys Lys
     50                  55                  60

cag ccc gaa agc aag gcc cgc gca cgt gcc atg gag ctg ctt gag cag  240
Gln Pro Glu Ser Lys Ala Arg Ala Arg Ala Met Glu Leu Leu Glu Gln
 65                  70                  75                  80

gtc ggc ctc gcc cac aag gcg gac gcc tac ccc gtc caa ctg tcg ggt  288
Val Gly Leu Ala His Lys Ala Asp Ala Tyr Pro Val Gln Leu Ser Gly
                 85                  90                  95

ggt cag cag cag cgc gtt gca att gcc cgc gcc gtc gcc atg gag cca  336
Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Ala Met Glu Pro
            100                 105                 110

aag ctc atg ctt ttc gac gaa ccc acc agc gct ttg gac cct gaa ctc  384
Lys Leu Met Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu
        115                 120                 125

gtc ggt gaa gtc ctg cga gtg atg aaa cag ctc gcc gac gac ggc atg  432
Val Gly Glu Val Leu Arg Val Met Lys Gln Leu Ala Asp Asp Gly Met
    130                 135                 140
```

```
acc atg ctt gtt gtc acc cac gaa atg ggc ttc gcc cac gaa gtc gcc   480
Thr Met Leu Val Val Thr His Glu Met Gly Phe Ala His Glu Val Ala
145                 150                 155                 160

gac cag gtc gtg ttc atg gcc gat gga gtt gtc gtt gaa gcc gga acc   528
Asp Gln Val Val Phe Met Ala Asp Gly Val Val Val Glu Ala Gly Thr
                165                 170                 175

ccc gaa caa gtt ctg gac aat cca aag gaa cag cgc acc aaa gac ttc   576
Pro Glu Gln Val Leu Asp Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe
            180                 185                 190

ctg tct tct ctg ctc taacctttc gggtcttaaa aaa                     614
Leu Ser Ser Leu Leu
        195
```

<210> 114
<211> 197
<212> PRT
<213> Corynebacterium glutamicum

<400> 114

```
Asn Ala Gly Arg Leu Tyr Val Asp Gly Asp Leu Ile Gly Tyr Arg Glu
  1               5                  10                  15

Arg Asp Gly Val Leu Tyr Glu Ile Ser Glu Lys Asp Ala Ala Lys Gln
             20                  25                  30

Arg Ser Asp Ile Gly Met Val Phe Gln Asn Phe Asn Leu Phe Pro His
         35                  40                  45

Arg Thr Val Ile Glu Asn Ile Ile Glu Ala Pro Ile His Val Lys Lys
     50                  55                  60

Gln Pro Glu Ser Lys Ala Arg Ala Arg Ala Met Glu Leu Leu Glu Gln
 65                  70                  75                  80

Val Gly Leu Ala His Lys Ala Asp Ala Tyr Pro Val Gln Leu Ser Gly
                 85                  90                  95

Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Ala Met Glu Pro
            100                 105                 110

Lys Leu Met Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu
        115                 120                 125

Val Gly Glu Val Leu Arg Val Met Lys Gln Leu Ala Asp Asp Gly Met
    130                 135                 140

Thr Met Leu Val Val Thr His Glu Met Gly Phe Ala His Glu Val Ala
145                 150                 155                 160

Asp Gln Val Val Phe Met Ala Asp Gly Val Val Val Glu Ala Gly Thr
                165                 170                 175

Pro Glu Gln Val Leu Asp Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe
            180                 185                 190

Leu Ser Ser Leu Leu
        195
```

<210> 115
<211> 765
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(742)
<223> RXN02570

<400> 115
ccattgttat gctcattgtg tttgtggtgg tcaagtcgct acccaagcgc accactaggg 60

cattggttcc gcagcgggtt ccggaggacg tcgcttaaac atg aat cct ttg aca 115
Met Asn Pro Leu Thr
1 5

tgg atc att ggc gca ttc agc atg tgg atc gtg gtg ctg ggc gtt aat 163
Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val Val Leu Gly Val Asn
10 15 20

aag ctt ggt tta agc atc gca gtg atc atc atc gcg cag gtc gtg gcg 211
Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile Ala Gln Val Val Ala
25 30 35

atg att cgg gtg cgc aat gta tct gtg ttg gct tca aca gca ttg tta 259
Met Ile Arg Val Arg Asn Val Ser Val Leu Ala Ser Thr Ala Leu Leu
40 45 50

tcg gtt cct gca ttg gcc tcg atg gcg ctg att cac atg ccg tat tct 307
Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile His Met Pro Tyr Ser
55 60 65

tcc gac ggc tgg ttg att gct ctt acc ttg acg gct cgt ttt agt gcg 355
Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr Ala Arg Phe Ser Ala
70 75 80 85

ttg atg tct att ttc ctc ctt gca gca aca gcg att act att cct gag 403
Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala Ile Thr Ile Pro Glu
90 95 100

ctg gtg aaa tcc cta tat cgt tgg ccc aag ctg gcg tat atc gtg ggt 451
Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu Ala Tyr Ile Val Gly
105 110 115

tct gca ttg cag atg att ccg cag ggt aaa cag acc ttg gcg ttg gtt 499
Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln Thr Leu Ala Leu Val
120 125 130

cgt gat gcc aat gct ttg cgc ggg cgc agc gtt aaa ggt ccc gtg cgc 547
Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val Lys Gly Pro Val Arg
135 140 145

gcg gtg aaa tat gtg ggt ttg ccc ctg att aca cat tta ctt agt gca 595
Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr His Leu Leu Ser Ala
150 155 160 165

ggt gcc gcg cga gcg att ccc ttg gag gtc gca ggc ctg gac agg ccg 643
Gly Ala Ala Arg Ala Ile Pro Leu Glu Val Ala Gly Leu Asp Arg Pro

```
                170                 175                 180

ggg ccg cgt acg gtg ttg gtt gag gtg gtg gag ggg cgc gtc gaa aag   691
Gly Pro Arg Thr Val Leu Val Glu Val Val Glu Gly Arg Val Glu Lys
            185                 190                 195

cat tgt cgc tgg ttg ttg ccg ctt ttg gca gtc ggg atg gcg tgg tgg   739
His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val Gly Met Ala Trp Trp
        200                 205                 210

ctc taactcaaat cgtcggaccg tcc                                     765
Leu
```

<210> 116
<211> 214
<212> PRT
<213> Corynebacterium glutamicum

<400> 116

```
Met Asn Pro Leu Thr Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val
  1               5                  10                  15

Val Leu Gly Val Asn Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile
             20                  25                  30

Ala Gln Val Val Ala Met Ile Arg Val Arg Asn Val Ser Val Leu Ala
         35                  40                  45

Ser Thr Ala Leu Leu Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile
     50                  55                  60

His Met Pro Tyr Ser Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr
 65                  70                  75                  80

Ala Arg Phe Ser Ala Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala
                 85                  90                  95

Ile Thr Ile Pro Glu Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu
            100                 105                 110

Ala Tyr Ile Val Gly Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln
        115                 120                 125

Thr Leu Ala Leu Val Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val
    130                 135                 140

Lys Gly Pro Val Arg Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr
145                 150                 155                 160

His Leu Leu Ser Ala Gly Ala Ala Arg Ala Ile Pro Leu Glu Val Ala
                165                 170                 175

Gly Leu Asp Arg Pro Gly Pro Arg Thr Val Leu Val Glu Val Val Glu
            180                 185                 190

Gly Arg Val Glu Lys His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val
        195                 200                 205

Gly Met Ala Trp Trp Leu
```

210

<210> 117
<211> 957
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(934)
<223> RXN02354

<400> 117
gaataaagaa aaagaaactg ggcggaacca aggatgagaa acccaccgct aaggatgctg 60

ttgtaaaggc cgattctgct gtgaaggaag ccgctaagcc atg act aaa cga aca 115
Met Thr Lys Arg Thr
1 5

aaa gga ctc atc ctc aac tac gcc gga gtg gtg ttc atc ctc ttc tgg 163
Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val Phe Ile Leu Phe Trp
10 15 20

gga cta gct ccc ttc tac tgg atg gtt atc acc gca ctg cgc gat tcc 211
Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr Ala Leu Arg Asp Ser
25 30 35

aag cac acc ttt gac acc acc cca tgg cca acg cac gtc acc ttg gat 259
Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr His Val Thr Leu Asp
40 45 50

aac ttc cgg gac gca ctg gcc acc gac aaa ggc aac aac ttc ctc gca 307
Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly Asn Asn Phe Leu Ala
55 60 65

gcc att ggc aac tca ctg gtc atc agc gtc acc aca aca gcg atc gct 355
Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr Thr Thr Ala Ile Ala
70 75 80 85

gtt ctc gtg gga gtg ttc acc gcc tac gct cta gcc cga ctg gaa ttc 403
Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu Ala Arg Leu Glu Phe
90 95 100

ccg ggc aaa ggc att gtc acc ggc atc atc ttg gca gcc tcc atg ttc 451
Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu Ala Ala Ser Met Phe
105 110 115

ccc ggc atc gcc ctg gtc act ccg ctg ttc cag ctc ttc ggt gac ctc 499
Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln Leu Phe Gly Asp Leu
120 125 130

aac tgg atc ggc acc tac caa gcg ctg att atc ccg aac att tcc ttc 547
Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile Pro Asn Ile Ser Phe
135 140 145

gcg cta cct ctg acg atc tac acg ctc gta tcc ttc ttc agg caa ctg 595
Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser Phe Phe Arg Gln Leu
150 155 160 165

ccc tgg gaa ctc gaa gaa tca gca cgt gtc gac ggc gcc aca cgt ggc 643

```
Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp Gly Ala Thr Arg Gly
                170                 175                 180

caa gcc ttc cgc atg atc ctg ctt cct cta gca gcg ccc gca cta ttt   691
Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala Ala Pro Ala Leu Phe
            185                 190                 195

acc acc gcg atc ctc gca ttc att gca acg tgg aac gaa ttc atg ctg   739
Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp Asn Glu Phe Met Leu
        200                 205                 210

gcc cgc caa cta tcc aac acc tcc aca gag cca gtg acc gtt gcg atc   787
Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro Val Thr Val Ala Ile
    215                 220                 225

gca agg ttc acc gga cca agc tcc ttc gaa tac ccc tac gcc tct gtc   835
Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr Pro Tyr Ala Ser Val
230                 235                 240                 245

atg gca gcg gga gct ttg gtg acc atc cca ctg atc atc atg gtt ctc   883
Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu Ile Ile Met Val Leu
                250                 255                 260

atc ttc caa cgc cgc atc gtc tcc gga ctc acc gca ggt ggc gtg aaa   931
Ile Phe Gln Arg Arg Ile Val Ser Gly Leu Thr Ala Gly Gly Val Lys
            265                 270                 275

gcc tagactagat actcatgagt gct                                    957
Ala
```

DO NOT ENTER

<210> 118
<211> 278
<212> PRT
<213> Corynebacterium glutamicum

<400> 118

```
Met Thr Lys Arg Thr Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val
  1               5                  10                  15

Phe Ile Leu Phe Trp Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr
             20                  25                  30

Ala Leu Arg Asp Ser Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr
         35                  40                  45

His Val Thr Leu Asp Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly
     50                  55                  60

Asn Asn Phe Leu Ala Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr
 65                  70                  75                  80

Thr Thr Ala Ile Ala Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu
                 85                  90                  95

Ala Arg Leu Glu Phe Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu
            100                 105                 110

Ala Ala Ser Met Phe Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln
        115                 120                 125
```

```
Leu Phe Gly Asp Leu Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile
    130                 135                 140

Pro Asn Ile Ser Phe Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser
145                 150                 155                 160

Phe Phe Arg Gln Leu Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp
                165                 170                 175

Gly Ala Thr Arg Gly Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala
            180                 185                 190

Ala Pro Ala Leu Phe Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp
        195                 200                 205

Asn Glu Phe Met Leu Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro
    210                 215                 220

Val Thr Val Ala Ile Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr
225                 230                 235                 240

Pro Tyr Ala Ser Val Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu
                245                 250                 255

Ile Ile Met Val Leu Ile Phe Gln Arg Arg Ile Val Ser Gly Leu Thr
            260                 265                 270

Ala Gly Gly Val Lys Ala
        275
```

08525360 "Pcd05"

<210> 119
<211> 889
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(889)
<223> FRXA02354

<400> 119

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gaataaagaa aaagaaactg ggcggaacca aggatgagaa acccaccgct aaggatgctg 60

ttgtaaaggc cgattctgct gtgaaggaag ccgctaagcc atg act aaa cga aca   115
                                            Met Thr Lys Arg Thr
                                              1               5

aaa gga ctc atc ctc aac tac gcc gga gtg gtg ttc atc ctc ttc tgg   163
Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val Phe Ile Leu Phe Trp
                  10                  15                  20

gga cta gct ccc ttc tac tgg atg gtt atc acc gca ctg cgc gat tcc   211
Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr Ala Leu Arg Asp Ser
              25                  30                  35

aag cac acc ttt gac acc acc cca tgg cca acg cac gtc acc ttg gat   259
Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr His Val Thr Leu Asp
          40                  45                  50
```

```
aac ttc cgg gac gca ctg gcc acc gac aaa ggc aac aac ttc ctc gca   307
Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly Asn Asn Phe Leu Ala
     55                  60                  65

gcc att ggc aac tca ctg gtc atc agc gtc acc aca aca gcg atc gct   355
Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr Thr Thr Ala Ile Ala
 70                  75                  80                  85

gtt ctc gtg gga gtg ttc acc gcc tac gct cta gcc cga ctg gaa ttc   403
Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu Ala Arg Leu Glu Phe
                 90                  95                 100

ccg ggc aaa ggc att gtc acc ggc atc atc ttg gca gcc tcc atg ttc   451
Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu Ala Ala Ser Met Phe
            105                 110                 115

ccc ggc atc gcc ctg gtc act ccg ctg ttc cag ctc ttc ggt gac ctc   499
Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln Leu Phe Gly Asp Leu
        120                 125                 130

aac tgg atc ggc acc tac caa gcg ctg att atc ccg aac att tcc ttc   547
Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile Pro Asn Ile Ser Phe
    135                 140                 145

gcg cta cct ctg acg atc tac acg ctc gta tcc ttc ttc agg caa ctg   595
Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser Phe Phe Arg Gln Leu
150                 155                 160                 165

ccc tgg gaa ctc gaa gaa tca gca cgt gtc gac ggc gcc aca cgt ggc   643
Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp Gly Ala Thr Arg Gly
                170                 175                 180

caa gcc ttc cgc atg atc ctg ctt cct cta gca gcg ccc gca cta ttt   691
Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala Ala Pro Ala Leu Phe
            185                 190                 195

acc acc gcg atc ctc gca ttc att gca acg tgg aac gaa ttc atg ctg   739
Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp Asn Glu Phe Met Leu
        200                 205                 210

gcc cgc caa cta tcc aac acc tcc aca gag cca gtg acc gtt gcg atc   787
Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro Val Thr Val Ala Ile
    215                 220                 225

gca agg ttc acc gga cca agc tcc ttc gaa tac ccc tac gcc tct gtc   835
Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr Pro Tyr Ala Ser Val
230                 235                 240                 245

atg gca gcg gga gct ttg gtg acc atc cca ctg atc atc atg gtt ctc   883
Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu Ile Ile Met Val Leu
                250                 255                 260

atc ttc                                                          889
Ile Phe
```

<210> 120
<211> 263
<212> PRT
<213> Corynebacterium glutamicum

<400> 120

```
Met Thr Lys Arg Thr Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val
  1               5                  10                  15

Phe Ile Leu Phe Trp Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr
             20                  25                  30

Ala Leu Arg Asp Ser Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr
         35                  40                  45

His Val Thr Leu Asp Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly
     50                  55                  60

Asn Asn Phe Leu Ala Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr
 65                  70                  75                  80

Thr Thr Ala Ile Ala Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu
                 85                  90                  95

Ala Arg Leu Glu Phe Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu
            100                 105                 110

Ala Ala Ser Met Phe Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln
        115                 120                 125

Leu Phe Gly Asp Leu Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile
    130                 135                 140

Pro Asn Ile Ser Phe Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser
145                 150                 155                 160

Phe Phe Arg Gln Leu Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp
                165                 170                 175

Gly Ala Thr Arg Gly Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala
            180                 185                 190

Ala Pro Ala Leu Phe Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp
        195                 200                 205

Asn Glu Phe Met Leu Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro
    210                 215                 220

Val Thr Val Ala Ile Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr
225                 230                 235                 240

Pro Tyr Ala Ser Val Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu
                245                 250                 255

Ile Ile Met Val Leu Ile Phe
            260
```

<210> 121
<211> 1251
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1228)
<223> RXN00001

<400> 121
tgtcataggc agcactctag atggcgcaca gtgactcact tcactgtttc tcacactacg 60

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gatcgttcgg cacgtacctg ccgatggagg agattctgca atg gca acc gta acg   115
                                              Met Ala Thr Val Thr
                                                1               5

ttc aaa gat gct tcc cta agc tac ccg gga gca aag gaa ccc acc gtc   163
Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala Lys Glu Pro Thr Val
                10                  15                  20

aag aaa ttc aac ctg gaa atc gcc gat ggc gag ttc ctc gtc ctc gtc   211
Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val
            25                  30                  35

ggc cct tcc ggc tgt ggt aaa tcc acc acg ctg cgc atg ctg gcc ggt   259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Met Leu Ala Gly
        40                  45                  50

ttg gaa aac gtt act gac ggt gcc att ttc atc gga gac aag gac gtt   307
Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile Gly Asp Lys Asp Val
    55                  60                  65

acc cac gtt gca ccg cgt gac cgt gac atc gcc atg gtt ttc cag aac   355
Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala Met Val Phe Gln Asn
70                  75                  80                  85

tat gct ctc tac ccc cac atg acc gtg ggc gag aac atg ggc ttc gca   403
Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu Asn Met Gly Phe Ala
                90                  95                  100

ctg aag atc gcc ggc aag tcc caa gac gag atc aat aag cgc gtc gac   451
Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile Asn Lys Arg Val Asp
            105                 110                 115

gaa gcc gcc gcc act ttg ggc ctg acc gaa ttc ttg gag cgc aag ccg   499
Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe Leu Glu Arg Lys Pro
        120                 125                 130

aag gcc ctg tcc ggt ggt cag cgt cag cgt gtg gcc atg ggc cgc gcc   547
Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
    135                 140                 145

att gtt cgc aac ccg cag gtc ttt ctc atg gat gag ccg ctg tct aac   595
Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp Glu Pro Leu Ser Asn
150                 155                 160                 165

ctc gat gcc aag ctg cgt gtt cag acc cgt acc cag att gca gcc ctg   643
Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr Gln Ile Ala Ala Leu
                170                 175                 180

cag cgc aag ctt ggg gtt acc acc gtt tac gtc acc cac gac cag acg   691
Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Thr
            185                 190                 195

gag gcc ttg acc atg ggt gac cgc atc gcg gtg ctg aag gat ggc tac   739
Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val Leu Lys Asp Gly Tyr
        200                 205                 210
```

```
ctg cag cag gtt ggc gcg ccc cga gag ctt tat gac cgc ccc gcc aac   787
Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr Asp Arg Pro Ala Asn
    215                 220                 225

gtc ttc gtc gcc ggc ttc atc ggc tcc cca gcc atg aac ttg ggc acc   835
Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala Met Asn Leu Gly Thr
230                 235                 240                 245

ttc tcg gtc aag gat ggt gac gct acc tct ggt cac gct cgc atc aag   883
Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly His Ala Arg Ile Lys
                250                 255                 260

ctt tcc ccg gaa acc ctc gcc gcc atg acg ccg gag gat aat ggc cgc   931
Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro Glu Asp Asn Gly Arg
            265                 270                 275

atc acc att ggt ttc cgc ccg gag gca ctg gag atc att ccg gaa ggc   979
Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu Ile Ile Pro Glu Gly
        280                 285                 290

gag tcc acc gat ctt tcc atc cca atc aag ctc gac ttc gtg gag gaa   1027
Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu Asp Phe Val Glu Glu
    295                 300                 305

ctc ggt tcc gat tcc ttc ctc tac ggc aag ctg gta ggc gag ggc gac   1075
Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu Val Gly Glu Gly Asp
310                 315                 320                 325

ctt gga tcc tcc agc gag gat gtc ccc gag tcc ggc caa atc gtc gtc   1123
Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser Gly Gln Ile Val Val
                330                 335                 340

cgc gct gct ccg aac gcc gcg cct gct ccg ggc agt gtt ttc cac gca   1171
Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly Ser Val Phe His Ala
            345                 350                 355

cgc atc gtg gag ggc ggc cag cac aac ttc tcg gcg tcg act ggc aag   1219
Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser Ala Ser Thr Gly Lys
        360                 365                 370

cgc ctc cct taagcccgcg taccggctac ccc                            1251
Arg Leu Pro
    375
```

<210> 122
<211> 376
<212> PRT
<213> Corynebacterium glutamicum

<400> 122

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Met Ala Thr Val Thr Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala
  1               5                  10                  15

Lys Glu Pro Thr Val Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu
            20                  25                  30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu
        35                  40                  45
```

Arg Met Leu Ala Gly Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile
50 55 60

Gly Asp Lys Asp Val Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala
65 70 75 80

Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu
85 90 95

Asn Met Gly Phe Ala Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile
100 105 110

Asn Lys Arg Val Asp Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe
115 120 125

Leu Glu Arg Lys Pro Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
130 135 140

Ala Met Gly Arg Ala Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp
145 150 155 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr
165 170 175

Gln Ile Ala Ala Leu Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val
180 185 190

Thr His Asp Gln Thr Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val
195 200 205

Leu Lys Asp Gly Tyr Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr
210 215 220

Asp Arg Pro Ala Asn Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala
225 230 235 240

Met Asn Leu Gly Thr Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly
245 250 255

His Ala Arg Ile Lys Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro
260 265 270

Glu Asp Asn Gly Arg Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu
275 280 285

Ile Ile Pro Glu Gly Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu
290 295 300

Asp Phe Val Glu Glu Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu
305 310 315 320

Val Gly Glu Gly Asp Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser
325 330 335

Gly Gln Ile Val Val Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly
340 345 350

Ser Val Phe His Ala Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser
355 360 365

Ala Ser Thr Gly Lys Arg Leu Pro

370 375

<210> 123
<211> 1251
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1228)
<223> FRXA00001

<400> 123
tgtcataggc agcactctag atggcgcaca gtgactcact tcactgtttc tcacactacg 60

gatcgttcgg cacgtacctg ccgatggagg agattctgca atg gca acc gta acg 115
Met Ala Thr Val Thr
1 5

ttc aaa gat gct tcc cta agc tac ccg gga gca aag gaa ccc acc gtc 163
Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala Lys Glu Pro Thr Val
10 15 20

aag aaa ttc aac ctg gaa atc gcc gat ggc gag ttc ctc gtc ctc gtc 211
Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val
25 30 35

ggc cct tcc ggc tgt ggt aaa tcc acc acg ctg cgc atg ctg gcc ggt 259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Met Leu Ala Gly
40 45 50

ttg gaa aac gtt act gac ggt gcc att ttc atc gga gac aag gac gtt 307
Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile Gly Asp Lys Asp Val
55 60 65

acc cac gtt gca ccg cgt gac cgt gac atc gcc atg gtt ttc cag aac 355
Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala Met Val Phe Gln Asn
70 75 80 85

tat gct ctc tac ccc cac atg acc gtg ggc gag aac atg ggc ttc gca 403
Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu Asn Met Gly Phe Ala
90 95 100

ctg aag atc gcc ggc aag tcc caa gac gag atc aat aag cgc gtc gac 451
Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile Asn Lys Arg Val Asp
105 110 115

gaa gcc gcc gcc act ttg ggc ctg acc gaa ttc ttg gag cgc aag ccg 499
Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe Leu Glu Arg Lys Pro
120 125 130

aag gcc ctg tcc ggt ggt cag cgt cag cgt gtg gcc atg ggc cgc gcc 547
Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
135 140 145

att gtt cgc aac ccg cag gtc ttt ctc atg gat gag ccg ctg tct aac 595
Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp Glu Pro Leu Ser Asn
150 155 160 165

ctc gat gcc aag ctg cgt gtt cag acc cgt acc cag att gca gcc ctg 643

```
Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr Gln Ile Ala Ala Leu
                170                 175                 180

cag cgc aag ctt ggg gtt acc acc gtt tac gtc acc cac gac cag acg   691
Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Thr
            185                 190                 195

gag gcc ttg acc atg ggt gac cgc atc gcg gtg ctg aag gat ggc tac   739
Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val Leu Lys Asp Gly Tyr
        200                 205                 210

ctg cag cag gtt ggc gcg ccc cga gag ctt tat gac cgc ccc gcc aac   787
Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr Asp Arg Pro Ala Asn
    215                 220                 225

gtc ttc gtc gcc ggc ttc atc ggc tcc cca gcc atg aac ttg ggc acc   835
Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala Met Asn Leu Gly Thr
230                 235                 240                 245

ttc tcg gtc aag gat ggt gac gct acc tct ggt cac gct cgc atc aag   883
Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly His Ala Arg Ile Lys
                250                 255                 260

ctt tcc ccg gaa acc ctc gcc gcc atg acg ccg gag gat aat ggc cgc   931
Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro Glu Asp Asn Gly Arg
            265                 270                 275

atc acc att ggt ttc cgc ccg gag gca ctg gag atc att ccg gaa ggc   979
Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu Ile Ile Pro Glu Gly
        280                 285                 290

gag tcc acc gat ctt tcc atc cca atc aag ctc gac ttc gtg gag gaa   1027
Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu Asp Phe Val Glu Glu
    295                 300                 305

ctc ggt tcc gat tcc ttc ctc tac ggc aag ctg gta ggc gag ggc gac   1075
Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu Val Gly Glu Gly Asp
310                 315                 320                 325

ctt gga tcc tcc agc gag gat gtc ccc gag tcc ggc caa atc gtc gtc   1123
Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser Gly Gln Ile Val Val
                330                 335                 340

cgc gct gct ccg aac gcc gcg cct gct ccg ggc agt gtt ttc cac gca   1171
Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly Ser Val Phe His Ala
            345                 350                 355

cgc atc gtg gag ggc ggc cag cac aac ttc tcg gcg tcg act ggc aag   1219
Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser Ala Ser Thr Gly Lys
        360                 365                 370

cgc ctc cct taagcccgcg taccggctac ccc                            1251
Arg Leu Pro
    375
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<210> 124
<211> 376
<212> PRT
<213> Corynebacterium glutamicum

<400> 124

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Met Ala Thr Val Thr Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala
  1               5                  10                  15

Lys Glu Pro Thr Val Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu
            20                  25                  30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu
        35                  40                  45

Arg Met Leu Ala Gly Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile
    50                  55                  60

Gly Asp Lys Asp Val Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala
65                  70                  75                  80

Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu
                85                  90                  95

Asn Met Gly Phe Ala Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile
            100                 105                 110

Asn Lys Arg Val Asp Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe
        115                 120                 125

Leu Glu Arg Lys Pro Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
    130                 135                 140

Ala Met Gly Arg Ala Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp
145                 150                 155                 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr
                165                 170                 175

Gln Ile Ala Ala Leu Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val
            180                 185                 190

Thr His Asp Gln Thr Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val
        195                 200                 205

Leu Lys Asp Gly Tyr Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr
    210                 215                 220

Asp Arg Pro Ala Asn Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala
225                 230                 235                 240

Met Asn Leu Gly Thr Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly
                245                 250                 255

His Ala Arg Ile Lys Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro
            260                 265                 270

Glu Asp Asn Gly Arg Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu
        275                 280                 285

Ile Ile Pro Glu Gly Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu
    290                 295                 300

Asp Phe Val Glu Glu Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu
305                 310                 315                 320
```

```
Val Gly Glu Gly Asp Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser
                325                 330                 335

Gly Gln Ile Val Val Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly
            340                 345                 350

Ser Val Phe His Ala Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser
        355                 360                 365

Ala Ser Thr Gly Lys Arg Leu Pro
    370                 375


<210> 125
<211> 1119
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXN02356

<400> 125
ttggcagtag ccatgcgttc tgctcctgac cttgaacagc ggtcccaatt tagacccgct 60

aaacccacaa tgtgtactgg tgctggtaat ttagtagaac atg gca acg gtc aca   115
                                          Met Ala Thr Val Thr
                                            1               5

ttc gac aag gtc aca atc cgg tac ccc ggc gcg gag cgc gca aca gtt   163
Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala Glu Arg Ala Thr Val
                10                  15                  20

cat gag ctt gat tta gat atc gct gat ggc gag ttt ttg gtg ctc gtc   211
His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu Phe Leu Val Leu Val
            25                  30                  35

ggc cct tcg ggt tgt ggt aaa tcc act acg ctg cgt gct ttg gcg ggg   259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Ala Leu Ala Gly
        40                  45                  50

ctt gag ggc gtg gag tcg ggt gtg atc aaa att gat ggc aag gat gtc   307
Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile Asp Gly Lys Asp Val
    55                  60                  65

act ggt cag gag ccg gcg gat cgc gat atc gcg atg gtg ttc cag aat   355
Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala Met Val Phe Gln Asn
70                  75                  80                  85

tat gct ctg tac cct cac atg acg gtg gcg aag aat atg ggt ttt gcg   403
Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys Asn Met Gly Phe Ala
                90                  95                  100

ctg aag ttg gct aag ctg ccg cag gcg cag atc gat gcg aag gtc aat   451
Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile Asp Ala Lys Val Asn
            105                 110                 115

gag gct gcg gaa att ctt ggg ttg acg gag ttt ttg gat cgc aag cct   499
Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe Leu Asp Arg Lys Pro
        120                 125                 130
```

```
aag gat tta tcg ggt ggt cag cgt cag cgt gtg gcg atg ggt cgc gcg   547
Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
    135                 140                 145

ttg gtg cgt gat ccg aag gtg ttc ctc atg gat gag ccg ctg tcc aac   595
Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp Glu Pro Leu Ser Asn
150                 155                 160                 165

ctg gat gcg aaa ttg cgc gtg caa acc cgc gcg gag gtc gct gct ttg   643
Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala Glu Val Ala Ala Leu
                170                 175                 180

cag cgt cgc ctg ggc acc acc acg gtg tat gtc acc cac gat cag gtt   691
Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val Thr His Asp Gln Val
            185                 190                 195

gag gca atg acg atg ggc gat cgg gtt gcg gtg ctc aag gac ggg ttg   739
Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Lys Asp Gly Leu
        200                 205                 210

ctg cag cag gtc gca ccg ccc agg gag ctt tac gac gcc ccg gtc aac   787
Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr Asp Ala Pro Val Asn
    215                 220                 225

gaa ttc gtt gcg ggc ttc atc ggc tcg ccg tcc atg aac ctc ttc cct   835
Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser Met Asn Leu Phe Pro
230                 235                 240                 245

gcc aac ggg cac aag atg ggt gtg cgc ccg gag aag atg ctg gtc aat   883
Ala Asn Gly His Lys Met Gly Val Arg Pro Glu Lys Met Leu Val Asn
                250                 255                 260

gag acc cct gag ggt ttc aca agc att gat gct gtg gtg gat atc gtc   931
Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala Val Val Asp Ile Val
            265                 270                 275

gag gag ctt ggc tcc gaa tcg tat gtt tat gcc act tgg gag ggc cac   979
Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala Thr Trp Glu Gly His
        280                 285                 290

cgc ctg gtg gcc cgt tgg gtg gaa ggc ccc gtg cca gcc cct ggc acg   1027
Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val Pro Ala Pro Gly Thr
    295                 300                 305

cct gtg act ttt tcc tat gat gcg gcg cag gcg cat cat ttc gat ctg   1075
Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala His His Phe Asp Leu
310                 315                 320                 325

gag tcg ggc gag cgt atc gct tagtttcgga cgtggggagg cgt             1119
Glu Ser Gly Glu Arg Ile Ala
                330
```

<210> 126
<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 126
Met Ala Thr Val Thr Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala

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  1               5                  10                  15

Glu Arg Ala Thr Val His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu
            20                  25                  30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu
        35                  40                  45

Arg Ala Leu Ala Gly Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile
    50                  55                  60

Asp Gly Lys Asp Val Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala
65                  70                  75                  80

Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys
                85                  90                  95

Asn Met Gly Phe Ala Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile
            100                 105                 110

Asp Ala Lys Val Asn Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe
        115                 120                 125

Leu Asp Arg Lys Pro Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val
    130                 135                 140

Ala Met Gly Arg Ala Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp
145                 150                 155                 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala
                165                 170                 175

Glu Val Ala Ala Leu Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val
            180                 185                 190

Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
        195                 200                 205

Leu Lys Asp Gly Leu Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr
    210                 215                 220

Asp Ala Pro Val Asn Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser
225                 230                 235                 240

Met Asn Leu Phe Pro Ala Asn Gly His Lys Met Gly Val Arg Pro Glu
                245                 250                 255

Lys Met Leu Val Asn Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala
            260                 265                 270

Val Val Asp Ile Val Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala
        275                 280                 285

Thr Trp Glu Gly His Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val
    290                 295                 300

Pro Ala Pro Gly Thr Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala
305                 310                 315                 320

His His Phe Asp Leu Glu Ser Gly Glu Arg Ile Ala
                325                 330
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<210> 127
<211> 1369
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1369)
<223> RXN02455

<400> 127
aagccttcgt tatgggaggt ctcccagaca caatcgaata cgggccggat atccatctcg 60

gctcatcacc ccgcttttta tcaagaaaga tgaggacctc ttg aag cgt ctt act 115
Leu Lys Arg Leu Thr
1 5

cgc atc gca tcc atc agc atg gcc tcc atg ctc gcc gcc gca agt ctc 163
Arg Ile Ala Ser Ile Ser Met Ala Ser Met Leu Ala Ala Ala Ser Leu
10 15 20

gtc gcg tgc tcc ggc tcc acc gac gag gaa ggc gat gtt tac ttc ctg 211
Val Ala Cys Ser Gly Ser Thr Asp Glu Glu Gly Asp Val Tyr Phe Leu
25 30 35

aac ttc aag cct gaa cag gac gtg gca tac cag gaa atc gca aag gcc 259
Asn Phe Lys Pro Glu Gln Asp Val Ala Tyr Gln Glu Ile Ala Lys Ala
40 45 50

tac act gaa gag acc ggc gtt aag gtc aag gtc gtt act gcc gcc tcc 307
Tyr Thr Glu Glu Thr Gly Val Lys Val Lys Val Val Thr Ala Ala Ser
55 60 65

ggc tcc tat gag cag acc ctc aag gcc gag att ggc aag gac gaa gcc 355
Gly Ser Tyr Glu Gln Thr Leu Lys Ala Glu Ile Gly Lys Asp Glu Ala
70 75 80 85

ccg act ctc ttc cag gtc aat ggc cca gcc ggc ttc atc act tgg cag 403
Pro Thr Leu Phe Gln Val Asn Gly Pro Ala Gly Phe Ile Thr Trp Gln
90 95 100

gac tac atg gca gat atg tcg gac acc gag gta gct aag cag ctg acc 451
Asp Tyr Met Ala Asp Met Ser Asp Thr Glu Val Ala Lys Gln Leu Thr
105 110 115

gac gac att ccg ccg ctg acc acc gag gat ggc gag gta cgt ggc gtt 499
Asp Asp Ile Pro Pro Leu Thr Thr Glu Asp Gly Glu Val Arg Gly Val
120 125 130

ccg ttc gcc gtc gag ggc ttc ggc atc atc tac aac gac gag atc ttc 547
Pro Phe Ala Val Glu Gly Phe Gly Ile Ile Tyr Asn Asp Glu Ile Phe
135 140 145

gac aag tac atc gcc acg tcc ggc gca aag atc aag tcc acg gat gag 595
Asp Lys Tyr Ile Ala Thr Ser Gly Ala Lys Ile Lys Ser Thr Asp Glu
150 155 160 165

atc acg agc tac cag aag ctc aag gaa gtc gcc gag gat atg cag gca 643
Ile Thr Ser Tyr Gln Lys Leu Lys Glu Val Ala Glu Asp Met Gln Ala

```
                    170                 175                 180

aag aag gac gag ctc ggt atc gaa ggc gcc ttc gcc tcc acc tcg ctg   691
Lys Lys Asp Glu Leu Gly Ile Glu Gly Ala Phe Ala Ser Thr Ser Leu
                185                 190                 195

aca tcc agt gag gac tgg cgt tgg cag acc cac ctg gcc aac gct ccg   739
Thr Ser Ser Glu Asp Trp Arg Trp Gln Thr His Leu Ala Asn Ala Pro
        200                 205                 210

atc tgg cag gag tac cag gac aag gga gtc gag gac acc aac gag atc   787
Ile Trp Gln Glu Tyr Gln Asp Lys Gly Val Glu Asp Thr Asn Glu Ile
    215                 220                 225

gag ttc tcc tac aac aag gag tac aag aac ctt ttc gat ctc tac ctt   835
Glu Phe Ser Tyr Asn Lys Glu Tyr Lys Asn Leu Phe Asp Leu Tyr Leu
230                 235                 240                 245

gag aac tcc acc gta gaa aag tct ctt gcg ccg tct aag acg gtg tct   883
Glu Asn Ser Thr Val Glu Lys Ser Leu Ala Pro Ser Lys Thr Val Ser
                250                 255                 260

gat tcc atg gct gag ttc gca cag ggc aag gcc gct atg gtt cag aac   931
Asp Ser Met Ala Glu Phe Ala Gln Gly Lys Ala Ala Met Val Gln Asn
            265                 270                 275

ggt aac tgg gca tgg tcc cag att tcc gag act tct ggc aac gtg gtc   979
Gly Asn Trp Ala Trp Ser Gln Ile Ser Glu Thr Ser Gly Asn Val Val
        280                 285                 290

aag gaa gac aag atc aag ttc ctg ccc atg tac atg ggt ctg cca gat   1027
Lys Glu Asp Lys Ile Lys Phe Leu Pro Met Tyr Met Gly Leu Pro Asp
    295                 300                 305

gaa gaa aag cac ggc atc aac gtc ggt acc gag aac tat ttg ggc gtg   1075
Glu Glu Lys His Gly Ile Asn Val Gly Thr Glu Asn Tyr Leu Gly Val
310                 315                 320                 325

aac tct gag gcc tcc gag gtc gac cag cag gcc acc aag gac ttc gtg   1123
Asn Ser Glu Ala Ser Glu Val Asp Gln Gln Ala Thr Lys Asp Phe Val
                330                 335                 340

gat tgg ctg ttt acc tct gaa gct ggc aag gag cac gtg gtg aag gac   1171
Asp Trp Leu Phe Thr Ser Glu Ala Gly Lys Glu His Val Val Lys Asp
            345                 350                 355

ctt ggc ttc atc gca ccg ttc gaa agc tac acc gct gag aac acc ccg   1219
Leu Gly Phe Ile Ala Pro Phe Glu Ser Tyr Thr Ala Glu Asn Thr Pro
        360                 365                 370

aat gac ccc ctt tct gag caa gtc gcg gaa gct atc gct aac aag gat   1267
Asn Asp Pro Leu Ser Glu Gln Val Ala Glu Ala Ile Ala Asn Lys Asp
    375                 380                 385

ctg acc acc tac ccg tgg aac ttc cag tac ttc ccg tcc cag cag ttc   1315
Leu Thr Thr Tyr Pro Trp Asn Phe Gln Tyr Phe Pro Ser Gln Gln Phe
390                 395                 400                 405

aag gat gac ttc ggc cag gat ctg tcg cag tac gcc tcc gga aag ctg   1363
Lys Asp Asp Phe Gly Gln Asp Leu Ser Gln Tyr Ala Ser Gly Lys Leu
                410                 415                 420
```

CN 1636570 A 20050713

aag tgg 1369
Lys Trp

<210> 128
<211> 423
<212> PRT
<213> Corynebacterium glutamicum

<400> 128

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Leu Lys Arg Leu Thr Arg Ile Ala Ser Ile Ser Met Ala Ser Met Leu
  1               5                  10                  15

Ala Ala Ala Ser Leu Val Ala Cys Ser Gly Ser Thr Asp Glu Glu Gly
             20                  25                  30

Asp Val Tyr Phe Leu Asn Phe Lys Pro Glu Gln Asp Val Ala Tyr Gln
         35                  40                  45

Glu Ile Ala Lys Ala Tyr Thr Glu Glu Thr Gly Val Lys Val Lys Val
     50                  55                  60

Val Thr Ala Ala Ser Gly Ser Tyr Glu Gln Thr Leu Lys Ala Glu Ile
 65                  70                  75                  80

Gly Lys Asp Glu Ala Pro Thr Leu Phe Gln Val Asn Gly Pro Ala Gly
                 85                  90                  95

Phe Ile Thr Trp Gln Asp Tyr Met Ala Asp Met Ser Asp Thr Glu Val
            100                 105                 110

Ala Lys Gln Leu Thr Asp Asp Ile Pro Pro Leu Thr Thr Glu Asp Gly
        115                 120                 125

Glu Val Arg Gly Val Pro Phe Ala Val Glu Gly Phe Gly Ile Ile Tyr
    130                 135                 140

Asn Asp Glu Ile Phe Asp Lys Tyr Ile Ala Thr Ser Gly Ala Lys Ile
145                 150                 155                 160

Lys Ser Thr Asp Glu Ile Thr Ser Tyr Gln Lys Leu Lys Glu Val Ala
                165                 170                 175

Glu Asp Met Gln Ala Lys Lys Asp Glu Leu Gly Ile Glu Gly Ala Phe
            180                 185                 190

Ala Ser Thr Ser Leu Thr Ser Ser Glu Asp Trp Arg Trp Gln Thr His
        195                 200                 205

Leu Ala Asn Ala Pro Ile Trp Gln Glu Tyr Gln Asp Lys Gly Val Glu
    210                 215                 220

Asp Thr Asn Glu Ile Glu Phe Ser Tyr Asn Lys Glu Tyr Lys Asn Leu
225                 230                 235                 240

Phe Asp Leu Tyr Leu Glu Asn Ser Thr Val Glu Lys Ser Leu Ala Pro
                245                 250                 255

Ser Lys Thr Val Ser Asp Ser Met Ala Glu Phe Ala Gln Gly Lys Ala
```

```
            260                 265                 270

Ala Met Val Gln Asn Gly Asn Trp Ala Trp Ser Gln Ile Ser Glu Thr
        275                 280                 285

Ser Gly Asn Val Val Lys Glu Asp Lys Ile Lys Phe Leu Pro Met Tyr
    290                 295                 300

Met Gly Leu Pro Asp Glu Glu Lys His Gly Ile Asn Val Gly Thr Glu
305                 310                 315                 320

Asn Tyr Leu Gly Val Asn Ser Glu Ala Ser Glu Val Asp Gln Gln Ala
                325                 330                 335

Thr Lys Asp Phe Val Asp Trp Leu Phe Thr Ser Glu Ala Gly Lys Glu
            340                 345                 350

His Val Val Lys Asp Leu Gly Phe Ile Ala Pro Phe Glu Ser Tyr Thr
        355                 360                 365

Ala Glu Asn Thr Pro Asn Asp Pro Leu Ser Glu Gln Val Ala Glu Ala
    370                 375                 380

Ile Ala Asn Lys Asp Leu Thr Thr Tyr Pro Trp Asn Phe Gln Tyr Phe
385                 390                 395                 400

Pro Ser Gln Gln Phe Lys Asp Asp Phe Gly Gln Asp Leu Ser Gln Tyr
                405                 410                 415

Ala Ser Gly Lys Leu Lys Trp
            420
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09/12/03 15:13:39

<210> 129
<211> 1560
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1537)
<223> RXN02795

<400> 129
gcggtgtggc ccggtgctgc gatcgctttg acggtccttg gttttaatct tttcggtgat 60

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ggtttacgcg atgccatcga tccaaagcgg gaggtcggcc gtg ctt aaa gtt tct   115
                                                Val Leu Lys Val Ser
                                                  1               5

gat tta acg gtt ggc aac aat ttt gtc cac aac gtc tcc ttc gag gtc   163
Asp Leu Thr Val Gly Asn Asn Phe Val His Asn Val Ser Phe Glu Val
                  10                  15                  20

aac ccc ggc gaa cgc gtc ggc atc atc ggc gag tcc ggc tca ggc aaa   211
Asn Pro Gly Glu Arg Val Gly Ile Ile Gly Glu Ser Gly Ser Gly Lys
              25                  30                  35

tca ctc acc gcg cta tcc atc atg ggt tta act gac ctg ccg acc acc   259
Ser Leu Thr Ala Leu Ser Ile Met Gly Leu Thr Asp Leu Pro Thr Thr
          40                  45                  50
```

```
ggc cag atc acc ttc aac ggc aaa ccc tcc gct aca ttc cgt ggc acc   307
Gly Gln Ile Thr Phe Asn Gly Lys Pro Ser Ala Thr Phe Arg Gly Thr
     55                  60                  65

cgc atc gcc atg gtt ttc caa gaa cca atg agc gca ctc aac ccg ctc   355
Arg Ile Ala Met Val Phe Gln Glu Pro Met Ser Ala Leu Asn Pro Leu
 70                  75                  80                  85

atg cgc atc ggc cgc caa atc gaa gaa atg atg acc ctg cac ggg gca   403
Met Arg Ile Gly Arg Gln Ile Glu Glu Met Met Thr Leu His Gly Ala
                 90                  95                 100

agc aaa aaa gac gcg cgg gcg cgc tta aaa agc ttg ctt atc gac gtc   451
Ser Lys Lys Asp Ala Arg Ala Arg Leu Lys Ser Leu Leu Ile Asp Val
            105                 110                 115

tcc ctc ccc gaa cgc acc gct tcg gcc tac cca cac gaa ctt tca ggc   499
Ser Leu Pro Glu Arg Thr Ala Ser Ala Tyr Pro His Glu Leu Ser Gly
        120                 125                 130

ggg caa cgc caa cgc gca cta atc gca atg gcg ctg gcc aat gat cct   547
Gly Gln Arg Gln Arg Ala Leu Ile Ala Met Ala Leu Ala Asn Asp Pro
    135                 140                 145

gac ctg ttg atc tgc gat gaa ccc acc acg gct ttg gat gtg gtt gtg   595
Asp Leu Leu Ile Cys Asp Glu Pro Thr Thr Ala Leu Asp Val Val Val
150                 155                 160                 165

caa aaa caa atc gtc gat ctg ctg ctg cgt ctc acc aaa gaa cgt ggc   643
Gln Lys Gln Ile Val Asp Leu Leu Leu Arg Leu Thr Lys Glu Arg Gly
                170                 175                 180

acc gct tta ttg ttc atc acc cac gat ctt gga ctc atc gcg cgc acc   691
Thr Ala Leu Leu Phe Ile Thr His Asp Leu Gly Leu Ile Ala Arg Thr
            185                 190                 195

tgc gaa cgc tta ttg gtg atg aaa tcc ggc gaa acc gta gaa cgc ggc   739
Cys Glu Arg Leu Leu Val Met Lys Ser Gly Glu Thr Val Glu Arg Gly
        200                 205                 210

gac acc gag gca att ctt cgc tcc ccc gcc cat tcg tat acc caa cag   787
Asp Thr Glu Ala Ile Leu Arg Ser Pro Ala His Ser Tyr Thr Gln Gln
    215                 220                 225

ctc ctt gat gct tca atc ctt gac cag cca gaa atc gcc tca gat tct   835
Leu Leu Asp Ala Ser Ile Leu Asp Gln Pro Glu Ile Ala Ser Asp Ser
230                 235                 240                 245

ggc gcg ccg gta gtg att gat gtg gag gag gcg tcg aaa agc ttt aaa   883
Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala Ser Lys Ser Phe Lys
                250                 255                 260

gaa acc acc gcc ctc cac aag gtt tca ttg gcg gtg cgc aaa ggt gac   931
Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala Val Arg Lys Gly Asp
            265                 270                 275

ctg ctt gga ata gtc ggc gga tca ggt tcc ggc aaa acg act ctg ctg   979
Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly Lys Thr Thr Leu Leu
        280                 285                 290
```

US 2005/0196750 A1

```
aag ctc atc gcc ggt ttg gat aag ccc aca acc ggt acc gtt gcg gta   1027
Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr Gly Thr Val Ala Val
    295                 300                 305

acc ggt ggt gtg cag atg gtg ttt cag gat ccc caa tca agc ctc aac   1075
Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro Gln Ser Ser Leu Asn
310                 315                 320                 325

cca cgg atg aaa atc aaa gac att gtc gcc gaa cca ctg ctt ggt tgg   1123
Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu Pro Leu Leu Gly Trp
                330                 335                 340

aac gcg gcg gag aaa acc aca cgg gtt gcg gaa gtc atc acc caa gtg   1171
Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu Val Ile Thr Gln Val
            345                 350                 355

gga ctg agc ccc gat gtc tta gat cgc tac ccc cac gaa ttc tcc gga   1219
Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro His Glu Phe Ser Gly
        360                 365                 370

gga cag cgc caa cga atc tcc atc gcc aga gcc ctc gcc atc aaa cca   1267
Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala Leu Ala Ile Lys Pro
    375                 380                 385

gcg atc ctg ctt gcc gac gaa cct gtc tcc gcc ctc gat gtg tcc gta   1315
Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala Leu Asp Val Ser Val
390                 395                 400                 405

cgt aaa caa gta ctg gat ctt ctc caa caa ctc gtc gaa gaa tac ggc   1363
Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu Val Glu Glu Tyr Gly
                410                 415                 420

atc acc ttg gtg ttc gtc tcc cac gat ctg gca gtg gtg aga cac ctg   1411
Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val Arg His Leu
            425                 430                 435

tgc aca acc gtg tgg gtg atg gaa cag gga cga gtc ctt gag caa ggg   1459
Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu Glu Gln Gly
        440                 445                 450

ccc atc gat tcg gtt tat gat cac cca cag acc gaa tac acc aag gag   1507
Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr Glu Tyr Thr Lys Glu
    455                 460                 465

ctg ctt gat gcc gtt ccg cgg ttg agc ctt taaaccagcg cagatgacaa     1557
Leu Leu Asp Ala Val Pro Arg Leu Ser Leu
470                 475

cgc                                                               1560
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<210> 130
<211> 479
<212> PRT
<213> Corynebacterium glutamicum

<400> 130

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Val Leu Lys Val Ser Asp Leu Thr Val Gly Asn Asn Phe Val His Asn
  1               5                  10                  15

Val Ser Phe Glu Val Asn Pro Gly Glu Arg Val Gly Ile Ile Gly Glu
```

```
                  20                  25                  30

Ser Gly Ser Gly Lys Ser Leu Thr Ala Leu Ser Ile Met Gly Leu Thr
          35                  40                  45

Asp Leu Pro Thr Thr Gly Gln Ile Thr Phe Asn Gly Lys Pro Ser Ala
      50                  55                  60

Thr Phe Arg Gly Thr Arg Ile Ala Met Val Phe Gln Glu Pro Met Ser
 65                  70                  75                  80

Ala Leu Asn Pro Leu Met Arg Ile Gly Arg Gln Ile Glu Glu Met Met
                 85                  90                  95

Thr Leu His Gly Ala Ser Lys Lys Asp Ala Arg Ala Arg Leu Lys Ser
            100                 105                 110

Leu Leu Ile Asp Val Ser Leu Pro Glu Arg Thr Ala Ser Ala Tyr Pro
        115                 120                 125

His Glu Leu Ser Gly Gly Gln Arg Gln Arg Ala Leu Ile Ala Met Ala
    130                 135                 140

Leu Ala Asn Asp Pro Asp Leu Leu Ile Cys Asp Glu Pro Thr Thr Ala
145                 150                 155                 160

Leu Asp Val Val Val Gln Lys Gln Ile Val Asp Leu Leu Leu Arg Leu
                165                 170                 175

Thr Lys Glu Arg Gly Thr Ala Leu Leu Phe Ile Thr His Asp Leu Gly
            180                 185                 190

Leu Ile Ala Arg Thr Cys Glu Arg Leu Leu Val Met Lys Ser Gly Glu
        195                 200                 205

Thr Val Glu Arg Gly Asp Thr Glu Ala Ile Leu Arg Ser Pro Ala His
    210                 215                 220

Ser Tyr Thr Gln Gln Leu Leu Asp Ala Ser Ile Leu Asp Gln Pro Glu
225                 230                 235                 240

Ile Ala Ser Asp Ser Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala
                245                 250                 255

Ser Lys Ser Phe Lys Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala
            260                 265                 270

Val Arg Lys Gly Asp Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly
        275                 280                 285

Lys Thr Thr Leu Leu Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr
    290                 295                 300

Gly Thr Val Ala Val Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro
305                 310                 315                 320

Gln Ser Ser Leu Asn Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu
                325                 330                 335

Pro Leu Leu Gly Trp Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu
            340                 345                 350
```

```
Val Ile Thr Gln Val Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro
        355                 360                 365

His Glu Phe Ser Gly Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala
    370                 375                 380

Leu Ala Ile Lys Pro Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala
385                 390                 395                 400

Leu Asp Val Ser Val Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu
                405                 410                 415

Val Glu Glu Tyr Gly Ile Thr Leu Val Phe Val Ser His Asp Leu Ala
            420                 425                 430

Val Val Arg His Leu Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg
        435                 440                 445

Val Leu Glu Gln Gly Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr
    450                 455                 460

Glu Tyr Thr Lys Glu Leu Leu Asp Ala Val Pro Arg Leu Ser Leu
465                 470                 475


<210> 131
<211> 1118
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1095)
<223> FRXA02795

<400> 131
atc gac gtc tcc ctc ccc gaa cgc acc gct tcg gcc tac cca cac gaa   48
Ile Asp Val Ser Leu Pro Glu Arg Thr Ala Ser Ala Tyr Pro His Glu
  1               5                  10                  15

ctt tca ggc ggg caa cgc caa cgc gca cta atc gca atg gcg ctg gcc   96
Leu Ser Gly Gly Gln Arg Gln Arg Ala Leu Ile Ala Met Ala Leu Ala
             20                  25                  30

aat gat cct gac ctg ttg atc tgc gat gaa ccc acc acg gct ttg gat   144
Asn Asp Pro Asp Leu Leu Ile Cys Asp Glu Pro Thr Thr Ala Leu Asp
         35                  40                  45

gtg gtt gtg caa aaa caa atc gtc gat ctg ctg ctg cgt ctc acc aaa   192
Val Val Val Gln Lys Gln Ile Val Asp Leu Leu Leu Arg Leu Thr Lys
     50                  55                  60

gaa cgt ggc acc gct tta ttg ttc atc acc cac gat ctt gga ctc atc   240
Glu Arg Gly Thr Ala Leu Leu Phe Ile Thr His Asp Leu Gly Leu Ile
 65                  70                  75                  80

gcg cgc acc tgc gaa cgc tta ttg gtg atg aaa tcc ggc gaa acc gta   288
Ala Arg Thr Cys Glu Arg Leu Leu Val Met Lys Ser Gly Glu Thr Val
                 85                  90                  95
```

```
gaa cgc ggc gac acc gag gca att ctt cgc tcc ccc gcc cat tcg tat   336
Glu Arg Gly Asp Thr Glu Ala Ile Leu Arg Ser Pro Ala His Ser Tyr
            100                 105                 110

acc caa cag ctc ctt gat gct tca atc ctt gac cag cca gaa atc gcc   384
Thr Gln Gln Leu Leu Asp Ala Ser Ile Leu Asp Gln Pro Glu Ile Ala
        115                 120                 125

tca gat tct ggc gcg ccg gta gtg att gat gtg gag gag gcg tcg aaa   432
Ser Asp Ser Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala Ser Lys
    130                 135                 140

agc ttt aaa gaa acc acc gcc ctc cac aag gtt tca ttg gcg gtg cgc   480
Ser Phe Lys Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala Val Arg
145                 150                 155                 160

aaa ggt gac ctg ctt gga ata gtc ggc gga tca ggt tcc ggc aaa acg   528
Lys Gly Asp Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly Lys Thr
                165                 170                 175

act ctg ctg aag ctc atc gcc ggt ttg gat aag ccc aca acc ggt acc   576
Thr Leu Leu Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr Gly Thr
            180                 185                 190

gtt gcg gta acc ggt ggt gtg cag atg gtg ttt cag gat ccc caa tca   624
Val Ala Val Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro Gln Ser
        195                 200                 205

agc ctc aac cca cgg atg aaa atc aaa gac att gtc gcc gaa cca ctg   672
Ser Leu Asn Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu Pro Leu
    210                 215                 220

ctt ggt tgg aac gcg gcg gag aaa acc aca cgg gtt gcg gaa gtc atc   720
Leu Gly Trp Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu Val Ile
225                 230                 235                 240

acc caa gtg gga ctg agc ccc gat gtc tta gat cgc tac ccc cac gaa   768
Thr Gln Val Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro His Glu
                245                 250                 255

ttc tcc gga gga cag cgc caa cga atc tcc atc gcc aga gcc ctc gcc   816
Phe Ser Gly Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala Leu Ala
            260                 265                 270

atc aaa cca gcg atc ctg ctt gcc gac gaa cct gtc tcc gcc ctc gat   864
Ile Lys Pro Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala Leu Asp
        275                 280                 285

gtg tcc gta cgt aaa caa gta ctg gat ctt ctc caa caa ctc gtc gaa   912
Val Ser Val Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu Val Glu
    290                 295                 300

gaa tac ggc atc acc ttg gtg ttc gtc tcc cac gat ctg gca gtg gtg   960
Glu Tyr Gly Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val
305                 310                 315                 320

aga cac ctg tgc aca acc gtg tgg gtg atg gaa cag gga cga gtc ctt  1008
Arg His Leu Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu
                325                 330                 335

gag caa ggg ccc atc gat tcg gtt tat gat cac cca cag acc gaa tac  1056
```

09534-4-09-09-09

```
Glu Gln Gly Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr Glu Tyr
            340                 345                 350

acc aag gag ctg ctt gat gcc gtt ccg cgg ttg agc ctt taaaccagcg    1105
Thr Lys Glu Leu Leu Asp Ala Val Pro Arg Leu Ser Leu
        355                 360                 365

cagatgacaa cgc                                                   1118
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<210> 132
<211> 365
<212> PRT
<213> Corynebacterium glutamicum

<400> 132

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Ile Asp Val Ser Leu Pro Glu Arg Thr Ala Ser Ala Tyr Pro His Glu
  1               5                  10                  15

Leu Ser Gly Gly Gln Arg Gln Arg Ala Leu Ile Ala Met Ala Leu Ala
            20                  25                  30

Asn Asp Pro Asp Leu Leu Ile Cys Asp Glu Pro Thr Thr Ala Leu Asp
        35                  40                  45

Val Val Val Gln Lys Gln Ile Val Asp Leu Leu Leu Arg Leu Thr Lys
    50                  55                  60

Glu Arg Gly Thr Ala Leu Leu Phe Ile Thr His Asp Leu Gly Leu Ile
65                  70                  75                  80

Ala Arg Thr Cys Glu Arg Leu Leu Val Met Lys Ser Gly Glu Thr Val
                85                  90                  95

Glu Arg Gly Asp Thr Glu Ala Ile Leu Arg Ser Pro Ala His Ser Tyr
            100                 105                 110

Thr Gln Gln Leu Leu Asp Ala Ser Ile Leu Asp Gln Pro Glu Ile Ala
        115                 120                 125

Ser Asp Ser Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala Ser Lys
    130                 135                 140

Ser Phe Lys Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala Val Arg
145                 150                 155                 160

Lys Gly Asp Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly Lys Thr
                165                 170                 175

Thr Leu Leu Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr Gly Thr
            180                 185                 190

Val Ala Val Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro Gln Ser
        195                 200                 205

Ser Leu Asn Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu Pro Leu
    210                 215                 220

Leu Gly Trp Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu Val Ile
225                 230                 235                 240
```

```
Thr Gln Val Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro His Glu
                245                 250                 255

Phe Ser Gly Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala Leu Ala
            260                 265                 270

Ile Lys Pro Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala Leu Asp
        275                 280                 285

Val Ser Val Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu Val Glu
    290                 295                 300

Glu Tyr Gly Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val
305                 310                 315                 320

Arg His Leu Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu
                325                 330                 335

Glu Gln Gly Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr Glu Tyr
            340                 345                 350

Thr Lys Glu Leu Leu Asp Ala Val Pro Arg Leu Ser Leu
        355                 360                 365


<210> 133
<211> 1854
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1831)
<223> RXN01939

<400> 133
tgctgttcta ccccgcaatg gcacttgcac taaccgtttt gagcttcatc atgatgggcg 60

atgtcgtccg cgacgctctg gatcctaagt cgaggaagcg atg acc acc aac atc   115
                                              Met Thr Thr Asn Ile
                                                1               5

cca caa acc ccc aac cac gag ggt gaa cag cca ctg ctc gag ctg aag   163
Pro Gln Thr Pro Asn His Glu Gly Glu Gln Pro Leu Leu Glu Leu Lys
                10                  15                  20

gat cta aag att tcc ttc acc tcc tcc acc ggt gtt gtc gac gct gtc   211
Asp Leu Lys Ile Ser Phe Thr Ser Ser Thr Gly Val Val Asp Ala Val
            25                  30                  35

cgt ggc gca aac ctc acc att tat cct ggc caa tct gtt gcc atc gtg   259
Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln Ser Val Ala Ile Val
        40                  45                  50

ggt gaa tcc ggt tca ggt aaa tcg acc acg gca atg tcg atc atc ggt   307
Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Met Ser Ile Ile Gly
    55                  60                  65

ctg ctt cca ggc acc ggc aaa gtg acc gaa ggt tcc atc atg ttt gat   355
Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly Ser Ile Met Phe Asp
70                  75                  80                  85
```

```
ggc caa gac atc aca ggc ttg agt aac aag cag atg gaa aag tac cgc   403
Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln Met Glu Lys Tyr Arg
                 90                  95                 100

ggt tca gaa atc gga ctg gtc ccc cag gat ccg atg acc aac ttg aac   451
Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro Met Thr Asn Leu Asn
            105                 110                 115

ccg gtg tgg cgc atc ggc acc cag gtc aag gaa tcc ctc cga gcc aac   499
Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu Ser Leu Arg Ala Asn
        120                 125                 130

cac gtg gtt cca ggc tca gag atg gac aag cgc gtg gca gaa gtt ctg   547
His Val Val Pro Gly Ser Glu Met Asp Lys Arg Val Ala Glu Val Leu
    135                 140                 145

gcc gag gca ggt ctt cct gat gct gag cgt cgc gca aag cag tac cca   595
Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg Ala Lys Gln Tyr Pro
150                 155                 160                 165

cat gag ttc tct ggc ggt atg cgc cag cgc gca ctg atc gcc att ggt   643
His Glu Phe Ser Gly Gly Met Arg Gln Arg Ala Leu Ile Ala Ile Gly
                170                 175                 180

ttg gcg gca cgc ccg aag ctc ttg atc gcc gac gag ccc acc tct gcg   691
Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp Glu Pro Thr Ser Ala
            185                 190                 195

ctg gat gtc acc gtg cag cgc caa atc ctt gat cac ctt gaa aca ctg   739
Leu Asp Val Thr Val Gln Arg Gln Ile Leu Asp His Leu Glu Thr Leu
        200                 205                 210

acc aag gat ctc ggc acc gca gtg cta ttt att acc cac gac ttg ggc   787
Thr Lys Asp Leu Gly Thr Ala Val Leu Phe Ile Thr His Asp Leu Gly
    215                 220                 225

ctt gcc gct gag cgc gcg gag cac ctc gtg gtg atg cac cgc gga cgc   835
Leu Ala Ala Glu Arg Ala Glu His Leu Val Val Met His Arg Gly Arg
230                 235                 240                 245

atc gtg gag tcc ggg cca tca ttg aag att ctg cgc aat cca cag cac   883
Ile Val Glu Ser Gly Pro Ser Leu Lys Ile Leu Arg Asn Pro Gln His
                250                 255                 260

cca tat acc caa cgc ttg gtt aag gct gcg ccg tct ctg gct tct gca   931
Pro Tyr Thr Gln Arg Leu Val Lys Ala Ala Pro Ser Leu Ala Ser Ala
            265                 270                 275

cgt att caa agt gcg cag gaa caa ggc att gaa tct gca gaa ctg ctc   979
Arg Ile Gln Ser Ala Gln Glu Gln Gly Ile Glu Ser Ala Glu Leu Leu
        280                 285                 290

tct gca acg gcc gtt gct gag ggc act att cca gag atg gaa gaa aaa   1027
Ser Ala Thr Ala Val Ala Glu Gly Thr Ile Pro Glu Met Glu Glu Lys
    295                 300                 305

gtt atc gag gtg aaa aac ctc acc cgc gaa ttt gat atc cgc ggt gcc   1075
Val Ile Glu Val Lys Asn Leu Thr Arg Glu Phe Asp Ile Arg Gly Ala
310                 315                 320                 325
```

```
cgt ggc gat aag aag aag ctg aag gcc gtt gat gat gtg tcc ttc ttc   1123
Arg Gly Asp Lys Lys Lys Leu Lys Ala Val Asp Asp Val Ser Phe Phe
                330                 335                 340

gta cgt aaa ggc acc acc acc gca ctt gtg ggt gaa tcc ggt tcg ggt   1171
Val Arg Lys Gly Thr Thr Thr Ala Leu Val Gly Glu Ser Gly Ser Gly
            345                 350                 355

aaa tcc acc gtg gcc aac atg gtg ctc aac ctt ctc gag cca acc agc   1219
Lys Ser Thr Val Ala Asn Met Val Leu Asn Leu Leu Glu Pro Thr Ser
        360                 365                 370

gga gag gtg ctc tac aac ggc acc gat ctt acg tcc ttg agc cac aag   1267
Gly Glu Val Leu Tyr Asn Gly Thr Asp Leu Thr Ser Leu Ser His Lys
    375                 380                 385

gaa atc ttc caa atg cga cgc aaa ctg cag gtg gtg ttc cag aac ccc   1315
Glu Ile Phe Gln Met Arg Arg Lys Leu Gln Val Val Phe Gln Asn Pro
390                 395                 400                 405

tac ggc tcg ctt gat ccg atg tac tcc atc tac cgg tgt att gag gaa   1363
Tyr Gly Ser Leu Asp Pro Met Tyr Ser Ile Tyr Arg Cys Ile Glu Glu
                410                 415                 420

ccg ctg acc atc cac aag gtt ggt gga gac cgc aag gca cgc gaa gct   1411
Pro Leu Thr Ile His Lys Val Gly Gly Asp Arg Lys Ala Arg Glu Ala
            425                 430                 435

cgc gtc gct gaa ctt ctc gat atg gtg tcc atg ccc agg tcc acc atg   1459
Arg Val Ala Glu Leu Leu Asp Met Val Ser Met Pro Arg Ser Thr Met
        440                 445                 450

cgc cgc tac ccc aac gag ctt tcc ggt ggc caa cgt cag cgc atc gcc   1507
Arg Arg Tyr Pro Asn Glu Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala
    455                 460                 465

atc gcc cgt gca ttg gca ctg aat cca gaa gtg atc gtg ttg gat gaa   1555
Ile Ala Arg Ala Leu Ala Leu Asn Pro Glu Val Ile Val Leu Asp Glu
470                 475                 480                 485

gcg gtt tcc gct ttg gac gtg ttg gtt cag aac cag atc ctc acc ctg   1603
Ala Val Ser Ala Leu Asp Val Leu Val Gln Asn Gln Ile Leu Thr Leu
                490                 495                 500

ctt gca gaa ctt cag cag gaa ctg aag ctc acc tat ttg ttc atc acc   1651
Leu Ala Glu Leu Gln Gln Glu Leu Lys Leu Thr Tyr Leu Phe Ile Thr
            505                 510                 515

cac gac ttg gcc gtt gtt cga caa acc gcc gac gat gtt gtg gtg atg   1699
His Asp Leu Ala Val Val Arg Gln Thr Ala Asp Asp Val Val Val Met
        520                 525                 530

caa aag gga cga atc gtt gaa aag ggt cgt acc gac gac atc ttc aac   1747
Gln Lys Gly Arg Ile Val Glu Lys Gly Arg Thr Asp Asp Ile Phe Asn
    535                 540                 545

gat cct cag cag cac tac acc cgc gat ttg atc aat gcg gta cct ggt   1795
Asp Pro Gln Gln His Tyr Thr Arg Asp Leu Ile Asn Ala Val Pro Gly
550                 555                 560                 565

ctg gga atc gag ttg ggt act gga gaa aac ctg gtt taacccgcac        1841
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Leu Gly Ile Glu Leu Gly Thr Gly Glu Asn Leu Val
570 575

agcctcacta aac 1854

<210> 134
<211> 577
<212> PRT
<213> Corynebacterium glutamicum

<400> 134
Met Thr Thr Asn Ile Pro Gln Thr Pro Asn His Glu Gly Glu Gln Pro
1 5 10 15

Leu Leu Glu Leu Lys Asp Leu Lys Ile Ser Phe Thr Ser Ser Thr Gly
20 25 30

Val Val Asp Ala Val Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln
35 40 45

Ser Val Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala
50 55 60

Met Ser Ile Ile Gly Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly
65 70 75 80

Ser Ile Met Phe Asp Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln
85 90 95

Met Glu Lys Tyr Arg Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro
100 105 110

Met Thr Asn Leu Asn Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu
115 120 125

Ser Leu Arg Ala Asn His Val Val Pro Gly Ser Glu Met Asp Lys Arg
130 135 140

Val Ala Glu Val Leu Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg
145 150 155 160

Ala Lys Gln Tyr Pro His Glu Phe Ser Gly Gly Met Arg Gln Arg Ala
165 170 175

Leu Ile Ala Ile Gly Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp
180 185 190

Glu Pro Thr Ser Ala Leu Asp Val Thr Val Gln Arg Gln Ile Leu Asp
195 200 205

His Leu Glu Thr Leu Thr Lys Asp Leu Gly Thr Ala Val Leu Phe Ile
210 215 220

Thr His Asp Leu Gly Leu Ala Ala Glu Arg Ala Glu His Leu Val Val
225 230 235 240

Met His Arg Gly Arg Ile Val Glu Ser Gly Pro Ser Leu Lys Ile Leu
245 250 255

Arg Asn Pro Gln His Pro Tyr Thr Gln Arg Leu Val Lys Ala Ala Pro

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260 265 270

Ser Leu Ala Ser Ala Arg Ile Gln Ser Ala Gln Glu Gln Gly Ile Glu
275 280 285

Ser Ala Glu Leu Leu Ser Ala Thr Ala Val Ala Glu Gly Thr Ile Pro
290 295 300

Glu Met Glu Glu Lys Val Ile Glu Val Lys Asn Leu Thr Arg Glu Phe
305 310 315 320

Asp Ile Arg Gly Ala Arg Gly Asp Lys Lys Lys Leu Lys Ala Val Asp
325 330 335

Asp Val Ser Phe Phe Val Arg Lys Gly Thr Thr Thr Ala Leu Val Gly
340 345 350

Glu Ser Gly Ser Gly Lys Ser Thr Val Ala Asn Met Val Leu Asn Leu
355 360 365

Leu Glu Pro Thr Ser Gly Glu Val Leu Tyr Asn Gly Thr Asp Leu Thr
370 375 380

Ser Leu Ser His Lys Glu Ile Phe Gln Met Arg Arg Lys Leu Gln Val
385 390 395 400

Val Phe Gln Asn Pro Tyr Gly Ser Leu Asp Pro Met Tyr Ser Ile Tyr
405 410 415

Arg Cys Ile Glu Glu Pro Leu Thr Ile His Lys Val Gly Gly Asp Arg
420 425 430

Lys Ala Arg Glu Ala Arg Val Ala Glu Leu Leu Asp Met Val Ser Met
435 440 445

Pro Arg Ser Thr Met Arg Arg Tyr Pro Asn Glu Leu Ser Gly Gly Gln
450 455 460

Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ala Leu Asn Pro Glu Val
465 470 475 480

Ile Val Leu Asp Glu Ala Val Ser Ala Leu Asp Val Leu Val Gln Asn
485 490 495

Gln Ile Leu Thr Leu Leu Ala Glu Leu Gln Gln Glu Leu Lys Leu Thr
500 505 510

Tyr Leu Phe Ile Thr His Asp Leu Ala Val Val Arg Gln Thr Ala Asp
515 520 525

Asp Val Val Val Met Gln Lys Gly Arg Ile Val Glu Lys Gly Arg Thr
530 535 540

Asp Asp Ile Phe Asn Asp Pro Gln Gln His Tyr Thr Arg Asp Leu Ile
545 550 555 560

Asn Ala Val Pro Gly Leu Gly Ile Glu Leu Gly Thr Gly Glu Asn Leu
565 570 575

Val

<210> 135
<211> 691
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(691)
<223> FRXA00761

<400> 135
tgctgttcta ccccgcaatg gcacttgcac taaccgtttt gagcttcatc atgatgggcg 60

atgtcgtccg cgacgctctg gatcctaagt cgaggaagcg atg acc acc aac atc 115
Met Thr Thr Asn Ile
1 5

cca caa acc ccc aac cac gag ggt gaa cag cca ctg ctc gag ctg aag 163
Pro Gln Thr Pro Asn His Glu Gly Glu Gln Pro Leu Leu Glu Leu Lys
10 15 20

gat cta aag att tcc ttc acc tcc tcc acc ggt gtt gtc gac gct gtc 211
Asp Leu Lys Ile Ser Phe Thr Ser Ser Thr Gly Val Val Asp Ala Val
25 30 35

cgt ggc gca aac ctc acc att tat cct ggc caa tct gtt gcc atc gtg 259
Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln Ser Val Ala Ile Val
40 45 50

ggt gaa tcc ggt tca ggt aaa tcg acc acg gca atg tcg atc atc ggt 307
Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Met Ser Ile Ile Gly
55 60 65

ctg ctt cca ggc acc ggc aaa gtg acc gaa ggt tcc atc atg ttt gat 355
Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly Ser Ile Met Phe Asp
70 75 80 85

ggc caa gac atc aca ggc ttg agt aac aag cag atg gaa aag tac cgc 403
Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln Met Glu Lys Tyr Arg
90 95 100

ggt tca gaa atc gga ctg gtc ccc cag gat ccg atg acc aac ttg aac 451
Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro Met Thr Asn Leu Asn
105 110 115

ccg gtg tgg cgc atc ggc acc cag gtc aag gaa tcc ctc cga gcc aac 499
Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu Ser Leu Arg Ala Asn
120 125 130

cac gtg gtt cca ggc tca gag atg gac aag cgc gtg gca gaa gtt ctg 547
His Val Val Pro Gly Ser Glu Met Asp Lys Arg Val Ala Glu Val Leu
135 140 145

gcc gag gca ggt ctt cct gat gct gag cgt cgc gca aag cag tac cca 595
Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg Ala Lys Gln Tyr Pro
150 155 160 165

cat gag ttc tct ggc ggt atg cgc cac cgc gca ctg atc gcc att ggt 643
His Glu Phe Ser Gly Gly Met Arg His Arg Ala Leu Ile Ala Ile Gly

170 175 180

ttg gcg gca cgc ccg aag ctc ttg atc gcc gac gag ccc acc tct gcg 691
Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp Glu Pro Thr Ser Ala
185 190 195

<210> 136
<211> 197
<212> PRT
<213> Corynebacterium glutamicum

<400> 136
Met Thr Thr Asn Ile Pro Gln Thr Pro Asn His Glu Gly Glu Gln Pro
1 5 10 15

Leu Leu Glu Leu Lys Asp Leu Lys Ile Ser Phe Thr Ser Ser Thr Gly
20 25 30

Val Val Asp Ala Val Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln
35 40 45

Ser Val Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala
50 55 60

Met Ser Ile Ile Gly Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly
65 70 75 80

Ser Ile Met Phe Asp Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln
85 90 95

Met Glu Lys Tyr Arg Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro
100 105 110

Met Thr Asn Leu Asn Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu
115 120 125

Ser Leu Arg Ala Asn His Val Val Pro Gly Ser Glu Met Asp Lys Arg
130 135 140

Val Ala Glu Val Leu Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg
145 150 155 160

Ala Lys Gln Tyr Pro His Glu Phe Ser Gly Gly Met Arg His Arg Ala
165 170 175

Leu Ile Ala Ile Gly Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp
180 185 190

Glu Pro Thr Ser Ala
195

<210> 137
<211> 626
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(603)

<223> FRXA01939

<400> 137

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tct aca agc ggc acc gat ctt acg tcc ttg agc cac aag gaa atc ttc   48
Ser Thr Ser Gly Thr Asp Leu Thr Ser Leu Ser His Lys Glu Ile Phe
  1               5                  10                  15

caa atg cga cgc aaa ctg cag gtg gtg ttc cag aac ccc tac ggc tcg   96
Gln Met Arg Arg Lys Leu Gln Val Val Phe Gln Asn Pro Tyr Gly Ser
             20                  25                  30

ctt gat ccg atg tac tcc atc tac cgg tgt att gag gaa ccg ctg acc  144
Leu Asp Pro Met Tyr Ser Ile Tyr Arg Cys Ile Glu Glu Pro Leu Thr
         35                  40                  45

atc cac aag gtt ggt gga gac cgc aag gca cgc gaa gct cgc gtc gtt  192
Ile His Lys Val Gly Gly Asp Arg Lys Ala Arg Glu Ala Arg Val Val
     50                  55                  60

gaa ctt ctc gat atg gtg tcc atg ccc agg tcc acc atg cgc cgc tac  240
Glu Leu Leu Asp Met Val Ser Met Pro Arg Ser Thr Met Arg Arg Tyr
 65                  70                  75                  80

ccc aac gag ctt tcc ggt ggc caa cgt cag cgc atc gcc atc gcc cgt  288
Pro Asn Glu Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg
                 85                  90                  95

gca ttg gca ctg aat cca gaa gtg atc gtg ttg gat gaa gcg gtt tcc  336
Ala Leu Ala Leu Asn Pro Glu Val Ile Val Leu Asp Glu Ala Val Ser
            100                 105                 110

gct ttg gac gtg ttg gtt cag aac cag atc ctc acc ctg ctt gca gaa  384
Ala Leu Asp Val Leu Val Gln Asn Gln Ile Leu Thr Leu Leu Ala Glu
        115                 120                 125

ctt cag cag gaa ctg aag ctc acc tat ttg ttc atc acc cac gac ttg  432
Leu Gln Gln Glu Leu Lys Leu Thr Tyr Leu Phe Ile Thr His Asp Leu
    130                 135                 140

gcc gtt gtt cga caa acc gcc gac gat gtt gtg gtg atg caa aag gga  480
Ala Val Val Arg Gln Thr Ala Asp Asp Val Val Val Met Gln Lys Gly
145                 150                 155                 160

cga atc gtt gaa aag ggt cgt acc gac gac atc ttc aac gat cct cag  528
Arg Ile Val Glu Lys Gly Arg Thr Asp Asp Ile Phe Asn Asp Pro Gln
                165                 170                 175

cag cac tac acc cgc gat ttg atc aat gcg gta cct ggt ctg gga atc  576
Gln His Tyr Thr Arg Asp Leu Ile Asn Ala Val Pro Gly Leu Gly Ile
            180                 185                 190

gag ttg ggt act gga gaa aac ctg gtt taacccgcac agcctcacta        623
Glu Leu Gly Thr Gly Glu Asn Leu Val
        195                 200

aac                                                              626
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<210> 138
<211> 201
<212> PRT

<213> Corynebacterium glutamicum

<400> 138

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Ser Thr Ser Gly Thr Asp Leu Thr Ser Leu Ser His Lys Glu Ile Phe
  1               5                  10                  15

Gln Met Arg Arg Lys Leu Gln Val Val Phe Gln Asn Pro Tyr Gly Ser
             20                  25                  30

Leu Asp Pro Met Tyr Ser Ile Tyr Arg Cys Ile Glu Glu Pro Leu Thr
         35                  40                  45

Ile His Lys Val Gly Gly Asp Arg Lys Ala Arg Glu Ala Arg Val Val
     50                  55                  60

Glu Leu Leu Asp Met Val Ser Met Pro Arg Ser Thr Met Arg Arg Tyr
 65                  70                  75                  80

Pro Asn Glu Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg
                 85                  90                  95

Ala Leu Ala Leu Asn Pro Glu Val Ile Val Leu Asp Glu Ala Val Ser
            100                 105                 110

Ala Leu Asp Val Leu Val Gln Asn Gln Ile Leu Thr Leu Leu Ala Glu
        115                 120                 125

Leu Gln Gln Glu Leu Lys Leu Thr Tyr Leu Phe Ile Thr His Asp Leu
    130                 135                 140

Ala Val Val Arg Gln Thr Ala Asp Asp Val Val Val Met Gln Lys Gly
145                 150                 155                 160

Arg Ile Val Glu Lys Gly Arg Thr Asp Asp Ile Phe Asn Asp Pro Gln
                165                 170                 175

Gln His Tyr Thr Arg Asp Leu Ile Asn Ala Val Pro Gly Leu Gly Ile
            180                 185                 190

Glu Leu Gly Thr Gly Glu Asn Leu Val
        195                 200
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<210> 139
<211> 1047
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1024)
<223> RXN00759

<400> 139

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tcaccttgaa cacttaaaac ataacttcat ccggcgcttt attagcttga agcgccccgc 60

accataatcc attccccagc aagcaaggac acccacgctc atg ctt cgt tac gtc   115
                                              Met Leu Arg Tyr Val
                                                1               5

ggg cga cgt ttg ctc caa atg att ccg gtc ttt ttc gga gcg acc tta   163
```

```
Gly Arg Arg Leu Leu Gln Met Ile Pro Val Phe Phe Gly Ala Thr Leu
                10                  15                  20

ctg att tac gcc ctc gtg ttc ctc atg cct ggt gac cca gtc cag gca   211
Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly Asp Pro Val Gln Ala
            25                  30                  35

ttg gga ggt gac cgc ggc cta acc gag gct gcg gcc gag aaa atc cgt   259
Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala Ala Glu Lys Ile Arg
        40                  45                  50

caa gaa tac aat ctt gat aaa ccc ttc atc gtt caa tac ctc ctg tac   307
Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val Gln Tyr Leu Leu Tyr
    55                  60                  65

atc aag ggc atc ttc gtc tta gat ttt gga aca acc ttc tct ggt cag   355
Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr Thr Phe Ser Gly Gln
70                  75                  80                  85

cca gtt att gat gtg atg gcc agg gcc ttc ccc gtc acc atc aaa ctc   403
Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro Val Thr Ile Lys Leu
                90                  95                  100

gcc atc atg gcc ctg ctg ttt gaa tca atc ctc ggc att atc ttt ggt   451
Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu Gly Ile Ile Phe Gly
            105                 110                 115

gtc atc gca ggt att cgc cgc gga gga atc ttc gac tcc acc gtg ctg   499
Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe Asp Ser Thr Val Leu
        120                 125                 130

gtc ctt tct ctg ata gtc atc gca gtc ccc acc ttc gtc att ggt ttc   547
Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr Phe Val Ile Gly Phe
    135                 140                 145

gtg ctg cag ttc tta gtc ggc gtg aaa tgg ggc tta ctg ccc gtc acc   595
Val Leu Gln Phe Leu Val Gly Val Lys Trp Gly Leu Leu Pro Val Thr
150                 155                 160                 165

gta ggt tcc aac aca tca ata acg gcg ctg atc atg ccg gct gtc gta   643
Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile Met Pro Ala Val Val
                170                 175                 180

ctg ggt gca gta tcg ttc gcc tac gtt ctt cgc ctc acc aga caa tcc   691
Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg Leu Thr Arg Gln Ser
            185                 190                 195

gtg agc gaa aac ctc cgc gct gat tac gtt cga acc gct cga gca aaa   739
Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg Thr Ala Arg Ala Lys
        200                 205                 210

ggc atg tcc gga ttc aac gtg atg aac cgc cat gtg ctt cga aac tca   787
Gly Met Ser Gly Phe Asn Val Met Asn Arg His Val Leu Arg Asn Ser
    215                 220                 225

ctg att ccc gtt gcc acc ttc ctg ggc gcc gat ctc ggt gca ctg atg   835
Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp Leu Gly Ala Leu Met
230                 235                 240                 245

ggt gga gcg att gtc acc gaa ggt atc ttc ggc atc aac ggt gtc ggt   883
Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly Ile Asn Gly Val Gly
```

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250 255 260

gga acg ctc tac cag gcc att ttg aaa ggt gaa ccc acc acg gtt gtc 931
Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu Pro Thr Thr Val Val
265 270 275

tcc att gtc act gtg ctg gtc atc gtc tac atc atc gcc aac ctt ctc 979
Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile Ile Ala Asn Leu Leu
280 285 290

gtg gac ttg atc tac gcc gtt ctc gat ccg agg atc cgc tat gcc 1024
Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg Ile Arg Tyr Ala
295 300 305

taataatgaa ttccacacaa acc 1047

<210> 140
<211> 308
<212> PRT
<213> Corynebacterium glutamicum

<400> 140
Met Leu Arg Tyr Val Gly Arg Arg Leu Leu Gln Met Ile Pro Val Phe
1 5 10 15

Phe Gly Ala Thr Leu Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly
20 25 30

Asp Pro Val Gln Ala Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala
35 40 45

Ala Glu Lys Ile Arg Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val
50 55 60

Gln Tyr Leu Leu Tyr Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr
65 70 75 80

Thr Phe Ser Gly Gln Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro
85 90 95

Val Thr Ile Lys Leu Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu
100 105 110

Gly Ile Ile Phe Gly Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe
115 120 125

Asp Ser Thr Val Leu Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr
130 135 140

Phe Val Ile Gly Phe Val Leu Gln Phe Leu Val Gly Val Lys Trp Gly
145 150 155 160

Leu Leu Pro Val Thr Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile
165 170 175

Met Pro Ala Val Val Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg
180 185 190

Leu Thr Arg Gln Ser Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg
195 200 205

```
Thr Ala Arg Ala Lys Gly Met Ser Gly Phe Asn Val Met Asn Arg His
    210                 215                 220

Val Leu Arg Asn Ser Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp
225                 230                 235                 240

Leu Gly Ala Leu Met Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly
                245                 250                 255

Ile Asn Gly Val Gly Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu
            260                 265                 270

Pro Thr Thr Val Val Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile
        275                 280                 285

Ile Ala Asn Leu Leu Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg
    290                 295                 300

Ile Arg Tyr Ala
305
```

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<210> 141
<211> 1047
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1024)
<223> FRXA00759


<400> 141

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tcaccttgaa cacttaaaac ataacttcat ccggcgcttt attagcttga agcgccccgc 60

accataatcc attccccagc aagcaaggac acccacgctc atg ctt cgt tac gtc   115
                                            Met Leu Arg Tyr Val
                                              1               5

ggg cga cgt ttg ctc caa atg att ccg gtc ttt ttc gga gcg acc tta   163
Gly Arg Arg Leu Leu Gln Met Ile Pro Val Phe Phe Gly Ala Thr Leu
                 10                  15                  20

ctg att tac gcc ctc gtg ttc ctc atg cct ggt gac cca gtc cag gca   211
Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly Asp Pro Val Gln Ala
             25                  30                  35

ttg gga ggt gac cgc ggc cta acc gag gct gcg gcc gag aaa atc cgt   259
Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala Ala Glu Lys Ile Arg
         40                  45                  50

caa gaa tac aat ctt gat aaa ccc ttc atc gtt caa tac ctc ctg tac   307
Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val Gln Tyr Leu Leu Tyr
     55                  60                  65

atc aag ggc atc ttc gtc tta gat ttt gga aca acc ttc tct ggt cag   355
Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr Thr Phe Ser Gly Gln
 70                  75                  80                  85

cca gtt att gat gtg atg gcc agg gcc ttc ccc gtc acc atc aaa ctc   403
```

```
Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro Val Thr Ile Lys Leu
                 90                  95                 100

gcc atc atg gcc ctg ctg ttt gaa tca atc ctc ggc att atc ttt ggt   451
Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu Gly Ile Ile Phe Gly
            105                 110                 115

gtc atc gca ggt att cgc cgc gga gga atc ttc gac tcc acc gtg ctg   499
Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe Asp Ser Thr Val Leu
        120                 125                 130

gtc ctt tct ctg ata gtc atc gca gtc ccc acc ttc gtc att ggt ttc   547
Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr Phe Val Ile Gly Phe
    135                 140                 145

gtg ctg cag ttc tta ntc ggc gtg aaa tgg ggc tta ctg ccc gtc acc   595
Val Leu Gln Phe Leu Xaa Gly Val Lys Trp Gly Leu Leu Pro Val Thr
150                 155                 160                 165

gta ggt tcc aac aca tca ata acg gcg ctg atc atg ccg gct gtc gta   643
Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile Met Pro Ala Val Val
                170                 175                 180

ctg ggt gca gta tcg ttc gcc tac gtt ctt cgc ctc acc aga caa tcc   691
Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg Leu Thr Arg Gln Ser
            185                 190                 195

gtg agc gaa aac ctc cgc gct gat tac gtt cga acc gct cga gca aaa   739
Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg Thr Ala Arg Ala Lys
        200                 205                 210

ggc atg tcc gga ttc aac gtg atg aac cgc cat gtg ctt cga aac tca   787
Gly Met Ser Gly Phe Asn Val Met Asn Arg His Val Leu Arg Asn Ser
    215                 220                 225

ctg att ccc gtt gcc acc ttc ctg ggc gcc gat ctc ggt gca ctg atg   835
Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp Leu Gly Ala Leu Met
230                 235                 240                 245

ggt gga gcg att gtc acc gaa ggt atc ttc ggc atc aac ggt gtc ggt   883
Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly Ile Asn Gly Val Gly
                250                 255                 260

gga acg ctc tac cag gcc att ttg aaa ggt gaa ccc acc acg gtt gtc   931
Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu Pro Thr Thr Val Val
            265                 270                 275

tcc att gtc act gtg ctg gtc atc gtc tac atc atc gcc aac ctt ctc   979
Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile Ile Ala Asn Leu Leu
        280                 285                 290

gtg gac ttg atc tac gcc gtt ctc gat ccg agg atc cgc tat gcc       1024
Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg Ile Arg Tyr Ala
    295                 300                 305

taataatgaa ttccacacaa acc                                        1047
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<210> 142
<211> 308
<212> PRT

<213> Corynebacterium glutamicum

<400> 142

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Met Leu Arg Tyr Val Gly Arg Arg Leu Leu Gln Met Ile Pro Val Phe
  1               5                  10                  15

Phe Gly Ala Thr Leu Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly
            20                  25                  30

Asp Pro Val Gln Ala Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala
        35                  40                  45

Ala Glu Lys Ile Arg Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val
    50                  55                  60

Gln Tyr Leu Leu Tyr Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr
65                  70                  75                  80

Thr Phe Ser Gly Gln Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro
                85                  90                  95

Val Thr Ile Lys Leu Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu
            100                 105                 110

Gly Ile Ile Phe Gly Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe
        115                 120                 125

Asp Ser Thr Val Leu Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr
    130                 135                 140

Phe Val Ile Gly Phe Val Leu Gln Phe Leu Xaa Gly Val Lys Trp Gly
145                 150                 155                 160

Leu Leu Pro Val Thr Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile
                165                 170                 175

Met Pro Ala Val Val Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg
            180                 185                 190

Leu Thr Arg Gln Ser Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg
        195                 200                 205

Thr Ala Arg Ala Lys Gly Met Ser Gly Phe Asn Val Met Asn Arg His
    210                 215                 220

Val Leu Arg Asn Ser Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp
225                 230                 235                 240

Leu Gly Ala Leu Met Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly
                245                 250                 255

Ile Asn Gly Val Gly Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu
            260                 265                 270

Pro Thr Thr Val Val Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile
        275                 280                 285

Ile Ala Asn Leu Leu Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg
    290                 295                 300

Ile Arg Tyr Ala
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305

<210> 143
<211> 912
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(889)
<223> RXN00431

<400> 143
tggatcgtcc tcgccttcac attcgtcggc cttggccttg ctctcctcgc gatgaagcaa 60

tggcgattcc gcgtcagcta ctgggtataa ggagcaccac atg gta tcc atc gat 115
Met Val Ser Ile Asp
1 5

aca tac aac gcc tgc gtc gac ttc ccc atc ttc gac gcc aaa tcc cgc 163
Thr Tyr Asn Ala Cys Val Asp Phe Pro Ile Phe Asp Ala Lys Ser Arg
10 15 20

tcc atg aag aaa gcc ttc ctc ggc gca gcc ggc gga gca atc ggg cgc 211
Ser Met Lys Lys Ala Phe Leu Gly Ala Ala Gly Gly Ala Ile Gly Arg
25 30 35

aat caa gac aac gtc gta gtc gtc gaa gcg ctg aag aac gtc aac ctg 259
Asn Gln Asp Asn Val Val Val Val Glu Ala Leu Lys Asn Val Asn Leu
40 45 50

cac ttg cgc gaa ggt gac cgg gtc gga ctc gtc ggc cac aac ggc gcc 307
His Leu Arg Glu Gly Asp Arg Val Gly Leu Val Gly His Asn Gly Ala
55 60 65

ggc aaa tcc acc ctc ctg cga ctc ctc tcc ggc atc tac gaa ccc acc 355
Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly Ile Tyr Glu Pro Thr
70 75 80 85

cgc gga agc gct gac atc cgt gga cgc gtc gcc ccc gtc ttc gac ctc 403
Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala Pro Val Phe Asp Leu
90 95 100

ggc gtc ggc atg gat cca gaa atc tcc ggc tac gaa aat atc atc atc 451
Gly Val Gly Met Asp Pro Glu Ile Ser Gly Tyr Glu Asn Ile Ile Ile
105 110 115

cgc ggc ctc ttc ctc ggt caa acc cgc aaa cag atg aaa gcc aaa atg 499
Arg Gly Leu Phe Leu Gly Gln Thr Arg Lys Gln Met Lys Ala Lys Met
120 125 130

gaa gaa atc gcc gac ttc acc gaa ctc ggc gaa tac ctc tcc atg cct 547
Glu Glu Ile Ala Asp Phe Thr Glu Leu Gly Glu Tyr Leu Ser Met Pro
135 140 145

ctc cga acc tac tcc acc ggc atg cgc atc cgc cta gcc ctc ggc gtg 595
Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg Leu Ala Leu Gly Val
150 155 160 165

gtc acc tcc atc gag ccc gaa att ctg ctt ctt gat gaa ggc atc ggc 643

```
Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Asp Glu Gly Ile Gly
                170                 175                 180

gcc gtc gac gcc gcc ttc atg gcc aaa gcc cgc gac cgc ctc caa gcc   691
Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg Asp Arg Leu Gln Ala
            185                 190                 195

ctc gtc gaa cga tcc ggc atc ctc gtc ttc gcc tcc cac tcc aac gac   739
Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala Ser His Ser Asn Asp
        200                 205                 210

ttc ctc gcc caa ctc tgc aac acc gca ctc tgg gtc gac cac gga caa   787
Phe Leu Ala Gln Leu Cys Asn Thr Ala Leu Trp Val Asp His Gly Gln
    215                 220                 225

atc cgc gaa gcg gga cta gtt cca gac gtg gtg gaa gcc tac gaa ggc   835
Ile Arg Glu Ala Gly Leu Val Pro Asp Val Val Glu Ala Tyr Glu Gly
230                 235                 240                 245

aag ggc gcc ggc gac cac gtc cgc aga ctc ctc acc cgc atg gaa gaa   883
Lys Gly Ala Gly Asp His Val Arg Arg Leu Leu Thr Arg Met Glu Glu
                250                 255                 260

gaa aag tagctcctgc gtttcgggtt tgc                                912
Glu Lys
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<210> 144
<211> 263
<212> PRT
<213> Corynebacterium glutamicum

<400> 144

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Met Val Ser Ile Asp Thr Tyr Asn Ala Cys Val Asp Phe Pro Ile Phe
  1               5                  10                  15

Asp Ala Lys Ser Arg Ser Met Lys Lys Ala Phe Leu Gly Ala Ala Gly
            20                  25                  30

Gly Ala Ile Gly Arg Asn Gln Asp Asn Val Val Val Val Glu Ala Leu
        35                  40                  45

Lys Asn Val Asn Leu His Leu Arg Glu Gly Asp Arg Val Gly Leu Val
    50                  55                  60

Gly His Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly
65                  70                  75                  80

Ile Tyr Glu Pro Thr Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala
                85                  90                  95

Pro Val Phe Asp Leu Gly Val Gly Met Asp Pro Glu Ile Ser Gly Tyr
            100                 105                 110

Glu Asn Ile Ile Ile Arg Gly Leu Phe Leu Gly Gln Thr Arg Lys Gln
        115                 120                 125

Met Lys Ala Lys Met Glu Glu Ile Ala Asp Phe Thr Glu Leu Gly Glu
    130                 135                 140
```

```
Tyr Leu Ser Met Pro Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg
145                 150                 155                 160

Leu Ala Leu Gly Val Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Leu
                165                 170                 175

Asp Glu Gly Ile Gly Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg
            180                 185                 190

Asp Arg Leu Gln Ala Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala
        195                 200                 205

Ser His Ser Asn Asp Phe Leu Ala Gln Leu Cys Asn Thr Ala Leu Trp
    210                 215                 220

Val Asp His Gly Gln Ile Arg Glu Ala Gly Leu Val Pro Asp Val Val
225                 230                 235                 240

Glu Ala Tyr Glu Gly Lys Gly Ala Gly Asp His Val Arg Arg Leu Leu
                245                 250                 255

Thr Arg Met Glu Glu Glu Lys
            260
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<210> 145
<211> 775
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> FRXA00431

<400> 145

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tggatcgtcc tcgccttcac attcgtcggc cttggccttg ctctcctcgc gatgaagcaa 60

tggcgattcc gcgtcagcta ctgggtataa ggagcaccac atg gta tcc atc gat   115
                                              Met Val Ser Ile Asp
                                                1               5

aca tac aac gcc tgc gtc gac ttc ccc atc ttc gac gcc aaa tcc cgc   163
Thr Tyr Asn Ala Cys Val Asp Phe Pro Ile Phe Asp Ala Lys Ser Arg
                10                  15                  20

tcc atg aag aaa gcc ttc ctc ggc gca gcc ggc gga gca atc ggg cgc   211
Ser Met Lys Lys Ala Phe Leu Gly Ala Ala Gly Gly Ala Ile Gly Arg
            25                  30                  35

aat caa gac aac gtc gta gtc gtc gaa gcg ctg aag aac gtc aac ctg   259
Asn Gln Asp Asn Val Val Val Val Glu Ala Leu Lys Asn Val Asn Leu
        40                  45                  50

cac ttg cgc gaa ggt gac cgg gtc gga ctc gtc ggc cac aac ggc gcc   307
His Leu Arg Glu Gly Asp Arg Val Gly Leu Val Gly His Asn Gly Ala
    55                  60                  65

ggc aaa tcc acc ctc ctg cga ctc ctc tcc ggc atc tac gaa ccc acc   355
Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly Ile Tyr Glu Pro Thr
70                  75                  80                  85
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```
cgc gga agc gct gac atc cgt gga cgc gtc gcc ccc gtc ttc gac ctc   403
Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala Pro Val Phe Asp Leu
                 90                  95                 100

ggc gtc ggc atg gat cca gaa atc tcc ggc tac gaa aat atc atc atc   451
Gly Val Gly Met Asp Pro Glu Ile Ser Gly Tyr Glu Asn Ile Ile Ile
            105                 110                 115

cgc ggc ctc ttc ctc ggt caa acc cgc aaa cag atg aaa gcc aaa atg   499
Arg Gly Leu Phe Leu Gly Gln Thr Arg Lys Gln Met Lys Ala Lys Met
        120                 125                 130

gaa gaa atc gcc gac ttc acc gaa ctc ggc gaa tac ctc tcc atg cct   547
Glu Glu Ile Ala Asp Phe Thr Glu Leu Gly Glu Tyr Leu Ser Met Pro
    135                 140                 145

ctc cga acc tac tcc acc ggc atg cgc atc cgc cta gcc ctc ggc gtg   595
Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg Leu Ala Leu Gly Val
150                 155                 160                 165

gtc acc tcc atc gag ccc gaa att ctg ctt ctt gat gaa ggc atc ggc   643
Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Leu Asp Glu Gly Ile Gly
                170                 175                 180

gcc gtc gac gcc gcc ttc atg gcc aaa gcc cgc gac cgg ctc caa gcc   691
Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg Asp Arg Leu Gln Ala
            185                 190                 195

ctc gtc gaa cga tcc ggc atc ctc gtc ttc gcc tcc act caa cga ctt   739
Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala Ser Thr Gln Arg Leu
        200                 205                 210

tct tgc caa ctc tgc aac acc gca ctc tgg gtc gac                   775
Ser Cys Gln Leu Cys Asn Thr Ala Leu Trp Val Asp
    215                 220                 225
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<210> 146
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 146

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Met Val Ser Ile Asp Thr Tyr Asn Ala Cys Val Asp Phe Pro Ile Phe
  1               5                  10                  15

Asp Ala Lys Ser Arg Ser Met Lys Lys Ala Phe Leu Gly Ala Ala Gly
             20                  25                  30

Gly Ala Ile Gly Arg Asn Gln Asp Asn Val Val Val Val Glu Ala Leu
         35                  40                  45

Lys Asn Val Asn Leu His Leu Arg Glu Gly Asp Arg Val Gly Leu Val
     50                  55                  60

Gly His Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly
 65                  70                  75                  80

Ile Tyr Glu Pro Thr Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala
                 85                  90                  95
```

```
Pro Val Phe Asp Leu Gly Val Gly Met Asp Pro Glu Ile Ser Gly Tyr
            100                 105                 110

Glu Asn Ile Ile Ile Arg Gly Leu Phe Leu Gly Gln Thr Arg Lys Gln
        115                 120                 125

Met Lys Ala Lys Met Glu Glu Ile Ala Asp Phe Thr Glu Leu Gly Glu
    130                 135                 140

Tyr Leu Ser Met Pro Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg
145                 150                 155                 160

Leu Ala Leu Gly Val Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Leu
                165                 170                 175

Asp Glu Gly Ile Gly Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg
            180                 185                 190

Asp Arg Leu Gln Ala Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala
        195                 200                 205

Ser Thr Gln Arg Leu Ser Cys Gln Leu Cys Asn Thr Ala Leu Trp Val
    210                 215                 220

Asp
225
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09529369.030905

<210> 147
<211> 1670
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1647)
<223> RXN00732

<400> 147

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aat cac ctc ctc cta ctc ccc acg gta aag gca gac atc att gac aat   48
Asn His Leu Leu Leu Leu Pro Thr Val Lys Ala Asp Ile Ile Asp Asn
  1               5                  10                  15

ggt gtg gtc aca ggt gac atc ggc tat att tgg cac acc ggt gga atc   96
Gly Val Val Thr Gly Asp Ile Gly Tyr Ile Trp His Thr Gly Gly Ile
             20                  25                  30

atg ctg gcc ctg aca tta gtc cag gtt gcc tgc gct atc gcc ggt gtt  144
Met Leu Ala Leu Thr Leu Val Gln Val Ala Cys Ala Ile Ala Gly Val
         35                  40                  45

tat ttc ggt tcc aaa cta tcc atg aga gtg ggc cgc gat ctg cgt tcg  192
Tyr Phe Gly Ser Lys Leu Ser Met Arg Val Gly Arg Asp Leu Arg Ser
     50                  55                  60

gcg atc ttt ggc aag gta gtg aac ttc tct gag cgt gag atg ggt cag  240
Ala Ile Phe Gly Lys Val Val Asn Phe Ser Glu Arg Glu Met Gly Gln
 65                  70                  75                  80

ttt ggc gca ccg tcg ctg atc acc cga aac acc aac gat gtg cag cag  288
```

```
Phe Gly Ala Pro Ser Leu Ile Thr Arg Asn Thr Asn Asp Val Gln Gln
                 85                  90                  95

gtt cag atg ctg gtg cag atg acc tcc act ttg atg att tcc gcc ccg   336
Val Gln Met Leu Val Gln Met Thr Ser Thr Leu Met Ile Ser Ala Pro
            100                 105                 110

atg ctg gcc att ggt ggc atc atc atg gcg gtg cgt cag gat ctt ggt   384
Met Leu Ala Ile Gly Gly Ile Ile Met Ala Val Arg Gln Asp Leu Gly
        115                 120                 125

ttg tct tgg ctg atg gtg gtc agt att ccg gtg ctc atc atc gtg gtg   432
Leu Ser Trp Leu Met Val Val Ser Ile Pro Val Leu Ile Ile Val Val
    130                 135                 140

gcg ctg atc att gtg cgc atg gtt ccg ttg ttc caa acc atg caa aag   480
Ala Leu Ile Ile Val Arg Met Val Pro Leu Phe Gln Thr Met Gln Lys
145                 150                 155                 160

cgc att gac cgc atc aat cag att ata cgc gag cag ctc acc ggt atc   528
Arg Ile Asp Arg Ile Asn Gln Ile Ile Arg Glu Gln Leu Thr Gly Ile
                165                 170                 175

cgc gtg atc cgc gcg ttc gtg cgt gaa gat gtg gaa cgc gaa cga ttc   576
Arg Val Ile Arg Ala Phe Val Arg Glu Asp Val Glu Arg Glu Arg Phe
            180                 185                 190

acc act gct agt aaa gat gtc gct gat atc ggc gtg cgc acc ggt aac   624
Thr Thr Ala Ser Lys Asp Val Ala Asp Ile Gly Val Arg Thr Gly Asn
        195                 200                 205

ctg atg gcg ttg atg ttc cct gcc gtg atg ctg atc atg aac ctt tct   672
Leu Met Ala Leu Met Phe Pro Ala Val Met Leu Ile Met Asn Leu Ser
    210                 215                 220

gcc gtt gct gtg att tgg ttt ggt gct ttc cag gtg gaa tcc ggc gag   720
Ala Val Ala Val Ile Trp Phe Gly Ala Phe Gln Val Glu Ser Gly Glu
225                 230                 235                 240

acg cag atc ggt acg ctc ttt gca ttc ttg cag tac atc atg cag atc   768
Thr Gln Ile Gly Thr Leu Phe Ala Phe Leu Gln Tyr Ile Met Gln Ile
                245                 250                 255

ctc atg ggc gtc atg atg gca gcg ttc atg ttt gtc atg gtt ccg cgc   816
Leu Met Gly Val Met Met Ala Ala Phe Met Phe Val Met Val Pro Arg
            260                 265                 270

gct gcc gtt tcc gct gat cgc atc ggt gag gtt ctg gaa acc aca ccg   864
Ala Ala Val Ser Ala Asp Arg Ile Gly Glu Val Leu Glu Thr Thr Pro
        275                 280                 285

tct gtg cag gcg cca gaa aca ccg gcg cag ccg tcg aca agc gct ggc   912
Ser Val Gln Ala Pro Glu Thr Pro Ala Gln Pro Ser Thr Ser Ala Gly
    290                 295                 300

gaa atc gtg ttc aac aac gcg act ttt gcc tac ccc ggc gcg gat gac   960
Glu Ile Val Phe Asn Asn Ala Thr Phe Ala Tyr Pro Gly Ala Asp Asp
305                 310                 315                 320

ccc gtg tta aat aat gtg agc ttc cgc gtt gcg cct ggt agc acg acg  1008
Pro Val Leu Asn Asn Val Ser Phe Arg Val Ala Pro Gly Ser Thr Thr
```

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                    325                 330                 335

gcg atc atc ggc tcg acg ggt tcg ggt aag acg acg ttg atc ggg ctg   1056
Ala Ile Ile Gly Ser Thr Gly Ser Gly Lys Thr Thr Leu Ile Gly Leu
            340                 345                 350

gtt cct agg ctt ttc gac gtc acc gaa ggc gac gtt acc gtc gat ggc   1104
Val Pro Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly
        355                 360                 365

acc gat gtt cgt gaa ttt gag ccg ctg aag ctg tgg gat cgg atc ggt   1152
Thr Asp Val Arg Glu Phe Glu Pro Leu Lys Leu Trp Asp Arg Ile Gly
    370                 375                 380

ctt gtt ccg cag aag tcg ttc ctg ttt tct gga acg atc gcc agc aac   1200
Leu Val Pro Gln Lys Ser Phe Leu Phe Ser Gly Thr Ile Ala Ser Asn
385                 390                 395                 400

ctg cgt tat ggc aat gaa gat gcc acg gaa acg cag ctg tgg cag gcg   1248
Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp Gln Ala
                405                 410                 415

ctt gca att gct cag gcg gcg gac ttt gtg cgt gag atg cca gag ggt   1296
Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro Glu Gly
            420                 425                 430

ctt gat tct gag att gct cag ggt gga acc aat gtt tct ggt ggt cag   1344
Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly Gly Gln
        435                 440                 445

cgc cag cga cta gcc att gcc agg gcg ttg ttg aag caa cct gag atc   1392
Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro Glu Ile
    450                 455                 460

tat att ttc gac gat tct ttc tcc gcc ctc gat gtg agc aca gac gcc   1440
Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr Asp Ala
465                 470                 475                 480

gct ctt cgc cga gcg ctg agc acc aac ctg ccg gat gca acc aag ttg   1488
Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr Lys Leu
                485                 490                 495

att gtc gcc cag cgt gtc agc acg att cga gat gcc gat cag att gtg   1536
Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln Ile Val
            500                 505                 510

gtg ctt gat aac ggc gag gtt gtc ggt att gga acg cac acg aat ttg   1584
Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr Asn Leu
        515                 520                 525

ctg aac acg tgc ggt acc tac cgt gaa att gtt gaa tcc caa gag act   1632
Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln Glu Thr
    530                 535                 540

gcg cag gcg caa tca tgagtaatac tgcaggcccc cgc                    1670
Ala Gln Ala Gln Ser
545
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<210> 148
<211> 549

<212> PRT
<213> Corynebacterium glutamicum

<400> 148

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Asn His Leu Leu Leu Leu Pro Thr Val Lys Ala Asp Ile Ile Asp Asn
  1               5                  10                  15

Gly Val Val Thr Gly Asp Ile Gly Tyr Ile Trp His Thr Gly Gly Ile
            20                  25                  30

Met Leu Ala Leu Thr Leu Val Gln Val Ala Cys Ala Ile Ala Gly Val
        35                  40                  45

Tyr Phe Gly Ser Lys Leu Ser Met Arg Val Gly Arg Asp Leu Arg Ser
    50                  55                  60

Ala Ile Phe Gly Lys Val Val Asn Phe Ser Glu Arg Glu Met Gly Gln
65                  70                  75                  80

Phe Gly Ala Pro Ser Leu Ile Thr Arg Asn Thr Asn Asp Val Gln Gln
                85                  90                  95

Val Gln Met Leu Val Gln Met Thr Ser Thr Leu Met Ile Ser Ala Pro
            100                 105                 110

Met Leu Ala Ile Gly Gly Ile Ile Met Ala Val Arg Gln Asp Leu Gly
        115                 120                 125

Leu Ser Trp Leu Met Val Val Ser Ile Pro Val Leu Ile Ile Val Val
    130                 135                 140

Ala Leu Ile Ile Val Arg Met Val Pro Leu Phe Gln Thr Met Gln Lys
145                 150                 155                 160

Arg Ile Asp Arg Ile Asn Gln Ile Ile Arg Glu Gln Leu Thr Gly Ile
                165                 170                 175

Arg Val Ile Arg Ala Phe Val Arg Glu Asp Val Glu Arg Glu Arg Phe
            180                 185                 190

Thr Thr Ala Ser Lys Asp Val Ala Asp Ile Gly Val Arg Thr Gly Asn
        195                 200                 205

Leu Met Ala Leu Met Phe Pro Ala Val Met Leu Ile Met Asn Leu Ser
    210                 215                 220

Ala Val Ala Val Ile Trp Phe Gly Ala Phe Gln Val Glu Ser Gly Glu
225                 230                 235                 240

Thr Gln Ile Gly Thr Leu Phe Ala Phe Leu Gln Tyr Ile Met Gln Ile
                245                 250                 255

Leu Met Gly Val Met Met Ala Ala Phe Met Phe Val Met Val Pro Arg
            260                 265                 270

Ala Ala Val Ser Ala Asp Arg Ile Gly Glu Val Leu Glu Thr Thr Pro
        275                 280                 285

Ser Val Gln Ala Pro Glu Thr Pro Ala Gln Pro Ser Thr Ser Ala Gly
    290                 295                 300
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DOCID: <WO 2004076659 A2>

Glu Ile Val Phe Asn Asn Ala Thr Phe Ala Tyr Pro Gly Ala Asp Asp
305 310 315 320

Pro Val Leu Asn Asn Val Ser Phe Arg Val Ala Pro Gly Ser Thr Thr
325 330 335

Ala Ile Ile Gly Ser Thr Gly Ser Gly Lys Thr Thr Leu Ile Gly Leu
340 345 350

Val Pro Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly
355 360 365

Thr Asp Val Arg Glu Phe Glu Pro Leu Lys Leu Trp Asp Arg Ile Gly
370 375 380

Leu Val Pro Gln Lys Ser Phe Leu Phe Ser Gly Thr Ile Ala Ser Asn
385 390 395 400

Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp Gln Ala
405 410 415

Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro Glu Gly
420 425 430

Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly Gly Gln
435 440 445

Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro Glu Ile
450 455 460

Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr Asp Ala
465 470 475 480

Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr Lys Leu
485 490 495

Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln Ile Val
500 505 510

Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr Asn Leu
515 520 525

Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln Glu Thr
530 535 540

Ala Gln Ala Gln Ser
545

<210> 149
<211> 922
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(922)
<223> FRXA00732

<400> 149
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WO 2004/063355 PCT/US2003/040510

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ctgatcaccc cgaaacacca acgatgtgca gcaggttcag atg ctg gtg cag atg   115
                                              Met Leu Val Gln Met
                                                1               5

acc tcc act ttg atg att tcc gcc ccg atg ctg gcc att ggt ggc atc   163
Thr Ser Thr Leu Met Ile Ser Ala Pro Met Leu Ala Ile Gly Gly Ile
               10                  15                  20

atc atg gcg gtg cgt cag gat ctt ggt ttg tct tgg ctg atg gtg gtc   211
Ile Met Ala Val Arg Gln Asp Leu Gly Leu Ser Trp Leu Met Val Val
           25                  30                  35

agt att ccg gtg ctc atc atc gtg gtg gcg ctg atc att gtg cgc atg   259
Ser Ile Pro Val Leu Ile Ile Val Val Ala Leu Ile Ile Val Arg Met
       40                  45                  50

gtt ccg ttg ttc caa acc atg caa aag cgc att gac cgc atc aat cag   307
Val Pro Leu Phe Gln Thr Met Gln Lys Arg Ile Asp Arg Ile Asn Gln
   55                  60                  65

att ata cgc gag cag ctc acc ggt atc cgc gtg atc cgc gcg ttc gtg   355
Ile Ile Arg Glu Gln Leu Thr Gly Ile Arg Val Ile Arg Ala Phe Val
70                  75                  80                  85

cgt gaa gat gtg gaa cgc gaa cga ttc acc act gct agt aaa gat gtc   403
Arg Glu Asp Val Glu Arg Glu Arg Phe Thr Thr Ala Ser Lys Asp Val
               90                  95                 100

gct gat atc ggc gtg cgc acc ggt aac ctg atg gcg ttg atg ttc cct   451
Ala Asp Ile Gly Val Arg Thr Gly Asn Leu Met Ala Leu Met Phe Pro
           105                 110                 115

gcc gtg atg ctg atc atg aac ctt tct gcc gtt gct gtg att tgg ttt   499
Ala Val Met Leu Ile Met Asn Leu Ser Ala Val Ala Val Ile Trp Phe
       120                 125                 130

ggt gct ttc cag gtg gaa tcc ggc gag acg cag atc ggt acg ctc ttt   547
Gly Ala Phe Gln Val Glu Ser Gly Glu Thr Gln Ile Gly Thr Leu Phe
   135                 140                 145

gca ttc ttg cag tac atc atg cag atc ctc atg ggc gtc atg atg gca   595
Ala Phe Leu Gln Tyr Ile Met Gln Ile Leu Met Gly Val Met Met Ala
150                 155                 160                 165

gcg ttc atg ttt gtc atg gtt ccg cgc gct gcc gtt tcc gct gat cgc   643
Ala Phe Met Phe Val Met Val Pro Arg Ala Ala Val Ser Ala Asp Arg
               170                 175                 180

atc ggt gag gtt ctg gaa acc aca ccg tct gtg cag gcg cca gaa aca   691
Ile Gly Glu Val Leu Glu Thr Thr Pro Ser Val Gln Ala Pro Glu Thr
           185                 190                 195

ccg gcg cag ccg tcg aca agc gct ggc gaa atc gtg ttc aac aac gcg   739
Pro Ala Gln Pro Ser Thr Ser Ala Gly Glu Ile Val Phe Asn Asn Ala
       200                 205                 210

act ttt gcc tac ccc ggc gcg gat gac ccc gtg tta aat aat gtg agc   787
Thr Phe Ala Tyr Pro Gly Ala Asp Asp Pro Val Leu Asn Asn Val Ser
   215                 220                 225
```

```
ttc cgc gtt gcg cct ggt agc acg acg gcg atc atc ggc tcg acg ggt   835
Phe Arg Val Ala Pro Gly Ser Thr Thr Ala Ile Ile Gly Ser Thr Gly
230                 235                 240                 245

tcg ggt aag acg acg ttg atc ggg ctg gtt cct agg ctt ttc gac gtc   883
Ser Gly Lys Thr Thr Leu Ile Gly Leu Val Pro Arg Leu Phe Asp Val
                250                 255                 260

acc gaa ggc gac gtt acc gtc gat ggc acc gat gtt cgt               922
Thr Glu Gly Asp Val Thr Val Asp Gly Thr Asp Val Arg
            265                 270
```

<210> 150
<211> 274
<212> PRT
<213> Corynebacterium glutamicum

<400> 150

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Met Leu Val Gln Met Thr Ser Thr Leu Met Ile Ser Ala Pro Met Leu
  1               5                  10                  15

Ala Ile Gly Gly Ile Ile Met Ala Val Arg Gln Asp Leu Gly Leu Ser
            20                  25                  30

Trp Leu Met Val Val Ser Ile Pro Val Leu Ile Ile Val Val Ala Leu
        35                  40                  45

Ile Ile Val Arg Met Val Pro Leu Phe Gln Thr Met Gln Lys Arg Ile
    50                  55                  60

Asp Arg Ile Asn Gln Ile Ile Arg Glu Gln Leu Thr Gly Ile Arg Val
65                  70                  75                  80

Ile Arg Ala Phe Val Arg Glu Asp Val Glu Arg Glu Arg Phe Thr Thr
                85                  90                  95

Ala Ser Lys Asp Val Ala Asp Ile Gly Val Arg Thr Gly Asn Leu Met
            100                 105                 110

Ala Leu Met Phe Pro Ala Val Met Leu Ile Met Asn Leu Ser Ala Val
        115                 120                 125

Ala Val Ile Trp Phe Gly Ala Phe Gln Val Glu Ser Gly Glu Thr Gln
    130                 135                 140

Ile Gly Thr Leu Phe Ala Phe Leu Gln Tyr Ile Met Gln Ile Leu Met
145                 150                 155                 160

Gly Val Met Met Ala Ala Phe Met Phe Val Met Val Pro Arg Ala Ala
                165                 170                 175

Val Ser Ala Asp Arg Ile Gly Glu Val Leu Glu Thr Thr Pro Ser Val
            180                 185                 190

Gln Ala Pro Glu Thr Pro Ala Gln Pro Ser Thr Ser Ala Gly Glu Ile
        195                 200                 205

Val Phe Asn Asn Ala Thr Phe Ala Tyr Pro Gly Ala Asp Asp Pro Val
    210                 215                 220
```

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```
Leu Asn Asn Val Ser Phe Arg Val Ala Pro Gly Ser Thr Thr Ala Ile
225                 230                 235                 240

Ile Gly Ser Thr Gly Ser Gly Lys Thr Thr Leu Ile Gly Leu Val Pro
                245                 250                 255

Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly Thr Asp
            260                 265                 270

Val Arg
```

<210> 151
<211> 476
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(453)
<223> FRXA00734

<400> 151

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agg cac ctg cgt tat ggc aat gaa gat gcc acg gaa acg cag ctg tgg   48
Arg His Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp
  1               5                  10                  15

cag gcg ctt gca att gct cag gcg gcg gac ttt gtg cgt gag atg cca   96
Gln Ala Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro
             20                  25                  30

gag ggt ctt gat tct gag att gct cag ggt gga acc aat gtt tct ggt   144
Glu Gly Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly
         35                  40                  45

ggt cag cgc cag cga cta gcc att gcc agg gcg ttg ttg aag caa cct   192
Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro
     50                  55                  60

gag atc tat att ttc gac gat tct ttc tcc gcc ctc gat gtg agc aca   240
Glu Ile Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr
 65                  70                  75                  80

gac gcc gct ctt cgc cga gcg ctg agc acc aac ctg ccg gat gca acc   288
Asp Ala Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr
                 85                  90                  95

aag ttg att gtc gcc cag cgt gtc agc acg att cga gat gcc gat cag   336
Lys Leu Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln
            100                 105                 110

att gtg gtg ctt gat aac ggc gag gtt gtc ggt att gga acg cac acg   384
Ile Val Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr
        115                 120                 125

aat ttg ctg aac acg tgc ggt acc tac cgt gaa att gtt gaa tcc caa   432
Asn Leu Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln
    130                 135                 140

gag act gcg cag gcg caa tca tgagtaatac tgcaggcccc cgc            476
```

Glu Thr Ala Gln Ala Gln Ser
145 150

<210> 152
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 152
Arg His Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp
1 5 10 15

Gln Ala Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro
20 25 30

Glu Gly Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly
35 40 45

Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro
50 55 60

Glu Ile Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr
65 70 75 80

Asp Ala Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr
85 90 95

Lys Leu Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln
100 105 110

Ile Val Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr
115 120 125

Asn Leu Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln
130 135 140

Glu Thr Ala Gln Ala Gln Ser
145 150

<210> 153
<211> 1172
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1149)
<223> RXN01808

<400> 153
cag agc ctc gcg tgt aaa gaa ctc gca tgg atg cgc ggc ggt gca cca 48
Gln Ser Leu Ala Cys Lys Glu Leu Ala Trp Met Arg Gly Gly Ala Pro
1 5 10 15

gcg cga acc tca aag cct gga ttc cgc ctt gaa gcc gcg gaa gct ttg 96
Ala Arg Thr Ser Lys Pro Gly Phe Arg Leu Glu Ala Ala Glu Ala Leu
20 25 30

atc gca gaa gtg cca gcg cca cgc gac aaa gtc gag ctc atg gca ttt 144

```
Ile Ala Glu Val Pro Ala Pro Arg Asp Lys Val Glu Leu Met Ala Phe
          35                  40                  45

tcc aag tcc agg caa ggc cgc gtt gtc att gaa ctt gaa gac gcc aca   192
Ser Lys Ser Arg Gln Gly Arg Val Val Ile Glu Leu Glu Asp Ala Thr
      50                  55                  60

gta gcc acc cct gat gat cgc atc ctg gta gaa gac ctc acc tgg cgt   240
Val Ala Thr Pro Asp Asp Arg Ile Leu Val Glu Asp Leu Thr Trp Arg
 65                  70                  75                  80

ttg gct cca gga gag cgc atc ggt ctt gtc ggc gtc aac ggc tcc ggc   288
Leu Ala Pro Gly Glu Arg Ile Gly Leu Val Gly Val Asn Gly Ser Gly
                 85                  90                  95

aaa acc acc ctg ctg cgc acc ctt gcc ggc gag cag cca ctt cag gca   336
Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly Glu Gln Pro Leu Gln Ala
            100                 105                 110

ggc aaa cgc atc gaa ggc caa acc gtc aaa ctg gga tgg ctc cgc cag   384
Gly Lys Arg Ile Glu Gly Gln Thr Val Lys Leu Gly Trp Leu Arg Gln
        115                 120                 125

gaa ctc gat gac cta gac ctc agc cgc cga ctc atc gac tgc gtt gaa   432
Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg Leu Ile Asp Cys Val Glu
    130                 135                 140

gat gtc gct tcc tac gtg atg atg ggc gac aag cag gtc tcc gct tcc   480
Asp Val Ala Ser Tyr Val Met Met Gly Asp Lys Gln Val Ser Ala Ser
145                 150                 155                 160

caa ttg gca gaa cgc ctc gga ttc tca ccc aag agg caa cgc acc cca   528
Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro Lys Arg Gln Arg Thr Pro
                165                 170                 175

gtt ggt gac ctg tcc ggt ggt gaa cgc cgc cga ctc caa ctc acc cgc   576
Val Gly Asp Leu Ser Gly Gly Glu Arg Arg Arg Leu Gln Leu Thr Arg
            180                 185                 190

gtg ctc atg gcc gaa cca aac gtg ctg ctc ctc gac gag ccc acc aac   624
Val Leu Met Ala Glu Pro Asn Val Leu Leu Leu Asp Glu Pro Thr Asn
        195                 200                 205

gac ctg gac att gac acc ctc caa gag ctg gaa tcc ctt ctc gac gga   672
Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu Glu Ser Leu Leu Asp Gly
    210                 215                 220

tgg cca ggc acc atg gtg gtt atc tcc cac gac cgt tac ctc atc gaa   720
Trp Pro Gly Thr Met Val Val Ile Ser His Asp Arg Tyr Leu Ile Glu
225                 230                 235                 240

cgc gtc acc gac tcc acc tgg gca ctc ttc ggc gat ggc aag ctc acc   768
Arg Val Thr Asp Ser Thr Trp Ala Leu Phe Gly Asp Gly Lys Leu Thr
                245                 250                 255

aac ctg cca ggc gga att gaa gag tac ctg cag cga cga gca gcg atg   816
Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu Gln Arg Arg Ala Ala Met
            260                 265                 270

gcc gcg gcc gaa gac agt gga gtg ctg aac ttg ggt gcg gcc acg cag   864
Ala Ala Ala Glu Asp Ser Gly Val Leu Asn Leu Gly Ala Ala Thr Gln
```

```
        275                 280                 285

gct gga acc ttt tct gct gca aca gag cag gct gcc act tct gtg gaa   912
Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln Ala Ala Thr Ser Val Glu
    290                 295                 300

agt tcc gga att tct tcc caa gaa cgc cac cgc atc acc aag gaa atg   960
Ser Ser Gly Ile Ser Ser Gln Glu Arg His Arg Ile Thr Lys Glu Met
305                 310                 315                 320

aac gcc ctg gag cgc aaa atg ggc aag ctt gac cag caa atg gac aag   1008
Asn Ala Leu Glu Arg Lys Met Gly Lys Leu Asp Gln Gln Met Asp Lys
                325                 330                 335

ctt aat cag cag ctc gct gat gca gcg gag gcc atg gac acc ata aag   1056
Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu Ala Met Asp Thr Ile Lys
            340                 345                 350

ctc acc gag ctg gac acc aag ctc cgc gca gtg cag gaa gaa cac ggc   1104
Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala Val Gln Glu Glu His Gly
        355                 360                 365

gag ctg gaa atg cag tgg ctg gaa ctc ggc gag gaa atc gag ggc       1149
Glu Leu Glu Met Gln Trp Leu Glu Leu Gly Glu Glu Ile Glu Gly
    370                 375                 380

tagttcatgc cgtcggcagg cga                                        1172


<210> 154
<211> 383
<212> PRT
<213> Corynebacterium glutamicum

<400> 154
Gln Ser Leu Ala Cys Lys Glu Leu Ala Trp Met Arg Gly Gly Ala Pro
  1               5                  10                  15

Ala Arg Thr Ser Lys Pro Gly Phe Arg Leu Glu Ala Ala Glu Ala Leu
             20                  25                  30

Ile Ala Glu Val Pro Ala Pro Arg Asp Lys Val Glu Leu Met Ala Phe
         35                  40                  45

Ser Lys Ser Arg Gln Gly Arg Val Val Ile Glu Leu Glu Asp Ala Thr
     50                  55                  60

Val Ala Thr Pro Asp Asp Arg Ile Leu Val Glu Asp Leu Thr Trp Arg
 65                  70                  75                  80

Leu Ala Pro Gly Glu Arg Ile Gly Leu Val Gly Val Asn Gly Ser Gly
                 85                  90                  95

Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly Glu Gln Pro Leu Gln Ala
            100                 105                 110

Gly Lys Arg Ile Glu Gly Gln Thr Val Lys Leu Gly Trp Leu Arg Gln
        115                 120                 125

Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg Leu Ile Asp Cys Val Glu
    130                 135                 140
```

```
Asp Val Ala Ser Tyr Val Met Met Gly Asp Lys Gln Val Ser Ala Ser
145                 150                 155                 160

Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro Lys Arg Gln Arg Thr Pro
                165                 170                 175

Val Gly Asp Leu Ser Gly Gly Glu Arg Arg Arg Leu Gln Leu Thr Arg
            180                 185                 190

Val Leu Met Ala Glu Pro Asn Val Leu Leu Leu Asp Glu Pro Thr Asn
        195                 200                 205

Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu Glu Ser Leu Leu Asp Gly
    210                 215                 220

Trp Pro Gly Thr Met Val Val Ile Ser His Asp Arg Tyr Leu Ile Glu
225                 230                 235                 240

Arg Val Thr Asp Ser Thr Trp Ala Leu Phe Gly Asp Gly Lys Leu Thr
                245                 250                 255

Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu Gln Arg Arg Ala Ala Met
            260                 265                 270

Ala Ala Ala Glu Asp Ser Gly Val Leu Asn Leu Gly Ala Ala Thr Gln
        275                 280                 285

Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln Ala Ala Thr Ser Val Glu
    290                 295                 300

Ser Ser Gly Ile Ser Ser Gln Glu Arg His Arg Ile Thr Lys Glu Met
305                 310                 315                 320

Asn Ala Leu Glu Arg Lys Met Gly Lys Leu Asp Gln Gln Met Asp Lys
                325                 330                 335

Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu Ala Met Asp Thr Ile Lys
            340                 345                 350

Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala Val Gln Glu Glu His Gly
        355                 360                 365

Glu Leu Glu Met Gln Trp Leu Glu Leu Gly Glu Glu Ile Glu Gly
    370                 375                 380
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<210> 155
<211> 1142
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1119)
<223> FRXA01808

<400> 155

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atg cgc ggc ggt gca cca gcg cga acc tca aag cct gga ttc cgc ctt   48
Met Arg Gly Gly Ala Pro Ala Arg Thr Ser Lys Pro Gly Phe Arg Leu
  1               5                  10                  15
```

```
gaa gcc gcg gaa gct ttg atc gca gaa gtg cca gcg cca cgc gac aaa    96
Glu Ala Ala Glu Ala Leu Ile Ala Glu Val Pro Ala Pro Arg Asp Lys
            20                  25                  30

gtc gag ctc atg gca ttt tcc aag tcc agg caa ggc cgc gtt gtc att   144
Val Glu Leu Met Ala Phe Ser Lys Ser Arg Gln Gly Arg Val Val Ile
        35                  40                  45

gaa ctt gaa gac gcc aca gta gcc acc cct gat gat cgc atc ctg gta   192
Glu Leu Glu Asp Ala Thr Val Ala Thr Pro Asp Asp Arg Ile Leu Val
    50                  55                  60

gaa gac ctc acc tgg cgt ttg gct cca gga gag cgc atc ggt ctt gtc   240
Glu Asp Leu Thr Trp Arg Leu Ala Pro Gly Glu Arg Ile Gly Leu Val
65                  70                  75                  80

ggc gtc aac ggc tcc ggc aaa acc acc ctg ctg cgc acc ctt gcc ggc   288
Gly Val Asn Gly Ser Gly Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly
                85                  90                  95

gag cag cca ctt cag gca ggc aaa cgc atc gaa ggc caa acc gtc aaa   336
Glu Gln Pro Leu Gln Ala Gly Lys Arg Ile Glu Gly Gln Thr Val Lys
            100                 105                 110

ctg gga tgg ctc cgc cag gaa ctc gat gac cta gac ctc agc cgc cga   384
Leu Gly Trp Leu Arg Gln Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg
        115                 120                 125

ctc atc gac tgc gtt gaa gat gtc gct tcc tac gtg atg atg ggc gac   432
Leu Ile Asp Cys Val Glu Asp Val Ala Ser Tyr Val Met Met Gly Asp
    130                 135                 140

aag cag gtc tcc gct tcc caa ttg gca gaa cgc ctc gga ttc tca ccc   480
Lys Gln Val Ser Ala Ser Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro
145                 150                 155                 160

aag agg caa cgc acc cca gtt ggt gac ctg tcc ggt ggt gaa cgc cgc   528
Lys Arg Gln Arg Thr Pro Val Gly Asp Leu Ser Gly Gly Glu Arg Arg
                165                 170                 175

cga ctc caa ctc acc cgc gtg ctc atg gcc gaa cca aac gtg ctg ctc   576
Arg Leu Gln Leu Thr Arg Val Leu Met Ala Glu Pro Asn Val Leu Leu
            180                 185                 190

ctc gac gag ccc acc aac gac ctg gac att gac acc ctc caa gag ctg   624
Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu
        195                 200                 205

gaa tcc ctt ctc gac gga tgg cca ggc acc atg gtg gtt atc tcc cac   672
Glu Ser Leu Leu Asp Gly Trp Pro Gly Thr Met Val Val Ile Ser His
    210                 215                 220

gac cgt tac ctc atc gaa cgc gtc acc gac tcc acc tgg gca ctc ttc   720
Asp Arg Tyr Leu Ile Glu Arg Val Thr Asp Ser Thr Trp Ala Leu Phe
225                 230                 235                 240

ggc gat ggc aag ctc acc aac ctg cca ggc gga att gaa gag tac ctg   768
Gly Asp Gly Lys Leu Thr Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu
                245                 250                 255
```

```
cag cga cga gca gcg atg gcc gcg gcc gaa gac agt gga gtg ctg aac   816
Gln Arg Arg Ala Ala Met Ala Ala Ala Glu Asp Ser Gly Val Leu Asn
            260                 265                 270

ttg ggt gcg gcc acg cag gct gga acc ttt tct gct gca aca gag cag   864
Leu Gly Ala Ala Thr Gln Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln
        275                 280                 285

gct gcc act tct gtg gaa agt tcc gga att tct tcc caa gaa cgc cac   912
Ala Ala Thr Ser Val Glu Ser Ser Gly Ile Ser Ser Gln Glu Arg His
    290                 295                 300

cgc atc acc aag gaa atg aac gcc ctg gag cgc aaa atg ggc aag ctt   960
Arg Ile Thr Lys Glu Met Asn Ala Leu Glu Arg Lys Met Gly Lys Leu
305                 310                 315                 320

gac cag caa atg gac aag ctt aat cag cag ctc gct gat gca gcg gag   1008
Asp Gln Gln Met Asp Lys Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu
                325                 330                 335

gcc atg gac acc ata aag ctc acc gag ctg gac acc aag ctc cgc gca   1056
Ala Met Asp Thr Ile Lys Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala
            340                 345                 350

gtg cag gaa gaa cac ggc gag ctg gaa atg cag tgg ctg gaa ctc ggc   1104
Val Gln Glu Glu His Gly Glu Leu Glu Met Gln Trp Leu Glu Leu Gly
        355                 360                 365

gag gaa atc gag ggc tagttcatgc cgtcggcagg cga                    1142
Glu Glu Ile Glu Gly
    370
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Doc. 2010-10-26 10:26:09 p.m.

<210> 156
<211> 373
<212> PRT
<213> Corynebacterium glutamicum

<400> 156

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Met Arg Gly Gly Ala Pro Ala Arg Thr Ser Lys Pro Gly Phe Arg Leu
  1               5                  10                  15

Glu Ala Ala Glu Ala Leu Ile Ala Glu Val Pro Ala Pro Arg Asp Lys
             20                  25                  30

Val Glu Leu Met Ala Phe Ser Lys Ser Arg Gln Gly Arg Val Val Ile
         35                  40                  45

Glu Leu Glu Asp Ala Thr Val Ala Thr Pro Asp Asp Arg Ile Leu Val
     50                  55                  60

Glu Asp Leu Thr Trp Arg Leu Ala Pro Gly Glu Arg Ile Gly Leu Val
 65                  70                  75                  80

Gly Val Asn Gly Ser Gly Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly
                 85                  90                  95

Glu Gln Pro Leu Gln Ala Gly Lys Arg Ile Glu Gly Gln Thr Val Lys
            100                 105                 110

Leu Gly Trp Leu Arg Gln Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg
```

```
        115                 120                 125

Leu Ile Asp Cys Val Glu Asp Val Ala Ser Tyr Val Met Met Gly Asp
    130                 135                 140

Lys Gln Val Ser Ala Ser Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro
145                 150                 155                 160

Lys Arg Gln Arg Thr Pro Val Gly Asp Leu Ser Gly Gly Glu Arg Arg
                165                 170                 175

Arg Leu Gln Leu Thr Arg Val Leu Met Ala Glu Pro Asn Val Leu Leu
            180                 185                 190

Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu
        195                 200                 205

Glu Ser Leu Leu Asp Gly Trp Pro Gly Thr Met Val Val Ile Ser His
    210                 215                 220

Asp Arg Tyr Leu Ile Glu Arg Val Thr Asp Ser Thr Trp Ala Leu Phe
225                 230                 235                 240

Gly Asp Gly Lys Leu Thr Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu
                245                 250                 255

Gln Arg Arg Ala Ala Met Ala Ala Ala Glu Asp Ser Gly Val Leu Asn
            260                 265                 270

Leu Gly Ala Ala Thr Gln Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln
        275                 280                 285

Ala Ala Thr Ser Val Glu Ser Ser Gly Ile Ser Ser Gln Glu Arg His
    290                 295                 300

Arg Ile Thr Lys Glu Met Asn Ala Leu Glu Arg Lys Met Gly Lys Leu
305                 310                 315                 320

Asp Gln Gln Met Asp Lys Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu
                325                 330                 335

Ala Met Asp Thr Ile Lys Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala
            340                 345                 350

Val Gln Glu Glu His Gly Glu Leu Glu Met Gln Trp Leu Glu Leu Gly
        355                 360                 365

Glu Glu Ile Glu Gly
    370
```

<210> 157
<211> 349
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(349)
<223> RXN02975

<400> 157
tcgtcggtgc agtcctcgga ttgcttaagt tgtaggtggc tgggggcgtc gaaaagcagc 60

tttattgacc tggcaacttc aattgataga ctgttaggtt gtg att gtc acc aat 115
Val Ile Val Thr Asn
1 5

gat tta gag gtg cgc gtt ggc gca cgt acc ctt ctc gat gcc cca ggt 163
Asp Leu Glu Val Arg Val Gly Ala Arg Thr Leu Leu Asp Ala Pro Gly
10 15 20

cag ctc ctt cgg gtg cag cca ggc gac cgt att ggt ctg gtt ggt aga 211
Gln Leu Leu Arg Val Gln Pro Gly Asp Arg Ile Gly Leu Val Gly Arg
25 30 35

aat ggt gcg ggc aaa acc acc acc atg cga atc ctc tcg ggc gaa acc 259
Asn Gly Ala Gly Lys Thr Thr Thr Met Arg Ile Leu Ser Gly Glu Thr
40 45 50

aag ccc tac gga gga tcc gta acc aca tct ggt gaa atc ggt tac ctg 307
Lys Pro Tyr Gly Gly Ser Val Thr Thr Ser Gly Glu Ile Gly Tyr Leu
55 60 65

ccc cag gac tcc cgc gaa ggc aac atc gaa caa acc gcc cgc 349
Pro Gln Asp Ser Arg Glu Gly Asn Ile Glu Gln Thr Ala Arg
70 75 80

<210> 158
<211> 83
<212> PRT
<213> Corynebacterium glutamicum

<400> 158
Val Ile Val Thr Asn Asp Leu Glu Val Arg Val Gly Ala Arg Thr Leu
1 5 10 15

Leu Asp Ala Pro Gly Gln Leu Leu Arg Val Gln Pro Gly Asp Arg Ile
20 25 30

Gly Leu Val Gly Arg Asn Gly Ala Gly Lys Thr Thr Thr Met Arg Ile
35 40 45

Leu Ser Gly Glu Thr Lys Pro Tyr Gly Gly Ser Val Thr Thr Ser Gly
50 55 60

Glu Ile Gly Tyr Leu Pro Gln Asp Ser Arg Glu Gly Asn Ile Glu Gln
65 70 75 80

Thr Ala Arg

<210> 159
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)

<223> RXN03116

<400> 159

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aggggaatgg cttaatatcg taggtcccaa cggctgcgga aagagtacgt tgctgcacgc 60

ttttgctcag gtactgtcac tggaatcggg aaggctgaaa atg ggg gag ggg gac   115
                                             Met Gly Glu Gly Asp
                                               1               5

gtc gaa aag cat ttt gct ttt ggt ctt aaa gct gcg aag cag cgt cgc   163
Val Glu Lys His Phe Ala Phe Gly Leu Lys Ala Ala Lys Gln Arg Arg
                 10                  15                  20

ttt ttc gcg cgt acc gtg gcc ctc atg cca cag aat cct act att cct   211
Phe Phe Ala Arg Thr Val Ala Leu Met Pro Gln Asn Pro Thr Ile Pro
             25                  30                  35

gca ggt ctg agc gtt ttt gat tat gtg ctg ctg ggg cgt cat ccg cac   259
Ala Gly Leu Ser Val Phe Asp Tyr Val Leu Leu Gly Arg His Pro His
         40                  45                  50

agt tac gcg ccg ggg cgt gct gat gat gag atc gtg aag cgg tgc ctc   307
Ser Tyr Ala Pro Gly Arg Ala Asp Asp Glu Ile Val Lys Arg Cys Leu
     55                  60                  65

gct gat ctg aaa ttg gag cat ttc agc gac cgc ggc tta gac gaa ttg   355
Ala Asp Leu Lys Leu Glu His Phe Ser Asp Arg Gly Leu Asp Glu Leu
 70                  75                  80                  85

tcc ggc ggc gag cgt caa cgc gtc agc ctt gcc cgc gcg ctc gcc caa   403
Ser Gly Gly Glu Arg Gln Arg Val Ser Leu Ala Arg Ala Leu Ala Gln
                 90                  95                 100

gaa ccg cgc atc gtg ctt ctc gac gag ccg acc tcc gcg ctt gac atc   451
Glu Pro Arg Ile Val Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Ile
            105                 110                 115

ggc cat gcg cag gaa acg ctt gag ctt atc gac gcc atc cgg cac cga   499
Gly His Ala Gln Glu Thr Leu Glu Leu Ile Asp Ala Ile Arg His Arg
        120                 125                 130

ctc ggc ctc acc gtg atc gcg gcg atg cat gac ctc acc ctg act gcg   547
Leu Gly Leu Thr Val Ile Ala Ala Met His Asp Leu Thr Leu Thr Ala
    135                 140                 145

caa tac ggc gat cgg gtg ctc atg atg aat ggt ggc cgc aaa gtt ttc   595
Gln Tyr Gly Asp Arg Val Leu Met Met Asn Gly Gly Arg Lys Val Phe
150                 155                 160                 165

gag ggc act gca gcc gaa gtg ctc acc gcg cag cgg att tcg gag att   643
Glu Gly Thr Ala Ala Glu Val Leu Thr Ala Gln Arg Ile Ser Glu Ile
                170                 175                 180

tat gat gcc act gtg att gtt gag gtt att gat ggg cgt ccc gtg gtg   691
Tyr Asp Ala Thr Val Ile Val Glu Val Ile Asp Gly Arg Pro Val Val
            185                 190                 195

att ccg caa cgg tcg cac tgacctgttg tggcagacca gac                732
Ile Pro Gln Arg Ser His
        200
```

<210> 160
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 160
Met Gly Glu Gly Asp Val Glu Lys His Phe Ala Phe Gly Leu Lys Ala
1 5 10 15

Ala Lys Gln Arg Arg Phe Phe Ala Arg Thr Val Ala Leu Met Pro Gln
20 25 30

Asn Pro Thr Ile Pro Ala Gly Leu Ser Val Phe Asp Tyr Val Leu Leu
35 40 45

Gly Arg His Pro His Ser Tyr Ala Pro Gly Arg Ala Asp Asp Glu Ile
50 55 60

Val Lys Arg Cys Leu Ala Asp Leu Lys Leu Glu His Phe Ser Asp Arg
65 70 75 80

Gly Leu Asp Glu Leu Ser Gly Gly Glu Arg Gln Arg Val Ser Leu Ala
85 90 95

Arg Ala Leu Ala Gln Glu Pro Arg Ile Val Leu Leu Asp Glu Pro Thr
100 105 110

Ser Ala Leu Asp Ile Gly His Ala Gln Glu Thr Leu Glu Leu Ile Asp
115 120 125

Ala Ile Arg His Arg Leu Gly Leu Thr Val Ile Ala Ala Met His Asp
130 135 140

Leu Thr Leu Thr Ala Gln Tyr Gly Asp Arg Val Leu Met Met Asn Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Gly Thr Ala Ala Glu Val Leu Thr Ala Gln
165 170 175

Arg Ile Ser Glu Ile Tyr Asp Ala Thr Val Ile Val Glu Val Ile Asp
180 185 190

Gly Arg Pro Val Val Ile Pro Gln Arg Ser His
195 200

<210> 161
<211> 390
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(367)
<223> RXN03108

<400> 161
caaccagcct gccacgttgc tggatggacc gtcgtaatca tcggcatcac cggcttaatc 60

cttgaccacc tcatcggtga gttgcagaaa gtagttcgct atg act aaa cca aac 115

```
                                                    Met Thr Lys Pro Asn
                                                      1               5

gct tcc gtc gag ctg aat acg atc acc aag tcc tac ggc tcc acc act   163
Ala Ser Val Glu Leu Asn Thr Ile Thr Lys Ser Tyr Gly Ser Thr Thr
                 10                  15                  20

atc att ggc gat acg agc atc acc atc aac gac ggt gaa ttc gtc tcc   211
Ile Ile Gly Asp Thr Ser Ile Thr Ile Asn Asp Gly Glu Phe Val Ser
             25                  30                  35

ctc ctc gac cct tcc ggc tgc gga aaa tca aca att ctc aaa atg atc   259
Leu Leu Asp Pro Ser Gly Cys Gly Lys Ser Thr Ile Leu Lys Met Ile
         40                  45                  50

gcc gga ctg gcc tcc cca tcc acc ggc aca gtc agc gca ggc aac gaa   307
Ala Gly Leu Ala Ser Pro Ser Thr Gly Thr Val Ser Ala Gly Asn Glu
     55                  60                  65

gaa att aaa gga cca gga cct gac cga ggc atg gtt ttc caa gac cac   355
Glu Ile Lys Gly Pro Gly Pro Asp Arg Gly Met Val Phe Gln Asp His
 70                  75                  80                  85

gcc ctc ctg ccc tgattgaccg cacgcggcaa cat                        390
Ala Leu Leu Pro
```

<210> 162
<211> 89
<212> PRT
<213> Corynebacterium glutamicum

<400> 162

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Met Thr Lys Pro Asn Ala Ser Val Glu Leu Asn Thr Ile Thr Lys Ser
  1               5                  10                  15

Tyr Gly Ser Thr Thr Ile Ile Gly Asp Thr Ser Ile Thr Ile Asn Asp
             20                  25                  30

Gly Glu Phe Val Ser Leu Leu Asp Pro Ser Gly Cys Gly Lys Ser Thr
         35                  40                  45

Ile Leu Lys Met Ile Ala Gly Leu Ala Ser Pro Ser Thr Gly Thr Val
     50                  55                  60

Ser Ala Gly Asn Glu Glu Ile Lys Gly Pro Gly Pro Asp Arg Gly Met
 65                  70                  75                  80

Val Phe Gln Asp His Ala Leu Leu Pro
                 85
```

<210> 163
<211> 1347
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1324)

<223> RXN03129

<400> 163

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gctgaggttg agaccaagct gaacaccatc tacacccgcg acatcgaacc acttatttaa 60

tccgagcact tcagctacac ctatttaagg aggctgtgac atg gcg tca atc gtc   115
                                          Met Ala Ser Ile Val
                                            1               5

ttt gaa aac gtc aca cgc aaa tac tct ccg ggc gca cgc ccg gcc gtc   163
Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly Ala Arg Pro Ala Val
                 10                  15                  20

gac aag ctt aat ttg gaa atc gcc gac ggc gag ttc cta gtt ctc gtt   211
Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val
             25                  30                  35

gga ccc tca ggc tgt gga aag tcc act tct ttg cgc atg ctg gct ggt   259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu Arg Met Leu Ala Gly
         40                  45                  50

ctt gag cct atc gac gag gga cgt cta ctc att gat ggt aaa gac gcc   307
Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile Asp Gly Lys Asp Ala
     55                  60                  65

acg gaa ctg cgt ccg cag gat cgt gac atc gct atg gtc ttc cag agc   355
Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala Met Val Phe Gln Ser
 70                  75                  80                  85

tac gcg ctg tac ccg aat atg act gtt cgg gac aac atg ggc ttt gcg   403
Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp Asn Met Gly Phe Ala
                 90                  95                 100

ctg aag aat cag aag gtg gct aag gct gag atc gaa aag cgt gtt gct   451
Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile Glu Lys Arg Val Ala
            105                 110                 115

gaa gcc tca cgc att ctg cag ctg gat ccg tat ctt gat cgt aag cct   499
Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr Leu Asp Arg Lys Pro
        120                 125                 130

gca gct ttg tct ggt ggt cag cgc cag cgc gtg gcc atg ggc cgt gca   547
Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
    135                 140                 145

att gtg cgt gag cca tcg gtg ttc tgc atg gat gag cca ctg tcc aac   595
Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp Glu Pro Leu Ser Asn
150                 155                 160                 165

cta gat gcg aag ctg cgt gtg tct acg cgt gcg gag atc tct ggt ttg   643
Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala Glu Ile Ser Gly Leu
                170                 175                 180

cag cgt cgc atg ggc gtg acc acg gtg tat gtg act cac gat cag gtc   691
Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Val
            185                 190                 195

gag gcc atg acc atg ggt gat cgc gtc gct gtg ctt ttg ctc ggt gtg   739
Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Leu Leu Gly Val
        200                 205                 210
```

```
ctg cag caa gta gac acc ccg cag aac ctg tac gac tac cca gca aat   787
Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr Asp Tyr Pro Ala Asn
    215                 220                 225

gcg ttc gtc gcc agc ttc att ggt tcc cct tcc atg aac ttg att gag   835
Ala Phe Val Ala Ser Phe Ile Gly Ser Pro Ser Met Asn Leu Ile Glu
230                 235                 240                 245

ggc acc atc cgt ggc gat aag gtc act ttg ggt act gga att cag att   883
Gly Thr Ile Arg Gly Asp Lys Val Thr Leu Gly Thr Gly Ile Gln Ile
                250                 255                 260

tca gtt cct gat gag gtg gca gca gag gtt cgc aac aac ccg gat cgc   931
Ser Val Pro Asp Glu Val Ala Ala Glu Val Arg Asn Asn Pro Asp Arg
            265                 270                 275

ttt gag ggt cgt cca gtc att gtt ggt gct cgt ccc gag cac atg tat   979
Phe Glu Gly Arg Pro Val Ile Val Gly Ala Arg Pro Glu His Met Tyr
        280                 285                 290

ttg acc acg gcg aat gag agt ggt gct gta ttg ggc gaa gtc agc cac   1027
Leu Thr Thr Ala Asn Glu Ser Gly Ala Val Leu Gly Glu Val Ser His
    295                 300                 305

att gat gag ctc ggc gcg gat tca atg gtc tac gta ttg gcg tct ggt   1075
Ile Asp Glu Leu Gly Ala Asp Ser Met Val Tyr Val Leu Ala Ser Gly
310                 315                 320                 325

gtg aag aac ccg aat act gat ctt ttg ggt gag ggc att cca gag gat   1123
Val Lys Asn Pro Asn Thr Asp Leu Leu Gly Glu Gly Ile Pro Glu Asp
                330                 335                 340

atg cgc gtg acc gtt gtc ggt gct gaa gag acc gat aag gcc cgg ctg   1171
Met Arg Val Thr Val Val Gly Ala Glu Glu Thr Asp Lys Ala Arg Leu
            345                 350                 355

ggt att cgt gtt gag cgc cat cac ggt ctg aag gcc ggc gat aag gtg   1219
Gly Ile Arg Val Glu Arg His His Gly Leu Lys Ala Gly Asp Lys Val
        360                 365                 370

cac gtt gtt gct gca ccg aag gat gtt cac ctc ttc gac ggt ctt gat   1267
His Val Val Ala Ala Pro Lys Asp Val His Leu Phe Asp Gly Leu Asp
    375                 380                 385

ggc cgt cga atc ggt gca tcg gtt cta gct cca gcc cat aca gtc cag   1315
Gly Arg Arg Ile Gly Ala Ser Val Leu Ala Pro Ala His Thr Val Gln
390                 395                 400                 405

tct ggt cac tagattattt accagtgcaa ctc                            1347
Ser Gly His
```

<210> 164
<211> 408
<212> PRT
<213> Corynebacterium glutamicum

<400> 164

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Met Ala Ser Ile Val Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly
  1               5                  10                  15
```

Ala Arg Pro Ala Val Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu
20 25 30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu
35 40 45

Arg Met Leu Ala Gly Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile
50 55 60

Asp Gly Lys Asp Ala Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala
65 70 75 80

Met Val Phe Gln Ser Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp
85 90 95

Asn Met Gly Phe Ala Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile
100 105 110

Glu Lys Arg Val Ala Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr
115 120 125

Leu Asp Arg Lys Pro Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
130 135 140

Ala Met Gly Arg Ala Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp
145 150 155 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala
165 170 175

Glu Ile Ser Gly Leu Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val
180 185 190

Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
195 200 205

Leu Leu Leu Gly Val Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr
210 215 220

Asp Tyr Pro Ala Asn Ala Phe Val Ala Ser Phe Ile Gly Ser Pro Ser
225 230 235 240

Met Asn Leu Ile Glu Gly Thr Ile Arg Gly Asp Lys Val Thr Leu Gly
245 250 255

Thr Gly Ile Gln Ile Ser Val Pro Asp Glu Val Ala Ala Glu Val Arg
260 265 270

Asn Asn Pro Asp Arg Phe Glu Gly Arg Pro Val Ile Val Gly Ala Arg
275 280 285

Pro Glu His Met Tyr Leu Thr Thr Ala Asn Glu Ser Gly Ala Val Leu
290 295 300

Gly Glu Val Ser His Ile Asp Glu Leu Gly Ala Asp Ser Met Val Tyr
305 310 315 320

Val Leu Ala Ser Gly Val Lys Asn Pro Asn Thr Asp Leu Leu Gly Glu
325 330 335

```
Gly Ile Pro Glu Asp Met Arg Val Thr Val Val Gly Ala Glu Glu Thr
            340                 345                 350

Asp Lys Ala Arg Leu Gly Ile Arg Val Glu Arg His His Gly Leu Lys
        355                 360                 365

Ala Gly Asp Lys Val His Val Val Ala Ala Pro Lys Asp Val His Leu
    370                 375                 380

Phe Asp Gly Leu Asp Gly Arg Arg Ile Gly Ala Ser Val Leu Ala Pro
385                 390                 395                 400

Ala His Thr Val Gln Ser Gly His
                405
```

<210> 165
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> FRXA01890

<400> 165

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gctgaggttg agaccaagct gaacaccatc tacacccgcg acatcgaacc acttatttaa 60

tccgagcact tcagctacac ctatttaagg aggctgtgac atg gcg tca atc gtc   115
                                            Met Ala Ser Ile Val
                                              1               5

ttt gaa aac gtc aca cgc aaa tac tct ccg ggc gca cgc ccg gcc gtc   163
Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly Ala Arg Pro Ala Val
                  10                  15                  20

gac aag ctt aat ttg gaa atc gcc gac ggc gag ttc cta gtt ctc gtt   211
Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val
              25                  30                  35

gga ccc tca ggc tgt gga aag tcc act tct ttg cgc atg ctg gct ggt   259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu Arg Met Leu Ala Gly
          40                  45                  50

ctt gag cct atc gac gag gga cgt cta ctc att gat ggt aaa gac gcc   307
Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile Asp Gly Lys Asp Ala
      55                  60                  65

acg gaa ctg cgt ccg cag gat cgt gac atc gct atg gtc ttc cag agc   355
Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala Met Val Phe Gln Ser
 70                  75                  80                  85

tac gcg ctg tac ccg aat atg act gtt cgg gac aac atg ggc ttt gcg   403
Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp Asn Met Gly Phe Ala
                  90                  95                 100

ctg aag aat cag aag gtg gct aag gct gag atc gaa aag cgt gtt gct   451
Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile Glu Lys Arg Val Ala
              105                 110                 115
```

```
gaa gcc tca cgc att ctg cag ctg gat ccg tat ctt gat cgt aag cct   499
Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr Leu Asp Arg Lys Pro
        120                 125                 130

gca gct ttg tct ggt ggt cag cgc cag cgc gtg gcc atg ggc cgt gca   547
Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
    135                 140                 145

att gtg cgt gag cca tcg gtg ttc tgc atg gat gag cca ctg tcc aac   595
Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp Glu Pro Leu Ser Asn
150                 155                 160                 165

cta gat gcg aag ctg cgt gtg tct acg cgt gcg gag atc tct ggt ttg   643
Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala Glu Ile Ser Gly Leu
                170                 175                 180

cag cgt cgc atg ggc gtg acc acg gtg tat gtg act cac gat cag gtc   691
Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Val
            185                 190                 195

gag gcc atg acc atg ggt gat cgc gtc gct gtg ctt ttg ctc ggt gtg   739
Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Leu Leu Gly Val
        200                 205                 210

ctg cag caa gta gac acc ccg cag aac ctg tac gac tac cca gca aat   787
Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr Asp Tyr Pro Ala Asn
    215                 220                 225

gcg ttc gtc gcc agc ttc att ggt tcc ctt cca tgaacttgat tgagggcacc 840
Ala Phe Val Ala Ser Phe Ile Gly Ser Leu Pro
230                 235                 240

atc                                                               843
```

<210> 166
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 166

```
Met Ala Ser Ile Val Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly
  1               5                  10                  15

Ala Arg Pro Ala Val Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu
             20                  25                  30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu
         35                  40                  45

Arg Met Leu Ala Gly Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile
     50                  55                  60

Asp Gly Lys Asp Ala Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala
 65                  70                  75                  80

Met Val Phe Gln Ser Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp
                 85                  90                  95

Asn Met Gly Phe Ala Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile
            100                 105                 110
```

```
Glu Lys Arg Val Ala Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr
        115                 120                 125

Leu Asp Arg Lys Pro Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
    130                 135                 140

Ala Met Gly Arg Ala Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp
145                 150                 155                 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala
                165                 170                 175

Glu Ile Ser Gly Leu Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val
            180                 185                 190

Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
        195                 200                 205

Leu Leu Leu Gly Val Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr
    210                 215                 220

Asp Tyr Pro Ala Asn Ala Phe Val Ala Ser Phe Ile Gly Ser Leu Pro
225                 230                 235                 240
```

20050130137

<210> 167
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXN02945

<400> 167

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ttccggtgcg atccttgccg gcctgctcag ctggtacctg gtccgcgcgt tggcgaggac 60

tggtgcactt gatcgtttcg ccgctggccg cgaggtataa atg acc acc gca ctt   115
                                                Met Thr Thr Ala Leu
                                                  1               5

gga acg cgc gtt gtt gcg cgc aac ttt ggc tac cgc cat gct tcc cgg   163
Gly Thr Arg Val Val Ala Arg Asn Phe Gly Tyr Arg His Ala Ser Arg
                  10                  15                  20

gaa aac ccc gcg ctc aaa gac atc aac ttc gag atc gca cct ggt gaa   211
Glu Asn Pro Ala Leu Lys Asp Ile Asn Phe Glu Ile Ala Pro Gly Glu
              25                  30                  35

cgc atc ctg ctc acc ggc gct tcc ggc gcc gga aaa tcc acg cta ctc   259
Arg Ile Leu Leu Thr Gly Ala Ser Gly Ala Gly Lys Ser Thr Leu Leu
          40                  45                  50

gcc gcg ctc gct ggc gtt tta ggc ggt tct gat gag ggc gtt tct acg   307
Ala Ala Leu Ala Gly Val Leu Gly Gly Ser Asp Glu Gly Val Ser Thr
      55                  60                  65
```

```
ggc gaa ttg ctt gtc gac gcc ccc tcc atc ggt ttg gtt ctc caa gat   355
Gly Glu Leu Leu Val Asp Ala Pro Ser Ile Gly Leu Val Leu Gln Asp
 70                  75                  80                  85

cca gat tcc caa gtc atc gcc tcc cgc atc ggc gat gat gtg gcg ttt   403
Pro Asp Ser Gln Val Ile Ala Ser Arg Ile Gly Asp Asp Val Ala Phe
                 90                  95                 100

ggc tgc gaa aac ctc caa att ccg cgc gag gaa atc tgg cca cgg gtg   451
Gly Cys Glu Asn Leu Gln Ile Pro Arg Glu Glu Ile Trp Pro Arg Val
            105                 110                 115

gaa cga gca ctt gaa ttg gtg ggc ttg gat cta cca ctg agc cac ccc   499
Glu Arg Ala Leu Glu Leu Val Gly Leu Asp Leu Pro Leu Ser His Pro
        120                 125                 130

acg aaa tat ctt tcc ggt ggc caa aaa caa cgc ctc gct ctt gcc ggt   547
Thr Lys Tyr Leu Ser Gly Gly Gln Lys Gln Arg Leu Ala Leu Ala Gly
    135                 140                 145

gtg atc gcc atg ggt gct cgt ctg att ctg ctt gat gaa ccc acc gca   595
Val Ile Ala Met Gly Ala Arg Leu Ile Leu Leu Asp Glu Pro Thr Ala
150                 155                 160                 165

aac ctt gat cct caa ggc caa aaa aat gtg gtc gca gca gtg gat cgc   643
Asn Leu Asp Pro Gln Gly Gln Lys Asn Val Val Ala Ala Val Asp Arg
                170                 175                 180

gtt gtt cag gaa act gga gca aca ctc atc gtg gtg gaa cac cgc cat   691
Val Val Gln Glu Thr Gly Ala Thr Leu Ile Val Val Glu His Arg His
            185                 190                 195

gag ctg tgg gtc aac atc att gac cgg atc atc agt att act gac ggc   739
Glu Leu Trp Val Asn Ile Ile Asp Arg Ile Ile Ser Ile Thr Asp Gly
        200                 205                 210

gaa gat gtc caa cct gca gag ttg atc aag gtg ggc cag ttg cct ggg   787
Glu Asp Val Gln Pro Ala Glu Leu Ile Lys Val Gly Gln Leu Pro Gly
    215                 220                 225

gcg cag ccg tcg aca agc aaa ccg atc ttg tgg gcg aat gat ttg ctg   835
Ala Gln Pro Ser Thr Ser Lys Pro Ile Leu Trp Ala Asn Asp Leu Leu
230                 235                 240                 245

tgc acc tgg ggc ggc ctg cgt agt ttt gag gtg ccg gaa ggc gcc tcg   883
Cys Thr Trp Gly Gly Leu Arg Ser Phe Glu Val Pro Glu Gly Ala Ser
                250                 255                 260

acg gtg atc acc ggg ccg aat ggc gct gga aaa tcc aca ctt gcg ctg   931
Thr Val Ile Thr Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Ala Leu
            265                 270                 275

acc atg ggt gga ttg ctt ccg cga aaa gtg ggc agc tgg aac tct ctg   979
Thr Met Gly Gly Leu Leu Pro Arg Lys Val Gly Ser Trp Asn Ser Leu
        280                 285                 290

aca cgg tgc gcg gcg gcc tta aca cgc ccc cgc aca agt ggc gtt cag   1027
Thr Arg Cys Ala Ala Ala Leu Thr Arg Pro Arg Thr Ser Gly Val Gln
    295                 300                 305
```

ctg atc tagctgcacg tattggcact gtc 1056
Leu Ile
310

<210> 168
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 168
Met Thr Thr Ala Leu Gly Thr Arg Val Val Ala Arg Asn Phe Gly Tyr
1 5 10 15

Arg His Ala Ser Arg Glu Asn Pro Ala Leu Lys Asp Ile Asn Phe Glu
20 25 30

Ile Ala Pro Gly Glu Arg Ile Leu Leu Thr Gly Ala Ser Gly Ala Gly
35 40 45

Lys Ser Thr Leu Leu Ala Ala Leu Ala Gly Val Leu Gly Gly Ser Asp
50 55 60

Glu Gly Val Ser Thr Gly Glu Leu Leu Val Asp Ala Pro Ser Ile Gly
65 70 75 80

Leu Val Leu Gln Asp Pro Asp Ser Gln Val Ile Ala Ser Arg Ile Gly
85 90 95

Asp Asp Val Ala Phe Gly Cys Glu Asn Leu Gln Ile Pro Arg Glu Glu
100 105 110

Ile Trp Pro Arg Val Glu Arg Ala Leu Glu Leu Val Gly Leu Asp Leu
115 120 125

Pro Leu Ser His Pro Thr Lys Tyr Leu Ser Gly Gly Gln Lys Gln Arg
130 135 140

Leu Ala Leu Ala Gly Val Ile Ala Met Gly Ala Arg Leu Ile Leu Leu
145 150 155 160

Asp Glu Pro Thr Ala Asn Leu Asp Pro Gln Gly Gln Lys Asn Val Val
165 170 175

Ala Ala Val Asp Arg Val Val Gln Glu Thr Gly Ala Thr Leu Ile Val
180 185 190

Val Glu His Arg His Glu Leu Trp Val Asn Ile Ile Asp Arg Ile Ile
195 200 205

Ser Ile Thr Asp Gly Glu Asp Val Gln Pro Ala Glu Leu Ile Lys Val
210 215 220

Gly Gln Leu Pro Gly Ala Gln Pro Ser Thr Ser Lys Pro Ile Leu Trp
225 230 235 240

Ala Asn Asp Leu Leu Cys Thr Trp Gly Gly Leu Arg Ser Phe Glu Val
245 250 255

Pro Glu Gly Ala Ser Thr Val Ile Thr Gly Pro Asn Gly Ala Gly Lys
260 265 270

```
Ser Thr Leu Ala Leu Thr Met Gly Gly Leu Leu Pro Arg Lys Val Gly
        275                 280                 285

Ser Trp Asn Ser Leu Thr Arg Cys Ala Ala Ala Leu Thr Arg Pro Arg
    290                 295                 300

Thr Ser Gly Val Gln Leu Ile
305                 310
```

<210> 169
<211> 357
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(334)
<223> RXA01247

<400> 169

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tccgatgacc accccgactt ccccttgct gccgctggcc tccgacggtt gtggatgctg 60

cgcgccctct acaccgtccg cgaccgtctc cgcctcggcc gtg gcc gcg gca acc   115
                                              Val Ala Ala Ala Thr
                                                1               5

gac gca aca cct gaa ggt ccc acc acc tac cag gtc aca ggc atg acc   163
Asp Ala Thr Pro Glu Gly Pro Thr Thr Tyr Gln Val Thr Gly Met Thr
                10                  15                  20

tgc gga cac tgc gcc gac aac gtc acc gag gcg gtg agc gct ctg ccc   211
Cys Gly His Cys Ala Asp Asn Val Thr Glu Ala Val Ser Ala Leu Pro
            25                  30                  35

cag gtc gac gac gtc cag gtc gac ctc atc gcc ggt ggg gtc tcc atc   259
Gln Val Asp Asp Val Gln Val Asp Leu Ile Ala Gly Gly Val Ser Ile
        40                  45                  50

gtc acg gtc acg ggt tcc gtg ccc ctg gaa acc gtc cac cgg gca att   307
Val Thr Val Thr Gly Ser Val Pro Leu Glu Thr Val His Arg Ala Ile
    55                  60                  65

gag gag acc ggc tac acc gtc ttg tcc tgatcgattc acccatcatc         354
Glu Glu Thr Gly Tyr Thr Val Leu Ser
70                  75

tcg                                                               357
```

<210> 170
<211> 78
<212> PRT
<213> Corynebacterium glutamicum

<400> 170

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Val Ala Ala Ala Thr Asp Ala Thr Pro Glu Gly Pro Thr Thr Tyr Gln
  1               5                  10                  15

Val Thr Gly Met Thr Cys Gly His Cys Ala Asp Asn Val Thr Glu Ala
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             20                  25                  30

Val Ser Ala Leu Pro Gln Val Asp Asp Val Gln Val Asp Leu Ile Ala
         35                  40                  45

Gly Gly Val Ser Ile Val Thr Val Thr Gly Ser Val Pro Leu Glu Thr
     50                  55                  60

Val His Arg Ala Ile Glu Glu Thr Gly Tyr Thr Val Leu Ser
 65                  70                  75


<210> 171
<211> 1296
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1273)
<223> RXN00099

<400> 171
ctctggtgaa gaggatgttg actcgggaga ttcttccact gattcactga ttaagtggta 60

ccgcgcaaat aggtagtcgc ttgcttatag ggtcaggggc gtg aag aat cct cgc   115
                                            Val Lys Asn Pro Arg
                                              1               5

ctc ata gca ctg gcc gct atc atc ctg acc tcg ttc aat ctg cga aca   163
Leu Ile Ala Leu Ala Ala Ile Ile Leu Thr Ser Phe Asn Leu Arg Thr
                 10                  15                  20

gct att act gct tta gct ccg ctg gtt tct gag att cgg gat gat tta   211
Ala Ile Thr Ala Leu Ala Pro Leu Val Ser Glu Ile Arg Asp Asp Leu
             25                  30                  35

ggg gtt agt gct tct ctt att ggt gtg ttg ggc atg atc ccg act gct   259
Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly Met Ile Pro Thr Ala
         40                  45                  50

atg ttc gcg gat gct gcg ttt gcg ctt ccg tcg ttg aag agg aag ttc   307
Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser Leu Lys Arg Lys Phe
     55                  60                  65

act act tcc caa ctg ttg atg ttt gcc atg ctg ttg act gct gcc ggt   355
Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu Leu Thr Ala Ala Gly
 70                  75                  80                  85

cag att att cgt gtc gct gga cct gct tcg ctg ttg atg gtc ggt act   403
Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu Leu Met Val Gly Thr
                 90                  95                 100

gtg ttc gcg atg ttt gcg atc gga gtt acc aat gtg ttg ctt ccg att   451
Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn Val Leu Leu Pro Ile
             105                 110                 115

gct gtt agg gag tat ttt ccg cgt cac gtc ggt gga atg tcg aca act   499
Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly Gly Met Ser Thr Thr
         120                 125                 130
```

```
tat ctg gtg tcg ttc cag att gtt cag gca ctt gct ccg acg ctt gcc   547
Tyr Leu Val Ser Phe Gln Ile Val Gln Ala Leu Ala Pro Thr Leu Ala
    135                 140                 145

gtg ccg att tct cag tgg gct aca cat gtg ggg ttg acc ggt tgg agg   595
Val Pro Ile Ser Gln Trp Ala Thr His Val Gly Leu Thr Gly Trp Arg
150                 155                 160                 165

gtg tcg ctc ggt tcg tgg gcg ctg ctg ggg ttg gtt gcg gcg att tcg   643
Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu Val Ala Ala Ile Ser
                170                 175                 180

tgg att ccg ctg ttg agt ttg cag ggt gcc agg gtt gtt gcg gcg ccg   691
Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg Val Val Ala Ala Pro
            185                 190                 195

tcg aag gtt tct ctt cct gtg tgg aag tct tcg gtt ggt gtg ggg ctc   739
Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser Val Gly Val Gly Leu
        200                 205                 210

ggg ttg atg ttt ggg ttt act tcg ttt gcg acg tat atc ctc atg ggt   787
Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr Tyr Ile Leu Met Gly
    215                 220                 225

ttt atg ccg cag atg gta ggt gat cct cag ctc ggt gcg gtg ttg tta   835
Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu Gly Ala Val Leu Leu
230                 235                 240                 245

ggc tgg tgg tca att ttg gga ttg ccg ctg aac att ctg gga ccg tgg   883
Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn Ile Leu Gly Pro Trp
                250                 255                 260

ttg gtg acg cgt ttc act aac tgc ttc ccg atg gtt gtt atc gcc agt   931
Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met Val Val Ile Ala Ser
            265                 270                 275

gtc atg ttt ctc atc ggt aat ggt ggg ttt tgt ttg gct ccg gat gtt   979
Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys Leu Ala Pro Asp Val
        280                 285                 290

gcg ccg tgg ttg tgg gcg acg ttg tct ggt ctt ggt ccc ctt gcg ttc  1027
Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu Gly Pro Leu Ala Phe
    295                 300                 305

ccg atg gcg ttg acg ctc att aat att cgt gct gaa act agt gct ggt  1075
Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala Glu Thr Ser Ala Gly
310                 315                 320                 325

gct tct gcg ttg agt tcc ttc ggg cag ggt ttg ggt tat acg att gcg  1123
Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu Gly Tyr Thr Ile Ala
                330                 335                 340

tgt ttc ggt ccc ttg ttg act ggt ttc att gtc gat gcg aca ggc agc  1171
Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val Asp Ala Thr Gly Ser
            345                 350                 355

ttc cga aca atc ttt gtg ctt ttt gcg gtt gca aca ctc ttc gtt att  1219
Phe Arg Thr Ile Phe Val Leu Phe Ala Val Ala Thr Leu Phe Val Ile
        360                 365                 370

aga ggc ggt tac ttt gcg aca agg cag gtt tac gtc gaa aag ctt tta  1267
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Arg Gly Gly Tyr Phe Ala Thr Arg Gln Val Tyr Val Glu Lys Leu Leu
375 380 385

aat cgc taggatggcg ctatgccgca aag 1296
Asn Arg
390

<210> 172
<211> 391
<212> PRT
<213> Corynebacterium glutamicum

<400> 172
Val Lys Asn Pro Arg Leu Ile Ala Leu Ala Ala Ile Ile Leu Thr Ser
1 5 10 15

Phe Asn Leu Arg Thr Ala Ile Thr Ala Leu Ala Pro Leu Val Ser Glu
20 25 30

Ile Arg Asp Asp Leu Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly
35 40 45

Met Ile Pro Thr Ala Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser
50 55 60

Leu Lys Arg Lys Phe Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu
65 70 75 80

Leu Thr Ala Ala Gly Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu
85 90 95

Leu Met Val Gly Thr Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn
100 105 110

Val Leu Leu Pro Ile Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly
115 120 125

Gly Met Ser Thr Thr Tyr Leu Val Ser Phe Gln Ile Val Gln Ala Leu
130 135 140

Ala Pro Thr Leu Ala Val Pro Ile Ser Gln Trp Ala Thr His Val Gly
145 150 155 160

Leu Thr Gly Trp Arg Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu
165 170 175

Val Ala Ala Ile Ser Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg
180 185 190

Val Val Ala Ala Pro Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser
195 200 205

Val Gly Val Gly Leu Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr
210 215 220

Tyr Ile Leu Met Gly Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu
225 230 235 240

Gly Ala Val Leu Leu Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn
245 250 255

5,595,889 - 4,208,529

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Ile Leu Gly Pro Trp Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met
            260                 265                 270

Val Val Ile Ala Ser Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys
        275                 280                 285

Leu Ala Pro Asp Val Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu
    290                 295                 300

Gly Pro Leu Ala Phe Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala
305                 310                 315                 320

Glu Thr Ser Ala Gly Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu
                325                 330                 335

Gly Tyr Thr Ile Ala Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val
            340                 345                 350

Asp Ala Thr Gly Ser Phe Arg Thr Ile Phe Val Leu Phe Ala Val Ala
        355                 360                 365

Thr Leu Phe Val Ile Arg Gly Gly Tyr Phe Ala Thr Arg Gln Val Tyr
    370                 375                 380

Val Glu Lys Leu Leu Asn Arg
385                 390


<210> 173
<211> 1296
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1273)
<223> FRXA00099

<400> 173
ctctggtgaa gaggatgttg actcgggaga ttcttccact gattcactga ttaagtggta 60

ccgcgcaaat aggtagtcgc ttgcttatag ggtcaggggc gtg aag aat cct cgc   115
                                            Val Lys Asn Pro Arg
                                              1               5

ctc ata gca ctg gcc gct atc atc ctg acc tcg ttc aat ctg cga aca   163
Leu Ile Ala Leu Ala Ala Ile Ile Leu Thr Ser Phe Asn Leu Arg Thr
                  10                  15                  20

gct att act gct tta gct ccg ctg gtt tct gag att cgg gat gat tta   211
Ala Ile Thr Ala Leu Ala Pro Leu Val Ser Glu Ile Arg Asp Asp Leu
              25                  30                  35

ggg gtt agt gct tct ctt att ggt gtg ttg ggc atg atc ccg act gct   259
Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly Met Ile Pro Thr Ala
          40                  45                  50

atg ttc gcg gat gct gcg ttt gcg ctt ccg tcg ttg aag agg aag ttc   307
Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser Leu Lys Arg Lys Phe
      55                  60                  65
```

```
act act tcc caa ctg ttg atg ttt gcc atg ctg ttg act gct gcc ggt   355
Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu Leu Thr Ala Ala Gly
 70                  75                  80                  85

cag att att cgt gtc gct gga cct gct tcg ctg ttg atg gtc ggt act   403
Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu Leu Met Val Gly Thr
                90                  95                 100

gtg ttc gcg atg ttt gcg atc gga gtt acc aat gtg ttg ctt ccg att   451
Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn Val Leu Leu Pro Ile
            105                 110                 115

gct gtt agg gag tat ttt ccg cgt cac gtc ggt gga atg tcg aca act   499
Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly Gly Met Ser Thr Thr
        120                 125                 130

tat ctg gtg tcg ttc cag att gtt cag gca ctt gct ccg acg ctt gcc   547
Tyr Leu Val Ser Phe Gln Ile Val Gln Ala Leu Ala Pro Thr Leu Ala
    135                 140                 145

gtg ccg att tct cag tgg gct aca cat gtg ggg ttg acc ggt tgg agg   595
Val Pro Ile Ser Gln Trp Ala Thr His Val Gly Leu Thr Gly Trp Arg
150                 155                 160                 165

gtg tcg ctc ggt tcg tgg gcg ctg ctg ggg ttg gtt gcg gcg att tcg   643
Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu Val Ala Ala Ile Ser
                170                 175                 180

tgg att ccg ctg ttg agt ttg cag ggt gcc agg gtt gtt gcg gcg ccg   691
Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg Val Val Ala Ala Pro
            185                 190                 195

tcg aag gtt tct ctt cct gtg tgg aag tct tcg gtt ggt gtg ggg ctc   739
Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser Val Gly Val Gly Leu
        200                 205                 210

ggg ttg atg ttt ggg ttt act tcg ttt gcg acg tat atc ctc atg ggt   787
Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr Tyr Ile Leu Met Gly
    215                 220                 225

ttt atg ccg cag atg gta ggt gat cct cag ctc ggt gcg gtg ttg tta   835
Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu Gly Ala Val Leu Leu
230                 235                 240                 245

ggc tgg tgg tca att ttg gga ttg ccg ctg aac att ctg gga ccg tgg   883
Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn Ile Leu Gly Pro Trp
                250                 255                 260

ttg gtg acg cgt ttc act aac tgc ttc ccg atg gtt gtt atc gcc agt   931
Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met Val Val Ile Ala Ser
            265                 270                 275

gtc atg ttt ctc atc ggt aat ggt ggg ttt tgt ttg gct ccg gat gtt   979
Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys Leu Ala Pro Asp Val
        280                 285                 290

gcg ccg tgg ttg tgg gcg acg ttg tct ggt ctt ggt ccc ctt gcg ttc  1027
Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu Gly Pro Leu Ala Phe
    295                 300                 305
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```
ccg atg gcg ttg acg ctc att aat att cgt gct gaa act agt gct ggt   1075
Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala Glu Thr Ser Ala Gly
310                 315                 320                 325

gct tct gcg ttg agt tcc ttc ggg cag ggt ttg ggt tat acg att gcg   1123
Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu Gly Tyr Thr Ile Ala
                330                 335                 340

tgt ttc ggt ccc ttg ttg act ggt ttc att gtc gat gca aca ggc agc   1171
Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val Asp Ala Thr Gly Ser
            345                 350                 355

ttc cga aca atc ttt ttg ctt ttt gcg ggt gca aca ctc ttc gtt att   1219
Phe Arg Thr Ile Phe Leu Leu Phe Ala Gly Ala Thr Leu Phe Val Ile
        360                 365                 370

aga ggc ggt tac ttt gcg aca agg cag gtt tac gtc gaa aag ctt tta   1267
Arg Gly Gly Tyr Phe Ala Thr Arg Gln Val Tyr Val Glu Lys Leu Leu
    375                 380                 385

aat cgc taggatggcg ctatgccgca aag                                1296
Asn Arg
390
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09/09/2005 15:09:09

<210> 174
<211> 391
<212> PRT
<213> Corynebacterium glutamicum

<400> 174

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Val Lys Asn Pro Arg Leu Ile Ala Leu Ala Ala Ile Ile Leu Thr Ser
  1               5                  10                  15

Phe Asn Leu Arg Thr Ala Ile Thr Ala Leu Ala Pro Leu Val Ser Glu
             20                  25                  30

Ile Arg Asp Asp Leu Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly
         35                  40                  45

Met Ile Pro Thr Ala Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser
     50                  55                  60

Leu Lys Arg Lys Phe Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu
 65                  70                  75                  80

Leu Thr Ala Ala Gly Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu
                 85                  90                  95

Leu Met Val Gly Thr Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn
            100                 105                 110

Val Leu Leu Pro Ile Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly
        115                 120                 125

Gly Met Ser Thr Thr Tyr Leu Val Ser Phe Gln Ile Val Gln Ala Leu
    130                 135                 140

Ala Pro Thr Leu Ala Val Pro Ile Ser Gln Trp Ala Thr His Val Gly
145                 150                 155                 160
```

Leu Thr Gly Trp Arg Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu
165 170 175

Val Ala Ala Ile Ser Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg
180 185 190

Val Val Ala Ala Pro Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser
195 200 205

Val Gly Val Gly Leu Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr
210 215 220

Tyr Ile Leu Met Gly Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu
225 230 235 240

Gly Ala Val Leu Leu Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn
245 250 255

Ile Leu Gly Pro Trp Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met
260 265 270

Val Val Ile Ala Ser Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys
275 280 285

Leu Ala Pro Asp Val Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu
290 295 300

Gly Pro Leu Ala Phe Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala
305 310 315 320

Glu Thr Ser Ala Gly Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu
325 330 335

Gly Tyr Thr Ile Ala Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val
340 345 350

Asp Ala Thr Gly Ser Phe Arg Thr Ile Phe Leu Leu Phe Ala Gly Ala
355 360 365

Thr Leu Phe Val Ile Arg Gly Gly Tyr Phe Ala Thr Arg Gln Val Tyr
370 375 380

Val Glu Lys Leu Leu Asn Arg
385 390

<210> 175
<211> 1506
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1483)
<223> RXA00634

<400> 175
aagtgttttt aattaccgca gctttgtctt aggagaagtc atggtccaac tggatcaacg 60

ggttaggttc aaaagcgcaa cctcaataat cagtattgaa atg tgg gag cga ttc 115
Met Trp Glu Arg Phe

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                                                                  1               5

agc ttc tac ggc atg caa gca ctc ttg gtg tac tac ctg tat ttt gat   163
Ser Phe Tyr Gly Met Gln Ala Leu Leu Val Tyr Tyr Leu Tyr Phe Asp
                10                  15                  20

gtt gca gcc ggt gga tta ggc ctt gat caa acc caa gca aca gga ctg   211
Val Ala Ala Gly Gly Leu Gly Leu Asp Gln Thr Gln Ala Thr Gly Leu
            25                  30                  35

gtc ggc gtt tat ggc gca ctg ctc tac ctc tgc tgt tgg gca ggc ggt   259
Val Gly Val Tyr Gly Ala Leu Leu Tyr Leu Cys Cys Trp Ala Gly Gly
        40                  45                  50

tgg gtc agt gac aga gtc ctg ggc gca gaa aaa acc ctg ctg ggc ggt   307
Trp Val Ser Asp Arg Val Leu Gly Ala Glu Lys Thr Leu Leu Gly Gly
    55                  60                  65

gcg atc tca gta acc atc gga cac ctt gtg ctt gct ggc ctc ggc ggg   355
Ala Ile Ser Val Thr Ile Gly His Leu Val Leu Ala Gly Leu Gly Gly
70                  75                  80                  85

aaa att ggt cta gcc att ggc ctt gga tgc atc gcg atc ggt tca gga   403
Lys Ile Gly Leu Ala Ile Gly Leu Gly Cys Ile Ala Ile Gly Ser Gly
                90                  95                  100

ttt gtg aaa aca gca gcc atc acc gtg ctg gga tcc agg cat ggt gaa   451
Phe Val Lys Thr Ala Ala Ile Thr Val Leu Gly Ser Arg His Gly Glu
            105                 110                 115

caa gaa gga gac gca aag gca gat ccc gca ttc caa ctc ttc tac cta   499
Gln Glu Gly Asp Ala Lys Ala Asp Pro Ala Phe Gln Leu Phe Tyr Leu
        120                 125                 130

ggc atc aac gtt ggt gca ctg ctc gga cca ctc ctg acc ggt tgg ctc   547
Gly Ile Asn Val Gly Ala Leu Leu Gly Pro Leu Leu Thr Gly Trp Leu
    135                 140                 145

tcc agc agg tat tcc ttt gaa atg gga ttc ggc gca gcc gca gtc ctt   595
Ser Ser Arg Tyr Ser Phe Glu Met Gly Phe Gly Ala Ala Ala Val Leu
150                 155                 160                 165

atg atc ggc gga ttg gga atc tac gca gcg ttg cgg aaa cca atg ctg   643
Met Ile Gly Gly Leu Gly Ile Tyr Ala Ala Leu Arg Lys Pro Met Leu
                170                 175                 180

caa tcg ttc ccg ctc gag gtg aag aaa gcg ctg ctc cgc gcc caa aac   691
Gln Ser Phe Pro Leu Glu Val Lys Lys Ala Leu Leu Arg Ala Gln Asn
            185                 190                 195

cct gca gaa aaa cat gtg att agc acg gca ttt gct gca gtg gct gtg   739
Pro Ala Glu Lys His Val Ile Ser Thr Ala Phe Ala Ala Val Ala Val
        200                 205                 210

ctt tgc gga gtg ctg ctt tat ctt ctc ctt aca gaa aca gtc agc gca   787
Leu Cys Gly Val Leu Leu Tyr Leu Leu Leu Thr Glu Thr Val Ser Ala
    215                 220                 225

gac caa cta gct gga gct ctg ctt tta gta aca atc ggt gca gca cta   835
Asp Gln Leu Ala Gly Ala Leu Leu Leu Val Thr Ile Gly Ala Ala Leu
230                 235                 240                 245
```

```
tgg ctc att atc cag ccc tta cga cac cca caa gtc agc tcc gaa gag   883
Trp Leu Ile Ile Gln Pro Leu Arg His Pro Gln Val Ser Ser Glu Glu
                250                 255                 260

aaa cga aaa gtg ctg gca ttc atc ccg atc ttc gtc tgc tca acc gca   931
Lys Arg Lys Val Leu Ala Phe Ile Pro Ile Phe Val Cys Ser Thr Ala
            265                 270                 275

ttc tgg gca gtg caa gca caa acc tac ggc gta cta gct gtg tac tcc   979
Phe Trp Ala Val Gln Ala Gln Thr Tyr Gly Val Leu Ala Val Tyr Ser
        280                 285                 290

caa gaa cgt gtt gac cgc atg gtt ggc gat ttt gag atc cca gca gcc   1027
Gln Glu Arg Val Asp Arg Met Val Gly Asp Phe Glu Ile Pro Ala Ala
    295                 300                 305

tgg tca caa tca ctc aat cct ttt ttc atc ctg gcg ctg tcc atc ccg   1075
Trp Ser Gln Ser Leu Asn Pro Phe Phe Ile Leu Ala Leu Ser Ile Pro
310                 315                 320                 325

att tcc ctg tgg ttt atg cgc gga tca cgc gcc cca aga gtg aaa att   1123
Ile Ser Leu Trp Phe Met Arg Gly Ser Arg Ala Pro Arg Val Lys Ile
                330                 335                 340

gga atc agc att gga gtg atc att gcg gga agt ggg ctt cta gtt ctt   1171
Gly Ile Ser Ile Gly Val Ile Ile Ala Gly Ser Gly Leu Leu Val Leu
            345                 350                 355

att cca ttt gtt gga atg ccg ctc gcg cca gtg tgg gtg ctg cct tta   1219
Ile Pro Phe Val Gly Met Pro Leu Ala Pro Val Trp Val Leu Pro Leu
        360                 365                 370

agt gtt ttc ctc atc tca ctg gga gaa ctt ttc atc gga ccc gga gga   1267
Ser Val Phe Leu Ile Ser Leu Gly Glu Leu Phe Ile Gly Pro Gly Gly
    375                 380                 385

atg gct gcg act gcg cac cac gca cca cga ata ttt gcc aca cga ttc   1315
Met Ala Ala Thr Ala His His Ala Pro Arg Ile Phe Ala Thr Arg Phe
390                 395                 400                 405

tcc gcc ctg tat ttc ctc aca ctc gcc atc ggc atg tct att gca ggt   1363
Ser Ala Leu Tyr Phe Leu Thr Leu Ala Ile Gly Met Ser Ile Ala Gly
                410                 415                 420

aat gtg tcc aaa ttt tac gac ccc acc aac cac acc tcc gag ctc cga   1411
Asn Val Ser Lys Phe Tyr Asp Pro Thr Asn His Thr Ser Glu Leu Arg
            425                 430                 435

tac ttc gcg gta ttt ggc att tcg atc atc gtc atc ggt gtc ggt tca   1459
Tyr Phe Ala Val Phe Gly Ile Ser Ile Ile Val Ile Gly Val Gly Ser
        440                 445                 450

ctg atg gtg gcc aag aag gtt gga taacagggtt aatcttgggt gat         1506
Leu Met Val Ala Lys Lys Val Gly
    455                 460
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<210> 176
<211> 461
<212> PRT

<213> Corynebacterium glutamicum

<400> 176

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Met Trp Glu Arg Phe Ser Phe Tyr Gly Met Gln Ala Leu Leu Val Tyr
  1               5                  10                  15

Tyr Leu Tyr Phe Asp Val Ala Ala Gly Gly Leu Gly Leu Asp Gln Thr
            20                  25                  30

Gln Ala Thr Gly Leu Val Gly Val Tyr Gly Ala Leu Leu Tyr Leu Cys
        35                  40                  45

Cys Trp Ala Gly Gly Trp Val Ser Asp Arg Val Leu Gly Ala Glu Lys
    50                  55                  60

Thr Leu Leu Gly Gly Ala Ile Ser Val Thr Ile Gly His Leu Val Leu
65                  70                  75                  80

Ala Gly Leu Gly Gly Lys Ile Gly Leu Ala Ile Gly Leu Gly Cys Ile
                85                  90                  95

Ala Ile Gly Ser Gly Phe Val Lys Thr Ala Ala Ile Thr Val Leu Gly
            100                 105                 110

Ser Arg His Gly Glu Gln Glu Gly Asp Ala Lys Ala Asp Pro Ala Phe
        115                 120                 125

Gln Leu Phe Tyr Leu Gly Ile Asn Val Gly Ala Leu Leu Gly Pro Leu
    130                 135                 140

Leu Thr Gly Trp Leu Ser Ser Arg Tyr Ser Phe Glu Met Gly Phe Gly
145                 150                 155                 160

Ala Ala Ala Val Leu Met Ile Gly Gly Leu Gly Ile Tyr Ala Ala Leu
                165                 170                 175

Arg Lys Pro Met Leu Gln Ser Phe Pro Leu Glu Val Lys Lys Ala Leu
            180                 185                 190

Leu Arg Ala Gln Asn Pro Ala Glu Lys His Val Ile Ser Thr Ala Phe
        195                 200                 205

Ala Ala Val Ala Val Leu Cys Gly Val Leu Leu Tyr Leu Leu Leu Thr
    210                 215                 220

Glu Thr Val Ser Ala Asp Gln Leu Ala Gly Ala Leu Leu Leu Val Thr
225                 230                 235                 240

Ile Gly Ala Ala Leu Trp Leu Ile Ile Gln Pro Leu Arg His Pro Gln
                245                 250                 255

Val Ser Ser Glu Glu Lys Arg Lys Val Leu Ala Phe Ile Pro Ile Phe
            260                 265                 270

Val Cys Ser Thr Ala Phe Trp Ala Val Gln Ala Gln Thr Tyr Gly Val
        275                 280                 285

Leu Ala Val Tyr Ser Gln Glu Arg Val Asp Arg Met Val Gly Asp Phe
    290                 295                 300

Glu Ile Pro Ala Ala Trp Ser Gln Ser Leu Asn Pro Phe Phe Ile Leu
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305                 310                 315                 320

Ala Leu Ser Ile Pro Ile Ser Leu Trp Phe Met Arg Gly Ser Arg Ala
                325                 330                 335

Pro Arg Val Lys Ile Gly Ile Ser Ile Gly Val Ile Ile Ala Gly Ser
            340                 345                 350

Gly Leu Leu Val Leu Ile Pro Phe Val Gly Met Pro Leu Ala Pro Val
        355                 360                 365

Trp Val Leu Pro Leu Ser Val Phe Leu Ile Ser Leu Gly Glu Leu Phe
    370                 375                 380

Ile Gly Pro Gly Gly Met Ala Ala Thr Ala His His Ala Pro Arg Ile
385                 390                 395                 400

Phe Ala Thr Arg Phe Ser Ala Leu Tyr Phe Leu Thr Leu Ala Ile Gly
                405                 410                 415

Met Ser Ile Ala Gly Asn Val Ser Lys Phe Tyr Asp Pro Thr Asn His
            420                 425                 430

Thr Ser Glu Leu Arg Tyr Phe Ala Val Phe Gly Ile Ser Ile Ile Val
        435                 440                 445

Ile Gly Val Gly Ser Leu Met Val Ala Lys Lys Val Gly
    450                 455                 460


<210> 177
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<222> (101)..(1624)
<223> RXA02451

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taattggagt tgtgctttta ggtggaggat catagaggtt atg aac acc gac aca   115
                                              Met Asn Thr Asp Thr
                                                1               5

act caa gac ggt gtg agt cct gaa cct tcc gac ccc cac cta ggg tct   163
Thr Gln Asp Gly Val Ser Pro Glu Pro Ser Asp Pro His Leu Gly Ser
                10                  15                  20

gaa gtg gcg gaa act cac cgc gaa aag aaa ttc ttc ggc cag cct tgg   211
Glu Val Ala Glu Thr His Arg Glu Lys Lys Phe Phe Gly Gln Pro Trp
            25                  30                  35

ggg ctg gca aat ctc ttc ggc gtg gag atg tgg gag cga ttc agc ttc   259
Gly Leu Ala Asn Leu Phe Gly Val Glu Met Trp Glu Arg Phe Ser Phe
        40                  45                  50

tac ggc atg cag tcc atc ctt gct ttc tat ctg tac tac tcc gtc acc   307
Tyr Gly Met Gln Ser Ile Leu Ala Phe Tyr Leu Tyr Tyr Ser Val Thr
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     55                  60                  65

gat ggc gga ctt ggt atg aat cag aca gct gca ctg tcc att gtg ggc   355
Asp Gly Gly Leu Gly Met Asn Gln Thr Ala Ala Leu Ser Ile Val Gly
 70                  75                  80                  85

gcc tac ggc ggc ttc gtc tac atg acc tcc ctc gtg gct tcg ttc att   403
Ala Tyr Gly Gly Phe Val Tyr Met Thr Ser Leu Val Ala Ser Phe Ile
                 90                  95                 100

gca gac cga gta ttg ggc tct gaa cgt aca ctc ttc tac tcc gcg atc   451
Ala Asp Arg Val Leu Gly Ser Glu Arg Thr Leu Phe Tyr Ser Ala Ile
            105                 110                 115

atc gtc atg ctg ggc cac att gcc ctg gcc ttg att ccg gga tat acg   499
Ile Val Met Leu Gly His Ile Ala Leu Ala Leu Ile Pro Gly Tyr Thr
        120                 125                 130

gga ctg tcc atc ggc ttg gtc ctc atc ggc ctt ggc tca ggt ggc gtg   547
Gly Leu Ser Ile Gly Leu Val Leu Ile Gly Leu Gly Ser Gly Gly Val
    135                 140                 145

aag acg gca gcg cag gtt gtg ctg ggc cag ctg tac tca cgc acg gac   595
Lys Thr Ala Ala Gln Val Val Leu Gly Gln Leu Tyr Ser Arg Thr Asp
150                 155                 160                 165

acg cgt cga gac gca ggc ttc tcc atc ttc tac atg ggc gtc aac ctc   643
Thr Arg Arg Asp Ala Gly Phe Ser Ile Phe Tyr Met Gly Val Asn Leu
                170                 175                 180

ggt ggc ctc ttt ggc ccg ctg atc acc aac gct ctg tgg gga tgg gga   691
Gly Gly Leu Phe Gly Pro Leu Ile Thr Asn Ala Leu Trp Gly Trp Gly
            185                 190                 195

gga ttc cac tgg ggc ttc ggt atc gcc gca gtc ggc atg gct ttg ggt   739
Gly Phe His Trp Gly Phe Gly Ile Ala Ala Val Gly Met Ala Leu Gly
        200                 205                 210

ctc atc caa tac gtg gcg atg cgt aaa acc acc atc ggt gcg gca ggc   787
Leu Ile Gln Tyr Val Ala Met Arg Lys Thr Thr Ile Gly Ala Ala Gly
    215                 220                 225

cat act gtt cct aac cca ctg cct aag aat gaa tat gcg cgc tgg att   835
His Thr Val Pro Asn Pro Leu Pro Lys Asn Glu Tyr Ala Arg Trp Ile
230                 235                 240                 245

atc ggt gca gtc gtg gtt gtc gca gca gtt gtc gct ctc atc gca acg   883
Ile Gly Ala Val Val Val Val Ala Ala Val Val Ala Leu Ile Ala Thr
                250                 255                 260

ggc atc atc aag ctg gaa tgg ctg tcc aac atc acc gca gcg atc gca   931
Gly Ile Ile Lys Leu Glu Trp Leu Ser Asn Ile Thr Ala Ala Ile Ala
            265                 270                 275

ctg att gcg gct att gct ctg ctt gct cag atg tac gtt tcc cca ctg   979
Leu Ile Ala Ala Ile Ala Leu Leu Ala Gln Met Tyr Val Ser Pro Leu
        280                 285                 290

acc acc gca gcg gaa aag tcc cgc ttg ttg gga ttc atc ccg atg ttc   1027
Thr Thr Ala Ala Glu Lys Ser Arg Leu Leu Gly Phe Ile Pro Met Phe
    295                 300                 305
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atc ggt ggc gtg ctt ttc ttc gcg atc ttc caa acc cag ttc acg gtc   1075
Ile Gly Gly Val Leu Phe Phe Ala Ile Phe Gln Thr Gln Phe Thr Val
310                 315                 320                 325

ctc gcg gtt tac tcc gac acc cgc ctg gac cgt aac ttc ttc ggc att   1123
Leu Ala Val Tyr Ser Asp Thr Arg Leu Asp Arg Asn Phe Phe Gly Ile
                330                 335                 340

gat ctt cct cca gga ttg atc aac tcc ttc aac cca atc ttc atc atc   1171
Asp Leu Pro Pro Gly Leu Ile Asn Ser Phe Asn Pro Ile Phe Ile Ile
            345                 350                 355

atc ttc tcc gga atc ttt gcc acc ttg tgg aca aaa ctc gga gca aag   1219
Ile Phe Ser Gly Ile Phe Ala Thr Leu Trp Thr Lys Leu Gly Ala Lys
        360                 365                 370

cag tgg tct act gca gtg aag ttc ggt gtc gcc aac att gtc att ggt   1267
Gln Trp Ser Thr Ala Val Lys Phe Gly Val Ala Asn Ile Val Ile Gly
    375                 380                 385

tgc gcg ctg ttc ttc ttc ctg ccg ttc gcc ggc ggt gca gag aac tct   1315
Cys Ala Leu Phe Phe Phe Leu Pro Phe Ala Gly Gly Ala Glu Asn Ser
390                 395                 400                 405

acc cca atg gca ctg atc att tgg gtc tac ttc ctc ttc acc atc gct   1363
Thr Pro Met Ala Leu Ile Ile Trp Val Tyr Phe Leu Phe Thr Ile Ala
                410                 415                 420

gag ctt ctg ctc tcc cct gtc ggc aac tca ctt gca acc aag gtc gca   1411
Glu Leu Leu Leu Ser Pro Val Gly Asn Ser Leu Ala Thr Lys Val Ala
            425                 430                 435

ccc gag gca ttc cag tcc cgc atg ttc gcc gtg tgg ctg atg gct gtc   1459
Pro Glu Ala Phe Gln Ser Arg Met Phe Ala Val Trp Leu Met Ala Val
        440                 445                 450

tcc atg ggt acg tcc ctg tcc ggc acc ctg ggt ggt tac tac gat cca   1507
Ser Met Gly Thr Ser Leu Ser Gly Thr Leu Gly Gly Tyr Tyr Asp Pro
    455                 460                 465

acc gat gca gga tct gaa aag gtc ttc ttc att acc gtt ggc gtt gca   1555
Thr Asp Ala Gly Ser Glu Lys Val Phe Phe Ile Thr Val Gly Val Ala
470                 475                 480                 485

gcc atc gtt ctt ggt gca atc gtc ata gca gcc aag ggc tgg gtg ctg   1603
Ala Ile Val Leu Gly Ala Ile Val Ile Ala Ala Lys Gly Trp Val Leu
                490                 495                 500

aag aag ttc atc gac gtc cga taggcctcac aaagcctcaa aac             1647
Lys Lys Phe Ile Asp Val Arg
            505
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<210> 178
<211> 508
<212> PRT
<213> Corynebacterium glutamicum

<400> 178
Met Asn Thr Asp Thr Thr Gln Asp Gly Val Ser Pro Glu Pro Ser Asp

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  1               5                  10                  15

Pro His Leu Gly Ser Glu Val Ala Glu Thr His Arg Glu Lys Lys Phe
            20                  25                  30

Phe Gly Gln Pro Trp Gly Leu Ala Asn Leu Phe Gly Val Glu Met Trp
        35                  40                  45

Glu Arg Phe Ser Phe Tyr Gly Met Gln Ser Ile Leu Ala Phe Tyr Leu
    50                  55                  60

Tyr Tyr Ser Val Thr Asp Gly Gly Leu Gly Met Asn Gln Thr Ala Ala
65                  70                  75                  80

Leu Ser Ile Val Gly Ala Tyr Gly Gly Phe Val Tyr Met Thr Ser Leu
                85                  90                  95

Val Ala Ser Phe Ile Ala Asp Arg Val Leu Gly Ser Glu Arg Thr Leu
            100                 105                 110

Phe Tyr Ser Ala Ile Ile Val Met Leu Gly His Ile Ala Leu Ala Leu
        115                 120                 125

Ile Pro Gly Tyr Thr Gly Leu Ser Ile Gly Leu Val Leu Ile Gly Leu
    130                 135                 140

Gly Ser Gly Gly Val Lys Thr Ala Ala Gln Val Val Leu Gly Gln Leu
145                 150                 155                 160

Tyr Ser Arg Thr Asp Thr Arg Arg Asp Ala Gly Phe Ser Ile Phe Tyr
                165                 170                 175

Met Gly Val Asn Leu Gly Gly Leu Phe Gly Pro Leu Ile Thr Asn Ala
            180                 185                 190

Leu Trp Gly Trp Gly Gly Phe His Trp Gly Phe Gly Ile Ala Ala Val
        195                 200                 205

Gly Met Ala Leu Gly Leu Ile Gln Tyr Val Ala Met Arg Lys Thr Thr
    210                 215                 220

Ile Gly Ala Ala Gly His Thr Val Pro Asn Pro Leu Pro Lys Asn Glu
225                 230                 235                 240

Tyr Ala Arg Trp Ile Ile Gly Ala Val Val Val Val Ala Ala Val Val
                245                 250                 255

Ala Leu Ile Ala Thr Gly Ile Ile Lys Leu Glu Trp Leu Ser Asn Ile
            260                 265                 270

Thr Ala Ala Ile Ala Leu Ile Ala Ala Ile Ala Leu Leu Ala Gln Met
        275                 280                 285

Tyr Val Ser Pro Leu Thr Thr Ala Ala Glu Lys Ser Arg Leu Leu Gly
    290                 295                 300

Phe Ile Pro Met Phe Ile Gly Gly Val Leu Phe Phe Ala Ile Phe Gln
305                 310                 315                 320

Thr Gln Phe Thr Val Leu Ala Val Tyr Ser Asp Thr Arg Leu Asp Arg
                325                 330                 335
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CN 102924590 A

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Asn Phe Phe Gly Ile Asp Leu Pro Pro Gly Leu Ile Asn Ser Phe Asn
            340                 345                 350

Pro Ile Phe Ile Ile Ile Phe Ser Gly Ile Phe Ala Thr Leu Trp Thr
        355                 360                 365

Lys Leu Gly Ala Lys Gln Trp Ser Thr Ala Val Lys Phe Gly Val Ala
    370                 375                 380

Asn Ile Val Ile Gly Cys Ala Leu Phe Phe Phe Leu Pro Phe Ala Gly
385                 390                 395                 400

Gly Ala Glu Asn Ser Thr Pro Met Ala Leu Ile Ile Trp Val Tyr Phe
                405                 410                 415

Leu Phe Thr Ile Ala Glu Leu Leu Leu Ser Pro Val Gly Asn Ser Leu
            420                 425                 430

Ala Thr Lys Val Ala Pro Glu Ala Phe Gln Ser Arg Met Phe Ala Val
        435                 440                 445

Trp Leu Met Ala Val Ser Met Gly Thr Ser Leu Ser Gly Thr Leu Gly
    450                 455                 460

Gly Tyr Tyr Asp Pro Thr Asp Ala Gly Ser Glu Lys Val Phe Phe Ile
465                 470                 475                 480

Thr Val Gly Val Ala Ala Ile Val Leu Gly Ala Ile Val Ile Ala Ala
                485                 490                 495

Lys Gly Trp Val Leu Lys Lys Phe Ile Asp Val Arg
            500                 505
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09/25/2003 15:09 FAX

<210> 179
<211> 1426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (93)..(1403)
<223> RXA02394

<400> 179

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ttctgcaagt tcagcggaag gtaggaacta atatg ttg tcg cca gca gct gta    113
                                      Met Leu Ser Pro Ala Ala Val
                                        1               5

gca gct tta att ctt gtc atc ggc att gtg gtg ctc atc atc gca tca   161
Ala Ala Leu Ile Leu Val Ile Gly Ile Val Val Leu Ile Ile Ala Ser
          10                  15                  20

gtg ccc gtt gcc att gcc atc ggt ttg cca tca ctt ttt gcc gcg atg   209
Val Pro Val Ala Ile Ala Ile Gly Leu Pro Ser Leu Phe Ala Ala Met
     25                  30                  35

gcc gtg ctt ggc cca gaa aac gcc gcg cag gcc gtc gcg cag cgc atg   257
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Ala Val Leu Gly Pro Glu Asn Ala Ala Gln Ala Val Ala Gln Arg Met
 40                  45                  50                  55

ttt acc ggc aca aac tcc ttt aca ctc ctt gcc att ccg ttc ttc gtg   305
Phe Thr Gly Thr Asn Ser Phe Thr Leu Leu Ala Ile Pro Phe Phe Val
                 60                  65                  70

ttg gcg ggt ttg ctg atg aac tcg ggt ggt att gcc acg cgg ctt atc   353
Leu Ala Gly Leu Leu Met Asn Ser Gly Gly Ile Ala Thr Arg Leu Ile
             75                  80                  85

gac gcc gcg aag gtg ctt gtc ggc cgc atg cct gcc tcc atg gcc aat   401
Asp Ala Ala Lys Val Leu Val Gly Arg Met Pro Ala Ser Met Ala Asn
         90                  95                 100

acg aat atc gca gca aat ggt ctc ttc gga gca gtt tca ggg gca gcg   449
Thr Asn Ile Ala Ala Asn Gly Leu Phe Gly Ala Val Ser Gly Ala Ala
    105                 110                 115

gta gca tca gct tct gcc gtg gga acc gtc atg aca cca aaa atg aag   497
Val Ala Ser Ala Ser Ala Val Gly Thr Val Met Thr Pro Lys Met Lys
120                 125                 130                 135

gaa gag ggc tac tcg cgc gct tac gca gcg gcc gtc aac gtg gct tca   545
Glu Glu Gly Tyr Ser Arg Ala Tyr Ala Ala Ala Val Asn Val Ala Ser
                140                 145                 150

gca cct gcg ggc atg ctg atc ccg cca tca aac act ttt att gtg tat   593
Ala Pro Ala Gly Met Leu Ile Pro Pro Ser Asn Thr Phe Ile Val Tyr
            155                 160                 165

tcc ttg gtg tcc tcg aca tca att gca gca cta ttt atg gcc ggt gtt   641
Ser Leu Val Ser Ser Thr Ser Ile Ala Ala Leu Phe Met Ala Gly Val
        170                 175                 180

gga ccc ggt ctg ctc tgg att ctg gcc tgt gtc atc gtg gga act tgg   689
Gly Pro Gly Leu Leu Trp Ile Leu Ala Cys Val Ile Val Gly Thr Trp
    185                 190                 195

tta gcg cga aag gaa aac tac aag cgc gag cag att cat cca aca ttc   737
Leu Ala Arg Lys Glu Asn Tyr Lys Arg Glu Gln Ile His Pro Thr Phe
200                 205                 210                 215

aag cag tcg ctc gtt gtg ctg tgg agg gcg ctg cct tca ctg ctc atg   785
Lys Gln Ser Leu Val Val Leu Trp Arg Ala Leu Pro Ser Leu Leu Met
                220                 225                 230

atc gtc att gtt gtt gga ggt atc ttg ctg ggc tgg ttc act cca act   833
Ile Val Ile Val Val Gly Gly Ile Leu Leu Gly Trp Phe Thr Pro Thr
            235                 240                 245

gaa tcc gct gct att gct gta gtg tac tgc ctg gtc ttg ggc ttt att   881
Glu Ser Ala Ala Ile Ala Val Val Tyr Cys Leu Val Leu Gly Phe Ile
        250                 255                 260

tac cgc aca atc aag gtg gga gat ctg gca gat att ttg ctc aag gca   929
Tyr Arg Thr Ile Lys Val Gly Asp Leu Ala Asp Ile Leu Leu Lys Ala
    265                 270                 275

act cgc acc aca tca att gtc atg ttg ctc att gca gtt tct gca gca   977
Thr Arg Thr Thr Ser Ile Val Met Leu Leu Ile Ala Val Ser Ala Ala
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09536790.1

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280                 285                 290                 295

ctg tcg tgg gtg atg gcc ttt gcc aag atc cct cag atg atc tct gat   1025
Leu Ser Trp Val Met Ala Phe Ala Lys Ile Pro Gln Met Ile Ser Asp
                300                 305                 310

gcg ctt ctt tcg gta tcc gat tcc aag gtt gtc atc ttg ttg atc atg   1073
Ala Leu Leu Ser Val Ser Asp Ser Lys Val Val Ile Leu Leu Ile Met
            315                 320                 325

atg ttc atc ctg tta ctc atc ggt acc gta atg gac cca aca cca gca   1121
Met Phe Ile Leu Leu Leu Ile Gly Thr Val Met Asp Pro Thr Pro Ala
        330                 335                 340

att ttg atc ttc gtc ccg atc ttc ctt cca gtg gtt acc gaa ctt ggt   1169
Ile Leu Ile Phe Val Pro Ile Phe Leu Pro Val Val Thr Glu Leu Gly
    345                 350                 355

gtg gac cca gtc cac ttc ggt gcg atg gtg gta atg aac ctg tcc gtg   1217
Val Asp Pro Val His Phe Gly Ala Met Val Val Met Asn Leu Ser Val
360                 365                 370                 375

ggc gtg att acc cca cca gta ggc aac gtg ttg ttc gtt ggt tcg caa   1265
Gly Val Ile Thr Pro Pro Val Gly Asn Val Leu Phe Val Gly Ser Gln
                380                 385                 390

gtg gca ggg ctg cgt gtg gaa act gtg atc aga cga ctg tgg ccg tat   1313
Val Ala Gly Leu Arg Val Glu Thr Val Ile Arg Arg Leu Trp Pro Tyr
            395                 400                 405

ctc att gcc att att gtt gcg ctg ttc gtg gtt gtt ttc gta ccg cag   1361
Leu Ile Ala Ile Ile Val Ala Leu Phe Val Val Val Phe Val Pro Gln
        410                 415                 420

atc tct atc tgg ctg ccc aca aca atg gga ttg atg gga ggc           1403
Ile Ser Ile Trp Leu Pro Thr Thr Met Gly Leu Met Gly Gly
    425                 430                 435

taaacctcca gccatcagct aag                                        1426


<210> 180
<211> 437
<212> PRT
<213> Corynebacterium glutamicum

<400> 180
Met Leu Ser Pro Ala Ala Val Ala Ala Leu Ile Leu Val Ile Gly Ile
  1               5                  10                  15

Val Val Leu Ile Ile Ala Ser Val Pro Val Ala Ile Ala Ile Gly Leu
             20                  25                  30

Pro Ser Leu Phe Ala Ala Met Ala Val Leu Gly Pro Glu Asn Ala Ala
         35                  40                  45

Gln Ala Val Ala Gln Arg Met Phe Thr Gly Thr Asn Ser Phe Thr Leu
     50                  55                  60

Leu Ala Ile Pro Phe Phe Val Leu Ala Gly Leu Leu Met Asn Ser Gly
 65                  70                  75                  80
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Gly Ile Ala Thr Arg Leu Ile Asp Ala Ala Lys Val Leu Val Gly Arg
85 90 95

Met Pro Ala Ser Met Ala Asn Thr Asn Ile Ala Ala Asn Gly Leu Phe
100 105 110

Gly Ala Val Ser Gly Ala Ala Val Ala Ser Ala Ser Ala Val Gly Thr
115 120 125

Val Met Thr Pro Lys Met Lys Glu Glu Gly Tyr Ser Arg Ala Tyr Ala
130 135 140

Ala Ala Val Asn Val Ala Ser Ala Pro Ala Gly Met Leu Ile Pro Pro
145 150 155 160

Ser Asn Thr Phe Ile Val Tyr Ser Leu Val Ser Ser Thr Ser Ile Ala
165 170 175

Ala Leu Phe Met Ala Gly Val Gly Pro Gly Leu Leu Trp Ile Leu Ala
180 185 190

Cys Val Ile Val Gly Thr Trp Leu Ala Arg Lys Glu Asn Tyr Lys Arg
195 200 205

Glu Gln Ile His Pro Thr Phe Lys Gln Ser Leu Val Val Leu Trp Arg
210 215 220

Ala Leu Pro Ser Leu Leu Met Ile Val Ile Val Val Gly Gly Ile Leu
225 230 235 240

Leu Gly Trp Phe Thr Pro Thr Glu Ser Ala Ala Ile Ala Val Val Tyr
245 250 255

Cys Leu Val Leu Gly Phe Ile Tyr Arg Thr Ile Lys Val Gly Asp Leu
260 265 270

Ala Asp Ile Leu Leu Lys Ala Thr Arg Thr Thr Ser Ile Val Met Leu
275 280 285

Leu Ile Ala Val Ser Ala Ala Leu Ser Trp Val Met Ala Phe Ala Lys
290 295 300

Ile Pro Gln Met Ile Ser Asp Ala Leu Leu Ser Val Ser Asp Ser Lys
305 310 315 320

Val Val Ile Leu Leu Ile Met Met Phe Ile Leu Leu Leu Ile Gly Thr
325 330 335

Val Met Asp Pro Thr Pro Ala Ile Leu Ile Phe Val Pro Ile Phe Leu
340 345 350

Pro Val Val Thr Glu Leu Gly Val Asp Pro Val His Phe Gly Ala Met
355 360 365

Val Val Met Asn Leu Ser Val Gly Val Ile Thr Pro Pro Val Gly Asn
370 375 380

Val Leu Phe Val Gly Ser Gln Val Ala Gly Leu Arg Val Glu Thr Val
385 390 395 400

Ile Arg Arg Leu Trp Pro Tyr Leu Ile Ala Ile Ile Val Ala Leu Phe
405 410 415

Val Val Val Phe Val Pro Gln Ile Ser Ile Trp Leu Pro Thr Thr Met
420 425 430

Gly Leu Met Gly Gly
435

<210> 181
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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1741)
<223> RXA01012

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caactaccta agccgcatca ttcagaagga ggcatagaaa atg act act ccc ttg 115
Met Thr Thr Pro Leu
1 5

tta gag atc aac gat ctg gtt gtc tcc tat caa act gct aaa ggt ttg 163
Leu Glu Ile Asn Asp Leu Val Val Ser Tyr Gln Thr Ala Lys Gly Leu
10 15 20

gtg cat gct gtc aac aat gtc agc ctg gag gtg cac cct ggc caa atc 211
Val His Ala Val Asn Asn Val Ser Leu Glu Val His Pro Gly Gln Ile
25 30 35

acc gcg att gtt ggt gag tcc ggt tct ggt aag tcc acc acc gct cag 259
Thr Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Gln
40 45 50

gcc gtg att ggt ttg ctg gct gat aat gct gaa gtg gat tct ggt cgg 307
Ala Val Ile Gly Leu Leu Ala Asp Asn Ala Glu Val Asp Ser Gly Arg
55 60 65

att tct ttc aac ggc cgt tcc ctt gtt ggc ttg aac gca cgt gag tgg 355
Ile Ser Phe Asn Gly Arg Ser Leu Val Gly Leu Asn Ala Arg Glu Trp
70 75 80 85

aaa aac gtt cgc ggt acc aaa att ggt ttg att ccg cag gac ccc aac 403
Lys Asn Val Arg Gly Thr Lys Ile Gly Leu Ile Pro Gln Asp Pro Asn
90 95 100

aac tct ctg aac ccg gtg aaa act atc ggc gct tca gtg ggg gag ggc 451
Asn Ser Leu Asn Pro Val Lys Thr Ile Gly Ala Ser Val Gly Glu Gly
105 110 115

ttg gct atc cac aag cgt gga acc gcc gcc gag cgc aaa aag aag gtc 499
Leu Ala Ile His Lys Arg Gly Thr Ala Ala Glu Arg Lys Lys Lys Val
120 125 130

att gag ctt cta gag cgc gtg ggt att gat aac cca gag gtc cgc tat 547
Ile Glu Leu Leu Glu Arg Val Gly Ile Asp Asn Pro Glu Val Arg Tyr

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    135                 140                 145

gac cag tac ccg cat gag ctg tct ggt ggc atg aag cag cgc gcg ttg   595
Asp Gln Tyr Pro His Glu Leu Ser Gly Gly Met Lys Gln Arg Ala Leu
150                 155                 160                 165

att gcc gct gcc att gca ctt gaa cca gag ctg atc att gcc gat gag   643
Ile Ala Ala Ala Ile Ala Leu Glu Pro Glu Leu Ile Ile Ala Asp Glu
                170                 175                 180

ccc aca tct gcg ctg gat gtg acc gtg cag aaa att att ctc gat ctg   691
Pro Thr Ser Ala Leu Asp Val Thr Val Gln Lys Ile Ile Leu Asp Leu
            185                 190                 195

ctg gaa gac atg cag cgt gaa ttg ggc atg ggt att ttg ttc att act   739
Leu Glu Asp Met Gln Arg Glu Leu Gly Met Gly Ile Leu Phe Ile Thr
        200                 205                 210

cac gat cta gcc gtg gca ggc gat cgg gcg gat cgc atc gtc gtc atg   787
His Asp Leu Ala Val Ala Gly Asp Arg Ala Asp Arg Ile Val Val Met
    215                 220                 225

caa aaa ggc gag gtg cgc gaa agt ggt tac gcg gct tcg gtc ttg acc   835
Gln Lys Gly Glu Val Arg Glu Ser Gly Tyr Ala Ala Ser Val Leu Thr
230                 235                 240                 245

gac ccc cag cat gag tat tcc aag aag ttg ctt gcc gac gcg ccc tcc   883
Asp Pro Gln His Glu Tyr Ser Lys Lys Leu Leu Ala Asp Ala Pro Ser
                250                 255                 260

ctc acc atc ggc gag atc ccc acg cga gtt ccg gcc gta gat ccg gag   931
Leu Thr Ile Gly Glu Ile Pro Thr Arg Val Pro Ala Val Asp Pro Glu
            265                 270                 275

gta gcg cag gcc aaa ggc ccg ctt ctg gta gtg gat aaa ttc cgc aag   979
Val Ala Gln Ala Lys Gly Pro Leu Leu Val Val Asp Lys Phe Arg Lys
        280                 285                 290

gaa cac caa cga ggc aaa gaa gga gca ttt gtt gcc gca aat gat att   1027
Glu His Gln Arg Gly Lys Glu Gly Ala Phe Val Ala Ala Asn Asp Ile
    295                 300                 305

tcc ttc gaa gta ctg cct ggc acc acg cat gcc atc gtc ggt gaa tcc   1075
Ser Phe Glu Val Leu Pro Gly Thr Thr His Ala Ile Val Gly Glu Ser
310                 315                 320                 325

ggt tct ggt aaa acc acg ctt ggc cgc gcg atc gcg atg ttt aat acg   1123
Gly Ser Gly Lys Thr Thr Leu Gly Arg Ala Ile Ala Met Phe Asn Thr
                330                 335                 340

ccg acc tct ggt tcc att tca gta agt ggc aag gac atc acc aac ctg   1171
Pro Thr Ser Gly Ser Ile Ser Val Ser Gly Lys Asp Ile Thr Asn Leu
            345                 350                 355

tcc aag gcc cag cag cgg gaa ctg cgc cag caa atc cag ctg gtg tac   1219
Ser Lys Ala Gln Gln Arg Glu Leu Arg Gln Gln Ile Gln Leu Val Tyr
        360                 365                 370

caa aac ccg tat tct tcc ctg gat cct cgc caa acc att ggc tcc acc   1267
Gln Asn Pro Tyr Ser Ser Leu Asp Pro Arg Gln Thr Ile Gly Ser Thr
    375                 380                 385
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atc gcg gaa cct ctg cgc aat ttc acc aag gtg agc aag cag gaa gcc   1315
Ile Ala Glu Pro Leu Arg Asn Phe Thr Lys Val Ser Lys Gln Glu Ala
390                 395                 400                 405

gac gaa aag gtg gca cac tac ctg gaa ctg gtg gcg ctt gac ccg gct   1363
Asp Glu Lys Val Ala His Tyr Leu Glu Leu Val Ala Leu Asp Pro Ala
                410                 415                 420

ctt gcc acc cgt cgc cca cgt gag ctc tct ggt ggt cag cgc cag cgc   1411
Leu Ala Thr Arg Arg Pro Arg Glu Leu Ser Gly Gly Gln Arg Gln Arg
            425                 430                 435

gtc gcc att gct cgt gcc atg att ttg gaa cct gaa ttg gtg gtt ttc   1459
Val Ala Ile Ala Arg Ala Met Ile Leu Glu Pro Glu Leu Val Val Phe
        440                 445                 450

gac gaa gcc gta tcc gcg ttg gat gtg act gtg cag gca caa atc ctg   1507
Asp Glu Ala Val Ser Ala Leu Asp Val Thr Val Gln Ala Gln Ile Leu
    455                 460                 465

cgc ctg ctc gac gat ctg caa cga gag cta ggc ttg act tac gtg ttt   1555
Arg Leu Leu Asp Asp Leu Gln Arg Glu Leu Gly Leu Thr Tyr Val Phe
470                 475                 480                 485

att tcc cac gac ctg gct gtg gtc cgt gaa atc tct gac act gtg tct   1603
Ile Ser His Asp Leu Ala Val Val Arg Glu Ile Ser Asp Thr Val Ser
                490                 495                 500

gtg atg agt cgc ggc aac cag gtg gaa ctt gga aaa acc gca gaa gta   1651
Val Met Ser Arg Gly Asn Gln Val Glu Leu Gly Lys Thr Ala Glu Val
            505                 510                 515

ttt aac aac ccg caa acc gat ttc act cgc cga ctc atc gac gcg atc   1699
Phe Asn Asn Pro Gln Thr Asp Phe Thr Arg Arg Leu Ile Asp Ala Ile
        520                 525                 530

cca gga tcg cgc tat cgt ggt ggc gaa ctc aat ctt gga cta           1741
Pro Gly Ser Arg Tyr Arg Gly Gly Glu Leu Asn Leu Gly Leu
    535                 540                 545

taggagcaga tcttaaaaat gtc                                        1764
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<210> 182
<211> 547
<212> PRT
<213> Corynebacterium glutamicum

<400> 182

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Met Thr Thr Pro Leu Leu Glu Ile Asn Asp Leu Val Val Ser Tyr Gln
  1               5                  10                  15

Thr Ala Lys Gly Leu Val His Ala Val Asn Asn Val Ser Leu Glu Val
             20                  25                  30

His Pro Gly Gln Ile Thr Ala Ile Val Gly Glu Ser Gly Ser Gly Lys
         35                  40                  45

Ser Thr Thr Ala Gln Ala Val Ile Gly Leu Leu Ala Asp Asn Ala Glu
     50                  55                  60
```

Val Asp Ser Gly Arg Ile Ser Phe Asn Gly Arg Ser Leu Val Gly Leu
65 70 75 80

Asn Ala Arg Glu Trp Lys Asn Val Arg Gly Thr Lys Ile Gly Leu Ile
85 90 95

Pro Gln Asp Pro Asn Asn Ser Leu Asn Pro Val Lys Thr Ile Gly Ala
100 105 110

Ser Val Gly Glu Gly Leu Ala Ile His Lys Arg Gly Thr Ala Ala Glu
115 120 125

Arg Lys Lys Lys Val Ile Glu Leu Leu Glu Arg Val Gly Ile Asp Asn
130 135 140

Pro Glu Val Arg Tyr Asp Gln Tyr Pro His Glu Leu Ser Gly Gly Met
145 150 155 160

Lys Gln Arg Ala Leu Ile Ala Ala Ala Ile Ala Leu Glu Pro Glu Leu
165 170 175

Ile Ile Ala Asp Glu Pro Thr Ser Ala Leu Asp Val Thr Val Gln Lys
180 185 190

Ile Ile Leu Asp Leu Leu Glu Asp Met Gln Arg Glu Leu Gly Met Gly
195 200 205

Ile Leu Phe Ile Thr His Asp Leu Ala Val Ala Gly Asp Arg Ala Asp
210 215 220

Arg Ile Val Val Met Gln Lys Gly Glu Val Arg Glu Ser Gly Tyr Ala
225 230 235 240

Ala Ser Val Leu Thr Asp Pro Gln His Glu Tyr Ser Lys Lys Leu Leu
245 250 255

Ala Asp Ala Pro Ser Leu Thr Ile Gly Glu Ile Pro Thr Arg Val Pro
260 265 270

Ala Val Asp Pro Glu Val Ala Gln Ala Lys Gly Pro Leu Leu Val Val
275 280 285

Asp Lys Phe Arg Lys Glu His Gln Arg Gly Lys Glu Gly Ala Phe Val
290 295 300

Ala Ala Asn Asp Ile Ser Phe Glu Val Leu Pro Gly Thr Thr His Ala
305 310 315 320

Ile Val Gly Glu Ser Gly Ser Gly Lys Thr Thr Leu Gly Arg Ala Ile
325 330 335

Ala Met Phe Asn Thr Pro Thr Ser Gly Ser Ile Ser Val Ser Gly Lys
340 345 350

Asp Ile Thr Asn Leu Ser Lys Ala Gln Gln Arg Glu Leu Arg Gln Gln
355 360 365

Ile Gln Leu Val Tyr Gln Asn Pro Tyr Ser Ser Leu Asp Pro Arg Gln
370 375 380

```
Thr Ile Gly Ser Thr Ile Ala Glu Pro Leu Arg Asn Phe Thr Lys Val
385                 390                 395                 400

Ser Lys Gln Glu Ala Asp Glu Lys Val Ala His Tyr Leu Glu Leu Val
                405                 410                 415

Ala Leu Asp Pro Ala Leu Ala Thr Arg Arg Pro Arg Glu Leu Ser Gly
            420                 425                 430

Gly Gln Arg Gln Arg Val Ala Ile Ala Arg Ala Met Ile Leu Glu Pro
        435                 440                 445

Glu Leu Val Val Phe Asp Glu Ala Val Ser Ala Leu Asp Val Thr Val
    450                 455                 460

Gln Ala Gln Ile Leu Arg Leu Leu Asp Asp Leu Gln Arg Glu Leu Gly
465                 470                 475                 480

Leu Thr Tyr Val Phe Ile Ser His Asp Leu Ala Val Val Arg Glu Ile
                485                 490                 495

Ser Asp Thr Val Ser Val Met Ser Arg Gly Asn Gln Val Glu Leu Gly
            500                 505                 510

Lys Thr Ala Glu Val Phe Asn Asn Pro Gln Thr Asp Phe Thr Arg Arg
        515                 520                 525

Leu Ile Asp Ala Ile Pro Gly Ser Arg Tyr Arg Gly Gly Glu Leu Asn
    530                 535                 540

Leu Gly Leu
545
```

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<210> 183
<211> 762
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(739)
<223> RXA02660

<400> 183

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catttttcag cacacttttt aagatctcat cgaaagcgcg atacccacta tgtccaatct 60

tttgagactt gtcggccgac ggctcatcgc tttaccgatc atg att att ggc gtc   115
                                              Met Ile Ile Gly Val
                                                1               5

acc ctg ctg gtt ttc atc gtc atg tca ttc tct cct gcc gac ccg gca   163
Thr Leu Leu Val Phe Ile Val Met Ser Phe Ser Pro Ala Asp Pro Ala
                10                  15                  20

cga ctt gcc cta ggc gaa tca gcc tcc ccc gaa gca ctt gaa gcc tac   211
Arg Leu Ala Leu Gly Glu Ser Ala Ser Pro Glu Ala Leu Glu Ala Tyr
            25                  30                  35

cgt gaa gcc aac ggc ctc aac gat cca atg atg gtt cgc tat ttc gac   259
Arg Glu Ala Asn Gly Leu Asn Asp Pro Met Met Val Arg Tyr Phe Asp
```

```
          40                  45                  50

ttc atc ctc ggc atg ctc aaa ggc gac ttg gga acc tct agc ggt ggc   307
Phe Ile Leu Gly Met Leu Lys Gly Asp Leu Gly Thr Ser Ser Gly Gly
     55                  60                  65

gta gct gtt acc gac att gtt gcc cgc gct ttc ccc atc acc ctg cag   355
Val Ala Val Thr Asp Ile Val Ala Arg Ala Phe Pro Ile Thr Leu Gln
 70                  75                  80                  85

cta aca ttc tgg gga ctc atc atc gct gtt gta gtg gcg ttg atc ctc   403
Leu Thr Phe Trp Gly Leu Ile Ile Ala Val Val Val Ala Leu Ile Leu
                 90                  95                 100

ggt gtc atc gcc gct cta tac cga gac cgc tgg cct gac cag ttg att   451
Gly Val Ile Ala Ala Leu Tyr Arg Asp Arg Trp Pro Asp Gln Leu Ile
            105                 110                 115

cgc gtg gtc tcc att gcg gct ctt gct act cct tca ttc tgg ttg gct   499
Arg Val Val Ser Ile Ala Ala Leu Ala Thr Pro Ser Phe Trp Leu Ala
        120                 125                 130

atc ttg ctg atc cag tgg ttg ggt act atc cct gga gcc tgg ggt ttc   547
Ile Leu Leu Ile Gln Trp Leu Gly Thr Ile Pro Gly Ala Trp Gly Phe
    135                 140                 145

ttc cca gca ctt gtc acc cgg tgg gtc cca ttc agc gaa gat ccc gcc   595
Phe Pro Ala Leu Val Thr Arg Trp Val Pro Phe Ser Glu Asp Pro Ala
150                 155                 160                 165

acc tac ttc aac aac atc gca ctt cag cga ttg cgt tgg cag tcc ccg   643
Thr Tyr Phe Asn Asn Ile Ala Leu Gln Arg Leu Arg Trp Gln Ser Pro
                170                 175                 180

ttg cag gtt ctt tgg ccc gcg ttg ttc gta cct cca tgg tgg aag aac   691
Leu Gln Val Leu Trp Pro Ala Leu Phe Val Pro Pro Trp Trp Lys Asn
            185                 190                 195

tgg aca agg act acg tcc gca cag caa tcg gtg cag gat ccc caa aac   739
Trp Thr Arg Thr Thr Ser Ala Gln Gln Ser Val Gln Asp Pro Gln Asn
        200                 205                 210

tgaagttgtt gcccgcaatg ttc                                        762


<210> 184
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 184
Met Ile Ile Gly Val Thr Leu Leu Val Phe Ile Val Met Ser Phe Ser
  1               5                  10                  15

Pro Ala Asp Pro Ala Arg Leu Ala Leu Gly Glu Ser Ala Ser Pro Glu
             20                  25                  30

Ala Leu Glu Ala Tyr Arg Glu Ala Asn Gly Leu Asn Asp Pro Met Met
         35                  40                  45

Val Arg Tyr Phe Asp Phe Ile Leu Gly Met Leu Lys Gly Asp Leu Gly
```

```
     50                  55                  60

Thr Ser Ser Gly Gly Val Ala Val Thr Asp Ile Val Ala Arg Ala Phe
 65                  70                  75                  80

Pro Ile Thr Leu Gln Leu Thr Phe Trp Gly Leu Ile Ile Ala Val Val
                85                  90                  95

Val Ala Leu Ile Leu Gly Val Ile Ala Ala Leu Tyr Arg Asp Arg Trp
            100                 105                 110

Pro Asp Gln Leu Ile Arg Val Val Ser Ile Ala Ala Leu Ala Thr Pro
        115                 120                 125

Ser Phe Trp Leu Ala Ile Leu Leu Ile Gln Trp Leu Gly Thr Ile Pro
    130                 135                 140

Gly Ala Trp Gly Phe Phe Pro Ala Leu Val Thr Arg Trp Val Pro Phe
145                 150                 155                 160

Ser Glu Asp Pro Ala Thr Tyr Phe Asn Asn Ile Ala Leu Gln Arg Leu
                165                 170                 175

Arg Trp Gln Ser Pro Leu Gln Val Leu Trp Pro Ala Leu Phe Val Pro
            180                 185                 190

Pro Trp Trp Lys Asn Trp Thr Arg Thr Thr Ser Ala Gln Gln Ser Val
        195                 200                 205

Gln Asp Pro Gln Asn
    210
```

09625950.1

<210> 185
<211> 342
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(319)
<223> RXA02661

<400> 185
tggacaagga ctacgtccgc acagcaatcg gtgcaggatc cccaaaactg aagttgttgc 60

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ccgcaatgtt ctgcgcaatg cgctgatcac cccaatcacc gtg att ggt ctt cgc   115
                                              Val Ile Gly Leu Arg
                                                1               5

gtt ggt tcc ctc atg ggt ggt gcg gtg atc att gag atc atc ttc aac   163
Val Gly Ser Leu Met Gly Gly Ala Val Ile Ile Glu Ile Ile Phe Asn
                10                  15                  20

atc caa gca atg gga cag ctc atc cta gac ggt gtg acc cga aat gac   211
Ile Gln Ala Met Gly Gln Leu Ile Leu Asp Gly Val Thr Arg Asn Asp
            25                  30                  35

gtc tac ctc gtc caa ggt gtc acc ctc acc gtt gcc atc gcc ttc atc   259
Val Tyr Leu Val Gln Gly Val Thr Leu Thr Val Ala Ile Ala Phe Ile
        40                  45                  50
```

```
atc gtc aat atc gcc gtg gac ctg ctc tac gtc ctg gtc aat cca cgt   307
Ile Val Asn Ile Ala Val Asp Leu Leu Tyr Val Leu Val Asn Pro Arg
     55                  60                  65

att agg agc atc tagatgcgcc gtaaactaac cac                        342
Ile Arg Ser Ile
 70
```

<210> 186
<211> 73
<212> PRT
<213> Corynebacterium glutamicum

<400> 186

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Val | Ile | Gly | Leu | Arg | Val | Gly | Ser | Leu | Met | Gly | Gly | Ala | Val | Ile | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Glu | Ile | Ile | Phe | Asn | Ile | Gln | Ala | Met | Gly | Gln | Leu | Ile | Leu | Asp | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Thr | Arg | Asn | Asp | Val | Tyr | Leu | Val | Gln | Gly | Val | Thr | Leu | Thr | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ala | Ile | Ala | Phe | Ile | Ile | Val | Asn | Ile | Ala | Val | Asp | Leu | Leu | Tyr | Val |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Val | Asn | Pro | Arg | Ile | Arg | Ser | Ile | | | | | | | |
| 65 | | | | | 70 | | | | | | | | | | |

<210> 187
<211> 1089
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1066)
<223> RXA02034

<400> 187

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tcgtggtgat gtcaccagag atcaccggca ttgatcccaa cgtggtgtcc ggggcgttgg 60

aattgtcgtt gattggtcgg aaagaatccg gggtagcgca gtg agt aaa aca atc   115
                                              Val Ser Lys Thr Ile
                                                1               5

gct tgg act gtg ctg cgg tac acc ctg act ttt gtg atc gcc agc atc   163
Ala Trp Thr Val Leu Arg Tyr Thr Leu Thr Phe Val Ile Ala Ser Ile
                10                  15                  20

atc att ttt gtg ctg att cga gtc atc ccc ggt gac ccc gcc gct gtt   211
Ile Ile Phe Val Leu Ile Arg Val Ile Pro Gly Asp Pro Ala Ala Val
            25                  30                  35

gcc ctg gga att acc gcg aca cca gaa gca atc gct gcg ttg caa tca   259
Ala Leu Gly Ile Thr Ala Thr Pro Glu Ala Ile Ala Ala Leu Gln Ser
        40                  45                  50
```

```
caa tta ggt act gat caa ccg ctt ttc caa cag tac ttt tcc tgg ata   307
Gln Leu Gly Thr Asp Gln Pro Leu Phe Gln Gln Tyr Phe Ser Trp Ile
     55                  60                  65

ggt gga atg ctc act ggc gat ttc ggc acc tcg ctg agc tct ggc caa   355
Gly Gly Met Leu Thr Gly Asp Phe Gly Thr Ser Leu Ser Ser Gly Gln
 70                  75                  80                  85

gac ctt tcc ccc atc att ttt gac cgc tta caa gtg agc ctc att ttg   403
Asp Leu Ser Pro Ile Ile Phe Asp Arg Leu Gln Val Ser Leu Ile Leu
                 90                  95                 100

gtg gga tgc tcc att gtg ttg tcg ttg ctc att gcc att cca ctt ggt   451
Val Gly Cys Ser Ile Val Leu Ser Leu Leu Ile Ala Ile Pro Leu Gly
            105                 110                 115

gtg ctt tcg gcc cgg cgc ggt ggc gtg atc att tcc ggc atc agc cag   499
Val Leu Ser Ala Arg Arg Gly Gly Val Ile Ile Ser Gly Ile Ser Gln
        120                 125                 130

att ggc att gcg atc cct agt ttc ctc gcc ggt att ttg ttg gtc gct   547
Ile Gly Ile Ala Ile Pro Ser Phe Leu Ala Gly Ile Leu Leu Val Ala
    135                 140                 145

gtc ttc gcc gtt ggt ttg ggg tgg ctg ccc gcc aat ggc tgg att ccg   595
Val Phe Ala Val Gly Leu Gly Trp Leu Pro Ala Asn Gly Trp Ile Pro
150                 155                 160                 165

ccg tcg gaa aac ttt gga ggt ttc tta gcc agg ctg atc ctc ccg gtt   643
Pro Ser Glu Asn Phe Gly Gly Phe Leu Ala Arg Leu Ile Leu Pro Val
                170                 175                 180

ctg gct ctt act gct gtt caa gca gca att ttg acc cgc tat gtc cgc   691
Leu Ala Leu Thr Ala Val Gln Ala Ala Ile Leu Thr Arg Tyr Val Arg
            185                 190                 195

tct gca gta atg gat gta atg ggg caa gat ttc atg cgc acc gcg agg   739
Ser Ala Val Met Asp Val Met Gly Gln Asp Phe Met Arg Thr Ala Arg
        200                 205                 210

tcg aaa ggt atg agc ttc aac cgc gcg ttg atc atc cac ggt ctt cgg   787
Ser Lys Gly Met Ser Phe Asn Arg Ala Leu Ile Ile His Gly Leu Arg
    215                 220                 225

aat gct gct ctt cct gtc ctt acc gtc act ggt ttg cag cta aca acc   835
Asn Ala Ala Leu Pro Val Leu Thr Val Thr Gly Leu Gln Leu Thr Thr
230                 235                 240                 245

ttg gtt atc ggc gcc gtg gtg att gaa caa gtc ttt gtc atc ccc gga   883
Leu Val Ile Gly Ala Val Val Ile Glu Gln Val Phe Val Ile Pro Gly
                250                 255                 260

atc ggt tcg atg ctg ctg gag tcc gtg tcc aac cgt gat ctc atc gct   931
Ile Gly Ser Met Leu Leu Glu Ser Val Ser Asn Arg Asp Leu Ile Ala
            265                 270                 275

gtg caa tct att gtc atg ctg ctg gtg gcg ttc acg ttg ctg gtt aat   979
Val Gln Ser Ile Val Met Leu Leu Val Ala Phe Thr Leu Leu Val Asn
        280                 285                 290

ttg gtg gtt gat ctg ctg tat cag gtg gtt gat cca aga gtc ggt gct   1027
```

```
Leu Val Val Asp Leu Leu Tyr Gln Val Val Asp Pro Arg Val Gly Ala
    295                 300                 305

gtt ggg gtt gct agc act aag gtt cca ggg agc gtg gct taagtgacaa    1076
Val Gly Val Ala Ser Thr Lys Val Pro Gly Ser Val Ala
310                 315                 320

cgatcaaaaa cat                                                  1089


<210> 188
<211> 322
<212> PRT
<213> Corynebacterium glutamicum

<400> 188
Val Ser Lys Thr Ile Ala Trp Thr Val Leu Arg Tyr Thr Leu Thr Phe
  1               5                  10                  15

Val Ile Ala Ser Ile Ile Ile Phe Val Leu Ile Arg Val Ile Pro Gly
            20                  25                  30

Asp Pro Ala Ala Val Ala Leu Gly Ile Thr Ala Thr Pro Glu Ala Ile
        35                  40                  45

Ala Ala Leu Gln Ser Gln Leu Gly Thr Asp Gln Pro Leu Phe Gln Gln
    50                  55                  60

Tyr Phe Ser Trp Ile Gly Gly Met Leu Thr Gly Asp Phe Gly Thr Ser
65                  70                  75                  80

Leu Ser Ser Gly Gln Asp Leu Ser Pro Ile Ile Phe Asp Arg Leu Gln
                85                  90                  95

Val Ser Leu Ile Leu Val Gly Cys Ser Ile Val Leu Ser Leu Leu Ile
            100                 105                 110

Ala Ile Pro Leu Gly Val Leu Ser Ala Arg Arg Gly Gly Val Ile Ile
        115                 120                 125

Ser Gly Ile Ser Gln Ile Gly Ile Ala Ile Pro Ser Phe Leu Ala Gly
    130                 135                 140

Ile Leu Leu Val Ala Val Phe Ala Val Gly Leu Gly Trp Leu Pro Ala
145                 150                 155                 160

Asn Gly Trp Ile Pro Pro Ser Glu Asn Phe Gly Gly Phe Leu Ala Arg
                165                 170                 175

Leu Ile Leu Pro Val Leu Ala Leu Thr Ala Val Gln Ala Ala Ile Leu
            180                 185                 190

Thr Arg Tyr Val Arg Ser Ala Val Met Asp Val Met Gly Gln Asp Phe
        195                 200                 205

Met Arg Thr Ala Arg Ser Lys Gly Met Ser Phe Asn Arg Ala Leu Ile
    210                 215                 220

Ile His Gly Leu Arg Asn Ala Ala Leu Pro Val Leu Thr Val Thr Gly
225                 230                 235                 240
```

```
Leu Gln Leu Thr Thr Leu Val Ile Gly Ala Val Val Ile Glu Gln Val
                245                 250                 255

Phe Val Ile Pro Gly Ile Gly Ser Met Leu Leu Glu Ser Val Ser Asn
            260                 265                 270

Arg Asp Leu Ile Ala Val Gln Ser Ile Val Met Leu Leu Val Ala Phe
        275                 280                 285

Thr Leu Leu Val Asn Leu Val Val Asp Leu Leu Tyr Gln Val Val Asp
    290                 295                 300

Pro Arg Val Gly Ala Val Gly Val Ala Ser Thr Lys Val Pro Gly Ser
305                 310                 315                 320

Val Ala
```

<210> 189
<211> 818
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(795)
<223> RXA01013

<400> 189

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ttg ggc aat cct tgg acg agg cct gct gct gtt att tcc atc gtg gta   48
Leu Gly Asn Pro Trp Thr Arg Pro Ala Ala Val Ile Ser Ile Val Val
  1               5                  10                  15

ctc gcc gtt gcg gtg ctg atg gca ctt gtt cct gga ctg ttt acc tcc   96
Leu Ala Val Ala Val Leu Met Ala Leu Val Pro Gly Leu Phe Thr Ser
             20                  25                  30

cag gat ccg ttc act ggc gat gat gtg gcg ctg ctt ggg cca agt ggc  144
Gln Asp Pro Phe Thr Gly Asp Asp Val Ala Leu Leu Gly Pro Ser Gly
         35                  40                  45

acc cac tgg ttt ggt acc gat tcc gtg gga cgc gat ctc tac agt cgt  192
Thr His Trp Phe Gly Thr Asp Ser Val Gly Arg Asp Leu Tyr Ser Arg
     50                  55                  60

gtt gtt tac ggc gcg agg gaa acc ctg ctc ggt gca ctg atc gca gtg  240
Val Val Tyr Gly Ala Arg Glu Thr Leu Leu Gly Ala Leu Ile Ala Val
 65                  70                  75                  80

ctg gtt ggt ctg atc gtg gga acc ctg atc gga ctg ctc gca ggt gca  288
Leu Val Gly Leu Ile Val Gly Thr Leu Ile Gly Leu Leu Ala Gly Ala
                 85                  90                  95

cag cgc ggt tgg gtt gac act gta tta atg cgt ttc gtg gat gtg ctg  336
Gln Arg Gly Trp Val Asp Thr Val Leu Met Arg Phe Val Asp Val Leu
            100                 105                 110

ttg tcc atc ccg gca ctg ctg ctc agc ttg act gtc att atc ctt ttg  384
Leu Ser Ile Pro Ala Leu Leu Leu Ser Leu Thr Val Ile Ile Leu Leu
        115                 120                 125
```

```
gga ttc ggc acc atg aac gca gcg atc gca gtc ggt att acc tct gtt   432
Gly Phe Gly Thr Met Asn Ala Ala Ile Ala Val Gly Ile Thr Ser Val
    130                 135                 140

gcc acc ttc gcg cgt ctg gcg cgt tcc cag gtg atg act gtt gca ggt   480
Ala Thr Phe Ala Arg Leu Ala Arg Ser Gln Val Met Thr Val Ala Gly
145                 150                 155                 160

tcc gat ttc gtg gaa gct gca tac ggt tcc ggt ggc acc cag gcg cag   528
Ser Asp Phe Val Glu Ala Ala Tyr Gly Ser Gly Gly Thr Gln Ala Gln
                165                 170                 175

gtg ttg ttc cgc cac att ctg cct aac tct ctg acc cca gtg ttt gct   576
Val Leu Phe Arg His Ile Leu Pro Asn Ser Leu Thr Pro Val Phe Ala
            180                 185                 190

ctt gca gca ctg cag ttc ggt tcc gcg att ttg cag ctg tcc gtg ttg   624
Leu Ala Ala Leu Gln Phe Gly Ser Ala Ile Leu Gln Leu Ser Val Leu
        195                 200                 205

ggc ttc ttg ggc tac ggc gct ccg gca cca aca cca gag tgg ggt ctg   672
Gly Phe Leu Gly Tyr Gly Ala Pro Ala Pro Thr Pro Glu Trp Gly Leu
    210                 215                 220

ctg atc tct gat gcc cgc gac tac atg gcg acc tca tgg tgg ctg act   720
Leu Ile Ser Asp Ala Arg Asp Tyr Met Ala Thr Ser Trp Trp Leu Thr
225                 230                 235                 240

gtg ctg cct ggt ttt gtc atc atc gcc gtg gtt atg tct gcc aac tac   768
Val Leu Pro Gly Phe Val Ile Ile Ala Val Val Met Ser Ala Asn Tyr
                245                 250                 255

cta agc cgc atc att cag aag gag gca tagaaaatga ctactccctt        815
Leu Ser Arg Ile Ile Gln Lys Glu Ala
            260                 265

gtt                                                              818
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<210> 190
<211> 265
<212> PRT
<213> Corynebacterium glutamicum

<400> 190

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Leu Gly Asn Pro Trp Thr Arg Pro Ala Ala Val Ile Ser Ile Val Val
  1               5                  10                  15

Leu Ala Val Ala Val Leu Met Ala Leu Val Pro Gly Leu Phe Thr Ser
            20                  25                  30

Gln Asp Pro Phe Thr Gly Asp Asp Val Ala Leu Leu Gly Pro Ser Gly
        35                  40                  45

Thr His Trp Phe Gly Thr Asp Ser Val Gly Arg Asp Leu Tyr Ser Arg
    50                  55                  60

Val Val Tyr Gly Ala Arg Glu Thr Leu Leu Gly Ala Leu Ile Ala Val
65                  70                  75                  80
```

Leu Val Gly Leu Ile Val Gly Thr Leu Ile Gly Leu Leu Ala Gly Ala
85 90 95

Gln Arg Gly Trp Val Asp Thr Val Leu Met Arg Phe Val Asp Val Leu
100 105 110

Leu Ser Ile Pro Ala Leu Leu Leu Ser Leu Thr Val Ile Ile Leu Leu
115 120 125

Gly Phe Gly Thr Met Asn Ala Ala Ile Ala Val Gly Ile Thr Ser Val
130 135 140

Ala Thr Phe Ala Arg Leu Ala Arg Ser Gln Val Met Thr Val Ala Gly
145 150 155 160

Ser Asp Phe Val Glu Ala Ala Tyr Gly Ser Gly Gly Thr Gln Ala Gln
165 170 175

Val Leu Phe Arg His Ile Leu Pro Asn Ser Leu Thr Pro Val Phe Ala
180 185 190

Leu Ala Ala Leu Gln Phe Gly Ser Ala Ile Leu Gln Leu Ser Val Leu
195 200 205

Gly Phe Leu Gly Tyr Gly Ala Pro Ala Pro Thr Pro Glu Trp Gly Leu
210 215 220

Leu Ile Ser Asp Ala Arg Asp Tyr Met Ala Thr Ser Trp Trp Leu Thr
225 230 235 240

Val Leu Pro Gly Phe Val Ile Ile Ala Val Val Met Ser Ala Asn Tyr
245 250 255

Leu Ser Arg Ile Ile Gln Lys Glu Ala
260 265

<210> 191
<211> 933
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> RXN02933

<400> 191
tgatctgctg tatcaggtgg ttgatccaag agtcggtgct gttggggttg ctagcactaa 60

ggttccaggg agcgtggctt aagtgacaac gatcaaaaac atg ccc ctt tca ggg 115
Met Pro Leu Ser Gly
1 5

aaa atc ggc ggc ttc atc gtt gcc gtt gta ttt gtt ctt gct gcg ctg 163
Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe Val Leu Ala Ala Leu
10 15 20

tct ttc att tgg act ccg ttt gat cca gtt caa gct ttc cca cag gag 211
Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln Ala Phe Pro Gln Glu
25 30 35

```
cgc ctt gag gga agt tct ttg agg cac ctg ttg gga acg gat cgt tat   259
Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu Gly Thr Asp Arg Tyr
          40                  45                  50

ggt cgc gat gtt tta tcc cag atc atg gtt ggt tcc cgc gtc acg ttg   307
Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly Ser Arg Val Thr Leu
     55                  60                  65

ttg gtg ggc atc att gcg gtg gcg atc gca gca tta atc ggc acg cca   355
Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala Leu Ile Gly Thr Pro
 70                  75                  80                  85

ctg ggt att gct gcg gga atg cgc cgt ggc atg gtg gaa acc ttt gtc   403
Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met Val Glu Thr Phe Val
                 90                  95                 100

atg cgt ggt gcc gat tta atg ttg gcg ttc cca gca ctg ttg ttg gcg   451
Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro Ala Leu Leu Leu Ala
            105                 110                 115

att att tcc ggc gcc gtt ttc ggc gcc tcc acg tgg tcc gcg atg gtc   499
Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr Trp Ser Ala Met Val
        120                 125                 130

gcg atc ggc atc gca ggc atc cct agt ttt gcc cgc gtg gct cgt gca   547
Ala Ile Gly Ile Ala Gly Ile Pro Ser Phe Ala Arg Val Ala Arg Ala
    135                 140                 145

ggc aca ttg cag gtg acc agt cag gat ttc atc gca gct gct cgg cta   595
Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile Ala Ala Ala Arg Leu
150                 155                 160                 165

tca aaa gta agt tcc gcc cgg atc gcg ctt cgc cat att ttg ccc aac   643
Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg His Ile Leu Pro Asn
                170                 175                 180

atc acc agc atg ttg atc gtt cag gca tca gta gct ttt gcc ctg gcg   691
Ile Thr Ser Met Leu Ile Val Gln Ala Ser Val Ala Phe Ala Leu Ala
            185                 190                 195

atc ctg gcg gaa gcc gca ttg agt ttc ctc ggt ttg ggc acc act ccc   739
Ile Leu Ala Glu Ala Ala Leu Ser Phe Leu Gly Leu Gly Thr Thr Pro
        200                 205                 210

ccg gat ccc agc tgg ggt cgc atg ttg caa acc gct caa gca tcc atc   787
Pro Asp Pro Ser Trp Gly Arg Met Leu Gln Thr Ala Gln Ala Ser Ile
    215                 220                 225

ggc gtc acc ccc atg ttg gcg gtg tgg ccc ggt gct gcg atc gct ttg   835
Gly Val Thr Pro Met Leu Ala Val Trp Pro Gly Ala Ala Ile Ala Leu
230                 235                 240                 245

acg gtc ctt ggt ttt aat ctt ttc ggt gat ggt tta cgc gat gcc atc   883
Thr Val Leu Gly Phe Asn Leu Phe Gly Asp Gly Leu Arg Asp Ala Ile
                250                 255                 260

gat cca aag cgg gag gtc ggc cgt gct taaagtttct gatttaacgg         930
Asp Pro Lys Arg Glu Val Gly Arg Ala
            265                 270
```

ttg 933

<210> 192
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 192

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Met Pro Leu Ser Gly Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe
  1               5                  10                  15

Val Leu Ala Ala Leu Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln
             20                  25                  30

Ala Phe Pro Gln Glu Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu
         35                  40                  45

Gly Thr Asp Arg Tyr Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly
     50                  55                  60

Ser Arg Val Thr Leu Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala
 65                  70                  75                  80

Leu Ile Gly Thr Pro Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met
                 85                  90                  95

Val Glu Thr Phe Val Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro
            100                 105                 110

Ala Leu Leu Leu Ala Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr
        115                 120                 125

Trp Ser Ala Met Val Ala Ile Gly Ile Ala Gly Ile Pro Ser Phe Ala
    130                 135                 140

Arg Val Ala Arg Ala Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile
145                 150                 155                 160

Ala Ala Ala Arg Leu Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg
                165                 170                 175

His Ile Leu Pro Asn Ile Thr Ser Met Leu Ile Val Gln Ala Ser Val
            180                 185                 190

Ala Phe Ala Leu Ala Ile Leu Ala Glu Ala Ala Leu Ser Phe Leu Gly
        195                 200                 205

Leu Gly Thr Thr Pro Pro Asp Pro Ser Trp Gly Arg Met Leu Gln Thr
    210                 215                 220

Ala Gln Ala Ser Ile Gly Val Thr Pro Met Leu Ala Val Trp Pro Gly
225                 230                 235                 240

Ala Ala Ile Ala Leu Thr Val Leu Gly Phe Asn Leu Phe Gly Asp Gly
                245                 250                 255

Leu Arg Asp Ala Ile Asp Pro Lys Arg Glu Val Gly Arg Ala
            260                 265                 270
```

<210> 193
<211> 900
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(889)
<223> FRXA02033

<400> 193
tgatctgctg tatcaggtgg ttgatccaag agtcggtgct gttggggttg ctagcactaa 60

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ggttccaggg agcgtggctt aagtgacaac gatcaaaaac atg ccc ctt tca ggg   115
                                              Met Pro Leu Ser Gly
                                                1               5

aaa atc ggc ggc ttc atc gtt gcc gtt gta ttt gtt ctt gct gcg ctg   163
Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe Val Leu Ala Ala Leu
                10                  15                  20

tct ttc att tgg act ccg ttt gat cca gtt caa gct ttc cca cag gag   211
Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln Ala Phe Pro Gln Glu
            25                  30                  35

cgc ctt gag gga agt tct ttg agg cac ctg ttg gga acg gat cgt tat   259
Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu Gly Thr Asp Arg Tyr
        40                  45                  50

ggt cgc gat gtt tta tcc cag atc atg gtt ggt tcc cgc gtc acg ttg   307
Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly Ser Arg Val Thr Leu
    55                  60                  65

ttg gtg ggc atc att gcg gtg gcg atc gca gca tta atc ggc acg cca   355
Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala Leu Ile Gly Thr Pro
70                  75                  80                  85

ctg ggt att gct gcg gga atg cgc cgt ggc atg gtg gaa acc ttt gtc   403
Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met Val Glu Thr Phe Val
                90                  95                  100

atg cgt ggt gcc gat tta atg ttg gcg ttc cca gca ctg ttg ttg gcg   451
Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro Ala Leu Leu Leu Ala
            105                 110                 115

att att tcc ggc gcc gtt ttc ggc gcc tcc acg tgg tcc gcg atg gtc   499
Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr Trp Ser Ala Met Val
        120                 125                 130

gcg atc ggc atc gca ggc atc cct agt ttt gcc cgc gtg gct cgt gca   547
Ala Ile Gly Ile Ala Gly Ile Pro Ser Phe Ala Arg Val Ala Arg Ala
    135                 140                 145

ggc aca ttg cag gtg acc agt cag gat ttc atc gca gct gct cgg cta   595
Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile Ala Ala Ala Arg Leu
150                 155                 160                 165

tca aaa gta agt tcc gcc cgg atc gcg ctt cgc cat att ttg ccc aac   643
Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg His Ile Leu Pro Asn
                170                 175                 180
```

```
atc acc agc atg ttg atc gtt cag gca tca gta gct ttt gcc ctg gcg   691
Ile Thr Ser Met Leu Ile Val Gln Ala Ser Val Ala Phe Ala Leu Ala
            185                 190                 195

atc ctg gcg gaa gcc gca ttg agt ttc ctc ggt ttg ggc acc act ccc   739
Ile Leu Ala Glu Ala Ala Leu Ser Phe Leu Gly Leu Gly Thr Thr Pro
        200                 205                 210

ccg gat ccc agc tgg ggt cgc atg ttg caa acc gct caa gca tcc atc   787
Pro Asp Pro Ser Trp Gly Arg Met Leu Gln Thr Ala Gln Ala Ser Ile
    215                 220                 225

ggc gtc acc ccc atg ttg gcg gtg tgg ccc ggt gct gcg atc gct ttg   835
Gly Val Thr Pro Met Leu Ala Val Trp Pro Gly Ala Ala Ile Ala Leu
230                 235                 240                 245

acg gtc ctt ggt ttt aat ctt ttc ggt gat ggt tta cgc gat gcc atc   883
Thr Val Leu Gly Phe Asn Leu Phe Gly Asp Gly Leu Arg Asp Ala Ile
                250                 255                 260

gat cca tagtattata t                                            900
Asp Pro
```

Sequence Listing.ST25.txt

<210> 194
<211> 263
<212> PRT
<213> Corynebacterium glutamicum

<400> 194

```
Met Pro Leu Ser Gly Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe
  1               5                  10                  15

Val Leu Ala Ala Leu Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln
            20                  25                  30

Ala Phe Pro Gln Glu Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu
        35                  40                  45

Gly Thr Asp Arg Tyr Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly
    50                  55                  60

Ser Arg Val Thr Leu Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala
65                  70                  75                  80

Leu Ile Gly Thr Pro Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met
                85                  90                  95

Val Glu Thr Phe Val Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro
            100                 105                 110

Ala Leu Leu Leu Ala Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr
        115                 120                 125

Trp Ser Ala Met Val Ala Ile Gly Ile Ala Gly Ile Pro Ser Phe Ala
    130                 135                 140

Arg Val Ala Arg Ala Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile
145                 150                 155                 160
```

Ala Ala Ala Arg Leu Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg
165 170 175

His Ile Leu Pro Asn Ile Thr Ser Met Leu Ile Val Gln Ala Ser Val
180 185 190

Ala Phe Ala Leu Ala Ile Leu Ala Glu Ala Ala Leu Ser Phe Leu Gly
195 200 205

Leu Gly Thr Thr Pro Pro Asp Pro Ser Trp Gly Arg Met Leu Gln Thr
210 215 220

Ala Gln Ala Ser Ile Gly Val Thr Pro Met Leu Ala Val Trp Pro Gly
225 230 235 240

Ala Ala Ile Ala Leu Thr Val Leu Gly Phe Asn Leu Phe Gly Asp Gly
245 250 255

Leu Arg Asp Ala Ile Asp Pro
260

<210> 195
<211> 958
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(958)
<223> RXA01006

<400> 195
gccttacgtg aagggcttta gccccgaagt gatcggccgc cccagcttct atgagaccta 60

cattgaccat tccagcgacc attccagtga ggaggactaa atg act acc tcg cag 115
Met Thr Thr Ser Gln
1 5

att ctg cgc cgc atc ggc caa gcc gtc ttg gtc ttg ttg gtc acc ttt 163
Ile Leu Arg Arg Ile Gly Gln Ala Val Leu Val Leu Leu Val Thr Phe
10 15 20

acc ttg gcg ttc atc atg ctt tcc gcc ctc cct ggc gat gct gtg tcc 211
Thr Leu Ala Phe Ile Met Leu Ser Ala Leu Pro Gly Asp Ala Val Ser
25 30 35

gcc cgc tat tcc agc cct gat ttg ggt ctg tca cct gag cag atc gca 259
Ala Arg Tyr Ser Ser Pro Asp Leu Gly Leu Ser Pro Glu Gln Ile Ala
40 45 50

cag atc cgt gaa tcc tat ggt gcc gat gaa tcc ctg atc gct cag tac 307
Gln Ile Arg Glu Ser Tyr Gly Ala Asp Glu Ser Leu Ile Ala Gln Tyr
55 60 65

ttc tcc acc ttg ggt ggc ttc ctt gta ggt aac ttc ggt tac tcc gta 355
Phe Ser Thr Leu Gly Gly Phe Leu Val Gly Asn Phe Gly Tyr Ser Val
70 75 80 85

caa acc gga act gcc gtg gca acc cag ctg gca gaa gcc cta cca ggc 403
Gln Thr Gly Thr Ala Val Ala Thr Gln Leu Ala Glu Ala Leu Pro Gly

```
                    90                  95                  100

acc ttg acc ttg gct att ttg gca ttc ttg ctc gca gcc att ttg gca   451
Thr Leu Thr Leu Ala Ile Leu Ala Phe Leu Leu Ala Ala Ile Leu Ala
            105                 110                 115

ctg gtt att tcc att ctt gcc acc atg gat cgc ttt gca tgg atc aag   499
Leu Val Ile Ser Ile Leu Ala Thr Met Asp Arg Phe Ala Trp Ile Lys
        120                 125                 130

ggc atc ttc cag gct ctg cct cca ttc ttt gtg tcc ctt cca agt ttc   547
Gly Ile Phe Gln Ala Leu Pro Pro Phe Phe Val Ser Leu Pro Ser Phe
    135                 140                 145

tgg ttg ggc atc atc ttg atc cag atc gtg tcc ttc cgc ctt ggt tgg   595
Trp Leu Gly Ile Ile Leu Ile Gln Ile Val Ser Phe Arg Leu Gly Trp
150                 155                 160                 165

gtc ccc gtt att ggg acc acc ccg gca caa gga ctg atc ctg ccg acc   643
Val Pro Val Ile Gly Thr Thr Pro Ala Gln Gly Leu Ile Leu Pro Thr
                170                 175                 180

atc acc ttg tcc atc cca att acc gct ccg ctt gca cag gtg ctc atc   691
Ile Thr Leu Ser Ile Pro Ile Thr Ala Pro Leu Ala Gln Val Leu Ile
            185                 190                 195

cgc tcg att gaa gag gtc aag gca caa ccg ttc atc gcg gct gtt cgt   739
Arg Ser Ile Glu Glu Val Lys Ala Gln Pro Phe Ile Ala Ala Val Arg
        200                 205                 210

gct cgc ggt gcg ggt gaa atg tgg atc ttc ttc cgc aac atc att cgc   787
Ala Arg Gly Ala Gly Glu Met Trp Ile Phe Phe Arg Asn Ile Ile Arg
    215                 220                 225

aac gcc ctt ttg cca acc ctg acg att gcc ggc atc ttg ttt ggt gaa   835
Asn Ala Leu Leu Pro Thr Leu Thr Ile Ala Gly Ile Leu Phe Gly Glu
230                 235                 240                 245

cta gtc ggt ggg gcc gtg gtc acc gag gca gtg ttc ggc cgc gct gga   883
Leu Val Gly Gly Ala Val Val Thr Glu Ala Val Phe Gly Arg Ala Gly
                250                 255                 260

ctt ggc caa atg acc gtc aac gca gtg gcc aac cgc gat atg cca gtg   931
Leu Gly Gln Met Thr Val Asn Ala Val Ala Asn Arg Asp Met Pro Val
            265                 270                 275

atg ctt gcc atc gtg gtg atc gca gct                              958
Met Leu Ala Ile Val Val Ile Ala Ala
        280                 285


<210> 196
<211> 286
<212> PRT
<213> Corynebacterium glutamicum

<400> 196
Met Thr Thr Ser Gln Ile Leu Arg Arg Ile Gly Gln Ala Val Leu Val
  1               5                  10                  15

Leu Leu Val Thr Phe Thr Leu Ala Phe Ile Met Leu Ser Ala Leu Pro
```

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```
                20                  25                  30

Gly Asp Ala Val Ser Ala Arg Tyr Ser Ser Pro Asp Leu Gly Leu Ser
          35                  40                  45

Pro Glu Gln Ile Ala Gln Ile Arg Glu Ser Tyr Gly Ala Asp Glu Ser
      50                  55                  60

Leu Ile Ala Gln Tyr Phe Ser Thr Leu Gly Gly Phe Leu Val Gly Asn
 65                  70                  75                  80

Phe Gly Tyr Ser Val Gln Thr Gly Thr Ala Val Ala Thr Gln Leu Ala
                 85                  90                  95

Glu Ala Leu Pro Gly Thr Leu Thr Leu Ala Ile Leu Ala Phe Leu Leu
            100                 105                 110

Ala Ala Ile Leu Ala Leu Val Ile Ser Ile Leu Ala Thr Met Asp Arg
        115                 120                 125

Phe Ala Trp Ile Lys Gly Ile Phe Gln Ala Leu Pro Pro Phe Phe Val
    130                 135                 140

Ser Leu Pro Ser Phe Trp Leu Gly Ile Ile Leu Ile Gln Ile Val Ser
145                 150                 155                 160

Phe Arg Leu Gly Trp Val Pro Val Ile Gly Thr Thr Pro Ala Gln Gly
                165                 170                 175

Leu Ile Leu Pro Thr Ile Thr Leu Ser Ile Pro Ile Thr Ala Pro Leu
            180                 185                 190

Ala Gln Val Leu Ile Arg Ser Ile Glu Glu Val Lys Ala Gln Pro Phe
        195                 200                 205

Ile Ala Ala Val Arg Ala Arg Gly Ala Gly Glu Met Trp Ile Phe Phe
    210                 215                 220

Arg Asn Ile Ile Arg Asn Ala Leu Leu Pro Thr Leu Thr Ile Ala Gly
225                 230                 235                 240

Ile Leu Phe Gly Glu Leu Val Gly Gly Ala Val Val Thr Glu Ala Val
                245                 250                 255

Phe Gly Arg Ala Gly Leu Gly Gln Met Thr Val Asn Ala Val Ala Asn
            260                 265                 270

Arg Asp Met Pro Val Met Leu Ala Ile Val Val Ile Ala Ala
        275                 280                 285
```

<210> 197
<211> 1482
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1459)
<223> RXA02312

<400> 197

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ttagcgccca ttaacgcttc acatccttat attcccaagg agcacgacca tttctgattc 60

agcagtccag gagaatcacg aaccgcacct caagcgcggt ttg agc aat aga cac   115
                                            Leu Ser Asn Arg His
                                              1               5

ctt cag ctc atc gcc atc ggc gga gcg atc ggt acg ggt ctg ttc atg   163
Leu Gln Leu Ile Ala Ile Gly Gly Ala Ile Gly Thr Gly Leu Phe Met
                10                  15                  20

ggg tcc ggc aag acg atc tcc gtt gcg ggg cca tca gta att ttg gtg   211
Gly Ser Gly Lys Thr Ile Ser Val Ala Gly Pro Ser Val Ile Leu Val
            25                  30                  35

tac gcc att att ggt ttc atg ctt ttc ttc gtc atg cgt gcc atg gga   259
Tyr Ala Ile Ile Gly Phe Met Leu Phe Phe Val Met Arg Ala Met Gly
        40                  45                  50

gag ctg ctg ctc gcc aat ttg aat tac aaa tct ttg cgc gat gcg gtc   307
Glu Leu Leu Leu Ala Asn Leu Asn Tyr Lys Ser Leu Arg Asp Ala Val
    55                  60                  65

tct gat att ttg ggt cct ggc gca ggt ttt gtc acc ggc tgg aca tat   355
Ser Asp Ile Leu Gly Pro Gly Ala Gly Phe Val Thr Gly Trp Thr Tyr
70                  75                  80                  85

tgg ttc tgc tgg att gcc aca ggc atg gcg gac atc gtg gcg atc act   403
Trp Phe Cys Trp Ile Ala Thr Gly Met Ala Asp Ile Val Ala Ile Thr
                90                  95                  100

gga tac acc caa tac tgg tgg cct gag atc cca ttg tgg ctt cca ggt   451
Gly Tyr Thr Gln Tyr Trp Trp Pro Glu Ile Pro Leu Trp Leu Pro Gly
            105                 110                 115

gtg ctc acc att gcg ttg ctg ttt gcc ctg aac ttg gct gcg gta cga   499
Val Leu Thr Ile Ala Leu Leu Phe Ala Leu Asn Leu Ala Ala Val Arg
        120                 125                 130

ctg ttc ggt gag atg gag ttt tgg ttc gcc atc atc aaa atc gtg gct   547
Leu Phe Gly Glu Met Glu Phe Trp Phe Ala Ile Ile Lys Ile Val Ala
    135                 140                 145

atc gtg tcc ttg atc gtc gtg gga ctt ttc atg gtg gtc aca gcc ttt   595
Ile Val Ser Leu Ile Val Val Gly Leu Phe Met Val Val Thr Ala Phe
150                 155                 160                 165

gaa tca cct aat ggc acc acc gcg cag ttc aac aac ctc att gag cat   643
Glu Ser Pro Asn Gly Thr Thr Ala Gln Phe Asn Asn Leu Ile Glu His
                170                 175                 180

ggc gga ttt ttc ccc aac ggc atc acc ggt ttc ttg gct ggt ttc cag   691
Gly Gly Phe Phe Pro Asn Gly Ile Thr Gly Phe Leu Ala Gly Phe Gln
            185                 190                 195

atc gct atc ttt gcg ttc gtc ggg att gaa ctt gcc ggc act gca gct   739
Ile Ala Ile Phe Ala Phe Val Gly Ile Glu Leu Ala Gly Thr Ala Ala
        200                 205                 210

gca gag act gag aat ccc acc aag acg ctt cct cgg gca atc aac tcc   787
Ala Glu Thr Glu Asn Pro Thr Lys Thr Leu Pro Arg Ala Ile Asn Ser
```

```
    215                 220                 225

att ccc atc cgc atc gtg gtg ttc tat gtt ttg gcg ttg gct gtc atc   835
Ile Pro Ile Arg Ile Val Val Phe Tyr Val Leu Ala Leu Ala Val Ile
230                 235                 240                 245

atg atg gtc acc cca tgg gat cag gtc cgt gct gac aac agc cca ttc   883
Met Met Val Thr Pro Trp Asp Gln Val Arg Ala Asp Asn Ser Pro Phe
                250                 255                 260

gtg cag atg ttc gcg ctg gca gga atc cca gcg gcg gca ggc atc att   931
Val Gln Met Phe Ala Leu Ala Gly Ile Pro Ala Ala Ala Gly Ile Ile
            265                 270                 275

aac ttt gtg gtc atc act tct gca gcg tcg tct gcc aac agt ggt att   979
Asn Phe Val Val Ile Thr Ser Ala Ala Ser Ser Ala Asn Ser Gly Ile
        280                 285                 290

ttc tcc acc tcc cgc atg ttg tat gga ttg tct ttg gaa ggc gca gct   1027
Phe Ser Thr Ser Arg Met Leu Tyr Gly Leu Ser Leu Glu Gly Ala Ala
    295                 300                 305

ccg aaa cgg tgg agc cgg ttg tcc aag aac ttg gtg cca gcc agg gga   1075
Pro Lys Arg Trp Ser Arg Leu Ser Lys Asn Leu Val Pro Ala Arg Gly
310                 315                 320                 325

ttg act ttt tct gtg att tgc ctc att cca gcg gtg ggt ttg ctg tac   1123
Leu Thr Phe Ser Val Ile Cys Leu Ile Pro Ala Val Gly Leu Leu Tyr
                330                 335                 340

gct ggc ggc act gtc atc gag gca ttc aca ctg atc acc acg gtt tct   1171
Ala Gly Gly Thr Val Ile Glu Ala Phe Thr Leu Ile Thr Thr Val Ser
            345                 350                 355

tcg gtg ttg ttc atg gtg gtg tgg tcc tac att ttg gtg gct tat atc   1219
Ser Val Leu Phe Met Val Val Trp Ser Tyr Ile Leu Val Ala Tyr Ile
        360                 365                 370

gtc tac cgc cgc aac agc ccg gaa tta cac aaa aag tcg att ttc aaa   1267
Val Tyr Arg Arg Asn Ser Pro Glu Leu His Lys Lys Ser Ile Phe Lys
    375                 380                 385

atg cct ggc ggc gtg gtc atg gca gtt gtg gtg ttg gtg ttc ttc gca   1315
Met Pro Gly Gly Val Val Met Ala Val Val Val Leu Val Phe Phe Ala
390                 395                 400                 405

gcg atg ttg gtg gtg ctg tcc ctg gag ccg gat acc cgt gca gcg ctc   1363
Ala Met Leu Val Val Leu Ser Leu Glu Pro Asp Thr Arg Ala Ala Leu
                410                 415                 420

atc gcg acg cca gtg tgg ttc atc att ttg ggt atc ggt tgg ttg tcc   1411
Ile Ala Thr Pro Val Trp Phe Ile Ile Leu Gly Ile Gly Trp Leu Ser
            425                 430                 435

atc ggt gga gct aag ggc gct aag cat cgc agc caa ata acc tcc cac   1459
Ile Gly Gly Ala Lys Gly Ala Lys His Arg Ser Gln Ile Thr Ser His
        440                 445                 450

taaagctcct gggttagact cga                                        1482
```

<210> 198
<211> 453
<212> PRT
<213> Corynebacterium glutamicum

<400> 198

```
Leu Ser Asn Arg His Leu Gln Leu Ile Ala Ile Gly Gly Ala Ile Gly
  1               5                  10                  15

Thr Gly Leu Phe Met Gly Ser Gly Lys Thr Ile Ser Val Ala Gly Pro
             20                  25                  30

Ser Val Ile Leu Val Tyr Ala Ile Ile Gly Phe Met Leu Phe Phe Val
         35                  40                  45

Met Arg Ala Met Gly Glu Leu Leu Leu Ala Asn Leu Asn Tyr Lys Ser
     50                  55                  60

Leu Arg Asp Ala Val Ser Asp Ile Leu Gly Pro Gly Ala Gly Phe Val
 65                  70                  75                  80

Thr Gly Trp Thr Tyr Trp Phe Cys Trp Ile Ala Thr Gly Met Ala Asp
                 85                  90                  95

Ile Val Ala Ile Thr Gly Tyr Thr Gln Tyr Trp Trp Pro Glu Ile Pro
            100                 105                 110

Leu Trp Leu Pro Gly Val Leu Thr Ile Ala Leu Leu Phe Ala Leu Asn
        115                 120                 125

Leu Ala Ala Val Arg Leu Phe Gly Glu Met Glu Phe Trp Phe Ala Ile
    130                 135                 140

Ile Lys Ile Val Ala Ile Val Ser Leu Ile Val Val Gly Leu Phe Met
145                 150                 155                 160

Val Val Thr Ala Phe Glu Ser Pro Asn Gly Thr Thr Ala Gln Phe Asn
                165                 170                 175

Asn Leu Ile Glu His Gly Gly Phe Phe Pro Asn Gly Ile Thr Gly Phe
            180                 185                 190

Leu Ala Gly Phe Gln Ile Ala Ile Phe Ala Phe Val Gly Ile Glu Leu
        195                 200                 205

Ala Gly Thr Ala Ala Ala Glu Thr Glu Asn Pro Thr Lys Thr Leu Pro
    210                 215                 220

Arg Ala Ile Asn Ser Ile Pro Ile Arg Ile Val Val Phe Tyr Val Leu
225                 230                 235                 240

Ala Leu Ala Val Ile Met Met Val Thr Pro Trp Asp Gln Val Arg Ala
                245                 250                 255

Asp Asn Ser Pro Phe Val Gln Met Phe Ala Leu Ala Gly Ile Pro Ala
            260                 265                 270

Ala Ala Gly Ile Ile Asn Phe Val Val Ile Thr Ser Ala Ala Ser Ser
        275                 280                 285

Ala Asn Ser Gly Ile Phe Ser Thr Ser Arg Met Leu Tyr Gly Leu Ser
```

```
    290                 295                 300

Leu Glu Gly Ala Ala Pro Lys Arg Trp Ser Arg Leu Ser Lys Asn Leu
305                 310                 315                 320

Val Pro Ala Arg Gly Leu Thr Phe Ser Val Ile Cys Leu Ile Pro Ala
                325                 330                 335

Val Gly Leu Leu Tyr Ala Gly Gly Thr Val Ile Glu Ala Phe Thr Leu
            340                 345                 350

Ile Thr Thr Val Ser Ser Val Leu Phe Met Val Val Trp Ser Tyr Ile
        355                 360                 365

Leu Val Ala Tyr Ile Val Tyr Arg Arg Asn Ser Pro Glu Leu His Lys
    370                 375                 380

Lys Ser Ile Phe Lys Met Pro Gly Gly Val Val Met Ala Val Val Val
385                 390                 395                 400

Leu Val Phe Phe Ala Ala Met Leu Val Val Leu Ser Leu Glu Pro Asp
                405                 410                 415

Thr Arg Ala Ala Leu Ile Ala Thr Pro Val Trp Phe Ile Ile Leu Gly
            420                 425                 430

Ile Gly Trp Leu Ser Ile Gly Gly Ala Lys Gly Ala Lys His Arg Ser
        435                 440                 445

Gln Ile Thr Ser His
    450
```

US 2006/0160180 A1 Jul. 20, 2006

<210> 199
<211> 1242
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1219)
<223> RXA00090

<400> 199
ttgatcagcc gaaccatcat cgcgcctttc gaaattccag tttcagtaat cctgggcatc 60

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atcggcgcag tggtcttcgt gatcatgatt gtgaggcaac gtg gcc gtg gat aaa   115
                                              Val Ala Val Asp Lys
                                                1               5

gat att gaa aac cgc acc tca gac ctt tct cga tgg gaa act atg gag   163
Asp Ile Glu Asn Arg Thr Ser Asp Leu Ser Arg Trp Glu Thr Met Glu
                10                  15                  20

gaa tca gca acg gtc gag gga cgc acc gat gtc gaa cta gca tca gcg   211
Glu Ser Ala Thr Val Glu Gly Arg Thr Asp Val Glu Leu Ala Ser Ala
            25                  30                  35

ccg agc aaa cga cgc acc tca ggt gca ttc caa aca gcg cgc gcc aag   259
Pro Ser Lys Arg Arg Thr Ser Gly Ala Phe Gln Thr Ala Arg Ala Lys
        40                  45                  50
```

```
cgc cgc tac tgg atc atc atg gcc gcg ctg ctg gtc acc gcg ctt gcc   307
Arg Arg Tyr Trp Ile Ile Met Ala Ala Leu Leu Val Thr Ala Leu Ala
     55                  60                  65

ttc acc tgg ggc ctc att tgg tac aag aac ccg atg ccc gtt ggg cat   355
Phe Thr Trp Gly Leu Ile Trp Tyr Lys Asn Pro Met Pro Val Gly His
 70                  75                  80                  85

ccg gcc ttc gcg ctg att gca gaa cga cgc atg gag tcg gtc ttt gtc   403
Pro Ala Phe Ala Leu Ile Ala Glu Arg Arg Met Glu Ser Val Phe Val
                 90                  95                 100

atg ctg att gtt gcg gtt tgc caa ggc ttt gcg acg gtt gcg ttc cag   451
Met Leu Ile Val Ala Val Cys Gln Gly Phe Ala Thr Val Ala Phe Gln
            105                 110                 115

acc gtc acc aac aac cgc att atc acg ccg tcg atc atg ggc ttt gaa   499
Thr Val Thr Asn Asn Arg Ile Ile Thr Pro Ser Ile Met Gly Phe Glu
        120                 125                 130

tct ctc tac aca ctg att cat acc tcc aca gtg ttc ttc ttc ggc gca   547
Ser Leu Tyr Thr Leu Ile His Thr Ser Thr Val Phe Phe Phe Gly Ala
    135                 140                 145

act gca ctg ctg gcc acc aga aat ctc gaa atg ttt gtc ggc cag ctg   595
Thr Ala Leu Leu Ala Thr Arg Asn Leu Glu Met Phe Val Gly Gln Leu
150                 155                 160                 165

gtg atc atg gtt ctt ttg acc ttg gtc ctc tac acc tgg ctg ctt tcc   643
Val Ile Met Val Leu Leu Thr Leu Val Leu Tyr Thr Trp Leu Leu Ser
                170                 175                 180

gga aaa cgc ggc gat atg cac gcc atg ctg ctt gtc ggc atc atc att   691
Gly Lys Arg Gly Asp Met His Ala Met Leu Leu Val Gly Ile Ile Ile
            185                 190                 195

ggt ggc gga ctc gga tcc atc tcc acc ttt atg cag cgc att ctg acc   739
Gly Gly Gly Leu Gly Ser Ile Ser Thr Phe Met Gln Arg Ile Leu Thr
        200                 205                 210

cca tca gaa ttc gat att ctt tcc gcc cga ctt ttc gga tca gta aac   787
Pro Ser Glu Phe Asp Ile Leu Ser Ala Arg Leu Phe Gly Ser Val Asn
    215                 220                 225

aac gcg gaa acc gaa tac ttc cca att gct gtt cca cta gta gta gtg   835
Asn Ala Glu Thr Glu Tyr Phe Pro Ile Ala Val Pro Leu Val Val Val
230                 235                 240                 245

gcg tcc gtc ttg ttg ctg cta agc tct cga cgc ctc aac gtt gta ggg   883
Ala Ser Val Leu Leu Leu Leu Ser Ser Arg Arg Leu Asn Val Val Gly
                250                 255                 260

ctt ggc aaa gat gcc gca acc aac ctt gga att aat cac cga cga tcc   931
Leu Gly Lys Asp Ala Ala Thr Asn Leu Gly Ile Asn His Arg Arg Ser
            265                 270                 275

tcc att tac aca ctg gtt ctc gtc tct gta tta atg gca gta tcc acc   979
Ser Ile Tyr Thr Leu Val Leu Val Ser Val Leu Met Ala Val Ser Thr
        280                 285                 290
```

```
gca ctt gtc gga ccg atg aca ttc ctc gga ttc ttg gtc gcg acc ttg   1027
Ala Leu Val Gly Pro Met Thr Phe Leu Gly Phe Leu Val Ala Thr Leu
    295                 300                 305

gca tat caa ttc gcc gac act tac gac cac cga tac atc ctt ccg atg   1075
Ala Tyr Gln Phe Ala Asp Thr Tyr Asp His Arg Tyr Ile Leu Pro Met
310                 315                 320                 325

tcc gca ctc atc gga ttc gtc gta ctc agc ggc gct tac ttt gtc atg   1123
Ser Ala Leu Ile Gly Phe Val Val Leu Ser Gly Ala Tyr Phe Val Met
                330                 335                 340

aac cac gtg ttc cgc gca caa ggc gtc gtg tcc atc att att gag atg   1171
Asn His Val Phe Arg Ala Gln Gly Val Val Ser Ile Ile Ile Glu Met
            345                 350                 355

gtc ggc ggt acc gtc ttc ctc atc gtc atc ctc aga aag ggc aga ctg   1219
Val Gly Gly Thr Val Phe Leu Ile Val Ile Leu Arg Lys Gly Arg Leu
        360                 365                 370

tgattacgtt aactaatgtc cgc                                        1242


<210> 200
<211> 373
<212> PRT
<213> Corynebacterium glutamicum

<400> 200
Val Ala Val Asp Lys Asp Ile Glu Asn Arg Thr Ser Asp Leu Ser Arg
  1               5                  10                  15

Trp Glu Thr Met Glu Glu Ser Ala Thr Val Glu Gly Arg Thr Asp Val
             20                  25                  30

Glu Leu Ala Ser Ala Pro Ser Lys Arg Arg Thr Ser Gly Ala Phe Gln
         35                  40                  45

Thr Ala Arg Ala Lys Arg Arg Tyr Trp Ile Ile Met Ala Ala Leu Leu
     50                  55                  60

Val Thr Ala Leu Ala Phe Thr Trp Gly Leu Ile Trp Tyr Lys Asn Pro
 65                  70                  75                  80

Met Pro Val Gly His Pro Ala Phe Ala Leu Ile Ala Glu Arg Arg Met
                85                  90                  95

Glu Ser Val Phe Val Met Leu Ile Val Ala Val Cys Gln Gly Phe Ala
            100                 105                 110

Thr Val Ala Phe Gln Thr Val Thr Asn Asn Arg Ile Ile Thr Pro Ser
        115                 120                 125

Ile Met Gly Phe Glu Ser Leu Tyr Thr Leu Ile His Thr Ser Thr Val
    130                 135                 140

Phe Phe Phe Gly Ala Thr Ala Leu Leu Ala Thr Arg Asn Leu Glu Met
145                 150                 155                 160

Phe Val Gly Gln Leu Val Ile Met Val Leu Leu Thr Leu Val Leu Tyr
                165                 170                 175
```

Thr Trp Leu Leu Ser Gly Lys Arg Gly Asp Met His Ala Met Leu Leu
180 185 190

Val Gly Ile Ile Ile Gly Gly Gly Leu Gly Ser Ile Ser Thr Phe Met
195 200 205

Gln Arg Ile Leu Thr Pro Ser Glu Phe Asp Ile Leu Ser Ala Arg Leu
210 215 220

Phe Gly Ser Val Asn Asn Ala Glu Thr Glu Tyr Phe Pro Ile Ala Val
225 230 235 240

Pro Leu Val Val Val Ala Ser Val Leu Leu Leu Leu Ser Ser Arg Arg
245 250 255

Leu Asn Val Val Gly Leu Gly Lys Asp Ala Ala Thr Asn Leu Gly Ile
260 265 270

Asn His Arg Arg Ser Ser Ile Tyr Thr Leu Val Leu Val Ser Val Leu
275 280 285

Met Ala Val Ser Thr Ala Leu Val Gly Pro Met Thr Phe Leu Gly Phe
290 295 300

Leu Val Ala Thr Leu Ala Tyr Gln Phe Ala Asp Thr Tyr Asp His Arg
305 310 315 320

Tyr Ile Leu Pro Met Ser Ala Leu Ile Gly Phe Val Val Leu Ser Gly
325 330 335

Ala Tyr Phe Val Met Asn His Val Phe Arg Ala Gln Gly Val Val Ser
340 345 350

Ile Ile Ile Glu Met Val Gly Gly Thr Val Phe Leu Ile Val Ile Leu
355 360 365

Arg Lys Gly Arg Leu
370

<210> 201
<211> 1122
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1099)
<223> RXA00089

<400> 201
acctcgtttt ggccgcaagt tctcgttagt taaaaactgt aggaaaccag gttccacaca 60

tgacacacaa tcggtttaac agggaagggg atcggcactg atg gca aca cca gca 115
Met Ala Thr Pro Ala
1 5

tcg gct ccc act tcc gaa cca cgt ctc aaa cgc acc aga gcc aag ctt 163
Ser Ala Pro Thr Ser Glu Pro Arg Leu Lys Arg Thr Arg Ala Lys Leu
10 15 20

```
ttt gat tgg aag ctt ctc atc ggc atc att ttc gtc gcc ggc ctc gtg   211
Phe Asp Trp Lys Leu Leu Ile Gly Ile Ile Phe Val Ala Gly Leu Val
            25                  30                  35

gtg ctt tcc ctc ctc acc ggc caa tac gac att ttc ggt ggc gat gat   259
Val Leu Ser Leu Leu Thr Gly Gln Tyr Asp Ile Phe Gly Gly Asp Asp
        40                  45                  50

ggc caa ctg atg ttc gag gca gtt cgc atc ccg cgt acc gtt tcc ctc   307
Gly Gln Leu Met Phe Glu Ala Val Arg Ile Pro Arg Thr Val Ser Leu
    55                  60                  65

att ttg tcc ggt gca gca atg gcg atg tgt ggc tta gtc atg cag ctg   355
Ile Leu Ser Gly Ala Ala Met Ala Met Cys Gly Leu Val Met Gln Leu
70                  75                  80                  85

ttg acc caa aac aaa ttc gtg gaa ccc agc acc aca gga aca acc gaa   403
Leu Thr Gln Asn Lys Phe Val Glu Pro Ser Thr Thr Gly Thr Thr Glu
                90                  95                  100

tgg gca ggt ctt ggc ctc ctc ttc gtg att tac ttc gtg cca gcc gcg   451
Trp Ala Gly Leu Gly Leu Leu Phe Val Ile Tyr Phe Val Pro Ala Ala
            105                 110                 115

acc gtt ttg gat cgc atg ctc ggt gcc gtg gtg ttt tcc ttc atc gga   499
Thr Val Leu Asp Arg Met Leu Gly Ala Val Val Phe Ser Phe Ile Gly
        120                 125                 130

acc atg gtg ttc ttc ctc ttt cta cgc cga gta aca ctg cgt tcc tca   547
Thr Met Val Phe Phe Leu Phe Leu Arg Arg Val Thr Leu Arg Ser Ser
    135                 140                 145

ttg atc gtc ccg att atc ggc atc atg ctc ggt gcc gtg gtg tca tcg   595
Leu Ile Val Pro Ile Ile Gly Ile Met Leu Gly Ala Val Val Ser Ser
150                 155                 160                 165

atc tcc agc ttc ttc gcc ttg caa ttc gac atg ctc cag caa ttg gga   643
Ile Ser Ser Phe Phe Ala Leu Gln Phe Asp Met Leu Gln Gln Leu Gly
                170                 175                 180

aca tgg ttt gcg ggt tcc ttt aat aca gtg ttc cgc gga cag tac gaa   691
Thr Trp Phe Ala Gly Ser Phe Asn Thr Val Phe Arg Gly Gln Tyr Glu
            185                 190                 195

gtg ctg tgg atc gtt gtc atc gtc gtt att gca gtg ttc ttc ttc gca   739
Val Leu Trp Ile Val Val Ile Val Val Ile Ala Val Phe Phe Phe Ala
        200                 205                 210

gac cgg ctc acc gta gct ggc ctt ggc gag gaa atc gcg aca aac gtg   787
Asp Arg Leu Thr Val Ala Gly Leu Gly Glu Glu Ile Ala Thr Asn Val
    215                 220                 225

ggt ctc aat tac aac cgc atg gtc ctt atc gga act ggc ctc atc gcc   835
Gly Leu Asn Tyr Asn Arg Met Val Leu Ile Gly Thr Gly Leu Ile Ala
230                 235                 240                 245

atc gca aca ggt gtg gtc acc gtc gtg gtt ggt agc ctg cca ttc ctc   883
Ile Ala Thr Gly Val Val Thr Val Val Val Gly Ser Leu Pro Phe Leu
                250                 255                 260
```

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```
gga ctc atc gtg ccc aac gtt gtg tcc atg ttc cgt ggc gat gac ctg   931
Gly Leu Ile Val Pro Asn Val Val Ser Met Phe Arg Gly Asp Asp Leu
            265                 270                 275

cgc tcg aac ctg cca tgg gta tgc cta acc ggc atc gcg atc gta acc   979
Arg Ser Asn Leu Pro Trp Val Cys Leu Thr Gly Ile Ala Ile Val Thr
        280                 285                 290

att tgt gac ttg atc agc cga acc atc atc gcg cct ttc gaa att cca   1027
Ile Cys Asp Leu Ile Ser Arg Thr Ile Ile Ala Pro Phe Glu Ile Pro
    295                 300                 305

gtt tca gta atc ctg ggc atc atc ggc gca gtg gtc ttc gtg atc atg   1075
Val Ser Val Ile Leu Gly Ile Ile Gly Ala Val Val Phe Val Ile Met
310                 315                 320                 325

att gtg agg caa cgt ggc cgt gga taaagatatt gaaaaccgca cct         1122
Ile Val Arg Gln Arg Gly Arg Gly
                330
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<210> 202
<211> 333
<212> PRT
<213> Corynebacterium glutamicum

<400> 202

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Met Ala Thr Pro Ala Ser Ala Pro Thr Ser Glu Pro Arg Leu Lys Arg
  1               5                  10                  15

Thr Arg Ala Lys Leu Phe Asp Trp Lys Leu Leu Ile Gly Ile Ile Phe
             20                  25                  30

Val Ala Gly Leu Val Val Leu Ser Leu Leu Thr Gly Gln Tyr Asp Ile
         35                  40                  45

Phe Gly Gly Asp Asp Gly Gln Leu Met Phe Glu Ala Val Arg Ile Pro
     50                  55                  60

Arg Thr Val Ser Leu Ile Leu Ser Gly Ala Ala Met Ala Met Cys Gly
 65                  70                  75                  80

Leu Val Met Gln Leu Leu Thr Gln Asn Lys Phe Val Glu Pro Ser Thr
                 85                  90                  95

Thr Gly Thr Thr Glu Trp Ala Gly Leu Gly Leu Leu Phe Val Ile Tyr
            100                 105                 110

Phe Val Pro Ala Ala Thr Val Leu Asp Arg Met Leu Gly Ala Val Val
        115                 120                 125

Phe Ser Phe Ile Gly Thr Met Val Phe Phe Leu Phe Leu Arg Arg Val
    130                 135                 140

Thr Leu Arg Ser Ser Leu Ile Val Pro Ile Ile Gly Ile Met Leu Gly
145                 150                 155                 160

Ala Val Val Ser Ser Ile Ser Ser Phe Phe Ala Leu Gln Phe Asp Met
                165                 170                 175

Leu Gln Gln Leu Gly Thr Trp Phe Ala Gly Ser Phe Asn Thr Val Phe
```

```
            180                 185                 190

Arg Gly Gln Tyr Glu Val Leu Trp Ile Val Val Ile Val Val Ile Ala
        195                 200                 205

Val Phe Phe Phe Ala Asp Arg Leu Thr Val Ala Gly Leu Gly Glu Glu
    210                 215                 220

Ile Ala Thr Asn Val Gly Leu Asn Tyr Asn Arg Met Val Leu Ile Gly
225                 230                 235                 240

Thr Gly Leu Ile Ala Ile Ala Thr Gly Val Val Thr Val Val Val Gly
                245                 250                 255

Ser Leu Pro Phe Leu Gly Leu Ile Val Pro Asn Val Val Ser Met Phe
            260                 265                 270

Arg Gly Asp Asp Leu Arg Ser Asn Leu Pro Trp Val Cys Leu Thr Gly
        275                 280                 285

Ile Ala Ile Val Thr Ile Cys Asp Leu Ile Ser Arg Thr Ile Ile Ala
    290                 295                 300

Pro Phe Glu Ile Pro Val Ser Val Ile Leu Gly Ile Ile Gly Ala Val
305                 310                 315                 320

Val Phe Val Ile Met Ile Val Arg Gln Arg Gly Arg Gly
                325                 330


<210> 203
<211> 749
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(726)
<223> RXN01285

<400> 203
ctc aac gtc acc atc ccc gac aac acc ttc acc gcc atc atc ggc ccc   48
Leu Asn Val Thr Ile Pro Asp Asn Thr Phe Thr Ala Ile Ile Gly Pro
  1               5                  10                  15

aac ggc tgc ggc aaa tcc acc ctg ctc cgc ggt ttc tcc cgc gtg ctc   96
Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Gly Phe Ser Arg Val Leu
             20                  25                  30

aat ccg cag cac ggc aaa gtg ctt ctc gac ggt cgg caa ctc gat tca   144
Asn Pro Gln His Gly Lys Val Leu Leu Asp Gly Arg Gln Leu Asp Ser
         35                  40                  45

ttc aag cct aaa gag atc gcc cga gaa cta ggc ctg ctg cca cag acc   192
Phe Lys Pro Lys Glu Ile Ala Arg Glu Leu Gly Leu Leu Pro Gln Thr
     50                  55                  60

tcc atc gcc cca gaa ggc atc cgg gtt tac gat ctc atc gcg cgc ggg   240
Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile Ala Arg Gly
 65                  70                  75                  80
```

```
cgc gct ccc tac caa agc ctc ata caa caa tgg cgc acc tcc gac gaa   288
Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr Ser Asp Glu
                 85                  90                  95

gac gcc gtc gcg caa gcg ctc gcc tcc acg aat ctc acc gaa ctt gca   336
Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr Glu Leu Ala
            100                 105                 110

gct cgc ctc gtc gat gaa ctc tcc ggt ggc cag cgc caa cga gtg tgg   384
Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Trp
        115                 120                 125

gtg gcc atg ttg ctc gcc cag caa aca ccg atc atg ctt ctc gac gag   432
Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu Leu Asp Glu
    130                 135                 140

ccc acc acc ttc ctc gac atc gcc cac caa tac gaa ctc ttg gaa ttg   480
Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu Leu Glu Leu
145                 150                 155                 160

ctg cgc gca ttc aac gag gcc ggg aaa act gtg gtc act gtg ctt cac   528
Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr Val Leu His
                165                 170                 175

gat ctc aac caa gcc gcc cgc tac gcc gac cac ctc atc gtg atg aaa   576
Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile Val Met Lys
            180                 185                 190

gat ggg cac gta cat gcc acg ggc aca ccg gag gaa gtc tta act gcc   624
Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val Leu Thr Ala
        195                 200                 205

gag atg gtt caa gga gtt ttt ggc ctg ccc tgc atc atc tcc cca gac   672
Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile Ser Pro Asp
    210                 215                 220

ccc gtc aca gga acc ccc acc gtc gtt ccc ctc agt cgg tct cgc gca   720
Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg Ser Arg Ala
225                 230                 235                 240

gga gct taagtagcta cccctccaac gga                                 749
Gly Ala
```

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<210> 204
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 204

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Leu Asn Val Thr Ile Pro Asp Asn Thr Phe Thr Ala Ile Ile Gly Pro
  1               5                  10                  15

Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Gly Phe Ser Arg Val Leu
             20                  25                  30

Asn Pro Gln His Gly Lys Val Leu Leu Asp Gly Arg Gln Leu Asp Ser
         35                  40                  45

Phe Lys Pro Lys Glu Ile Ala Arg Glu Leu Gly Leu Leu Pro Gln Thr
```

```
     50                  55                  60

Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile Ala Arg Gly
 65                  70                  75                  80

Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr Ser Asp Glu
                85                  90                  95

Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr Glu Leu Ala
            100                 105                 110

Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Trp
        115                 120                 125

Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu Leu Asp Glu
    130                 135                 140

Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu Leu Glu Leu
145                 150                 155                 160

Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr Val Leu His
                165                 170                 175

Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile Val Met Lys
            180                 185                 190

Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val Leu Thr Ala
        195                 200                 205

Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile Ser Pro Asp
    210                 215                 220

Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg Ser Arg Ala
225                 230                 235                 240

Gly Ala
```

Substitute Sheet (Rule 26)

<210> 205
<211> 566
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(543)
<223> FRXA01285

<400> 205

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cca cag acc tcc atc gcc cca gaa ggc atc cgg gtt tac gat ctc atc   48
Pro Gln Thr Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile
  1               5                  10                  15

gcg cgc ggg cgc gct ccc tac caa agc ctc ata caa caa tgg cgc acc   96
Ala Arg Gly Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr
             20                  25                  30

tcc gac gaa gac gcc gtc gcg caa gcg ctc gcc tcc acg aat ctc acc   144
Ser Asp Glu Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr
         35                  40                  45
```

```
gaa ctt gca gct cgc ctc gtc gat gaa ctc tcc ggt ggc cag cgc caa   192
Glu Leu Ala Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln
     50                  55                  60

cga gtg tgg gtg gcc atg ttg ctc gcc cag caa aca ccg atc atg ctt   240
Arg Val Trp Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu
 65                  70                  75                  80

ctc gac gag ccc acc acc ttc ctc gac atc gcc cac caa tac gaa ctc   288
Leu Asp Glu Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu
                85                  90                  95

ttg gaa ttg ctg cgc gca ttc aac gag gcc ggg aaa act gtg gtc act   336
Leu Glu Leu Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr
            100                 105                 110

gtg ctt cac gat ctc aac caa gcc gcc cgc tac gcc gac cac ctc atc   384
Val Leu His Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile
        115                 120                 125

gtg atg aaa gat ggg cac gta cat gcc acg ggc aca ccg gag gaa gtc   432
Val Met Lys Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val
    130                 135                 140

tta act gcc gag atg gtt caa gga gtt ttt ggc ctg ccc tgc atc atc   480
Leu Thr Ala Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile
145                 150                 155                 160

tcc cca gac ccc gtc aca gga acc ccc acc gtc gtt ccc ctc agt cgg   528
Ser Pro Asp Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg
                165                 170                 175

tct cgc gca gga gct taagtagcta ccctccaac gga                     566
Ser Arg Ala Gly Ala
            180
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09/25/2003 15:29 [ID: 0325]

<210> 206
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 206

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Pro Gln Thr Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile
  1               5                  10                  15

Ala Arg Gly Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr
             20                  25                  30

Ser Asp Glu Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr
         35                  40                  45

Glu Leu Ala Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln
     50                  55                  60

Arg Val Trp Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu
 65                  70                  75                  80

Leu Asp Glu Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu
                85                  90                  95
```

Leu Glu Leu Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr
100 105 110

Val Leu His Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile
115 120 125

Val Met Lys Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val
130 135 140

Leu Thr Ala Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile
145 150 155 160

Ser Pro Asp Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg
165 170 175

Ser Arg Ala Gly Ala
180

<210> 207
<211> 936
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(913)
<223> RXA02728

<400> 207
atcccatacg ttgccttccg atcggcattt tcacagcgct ggtcggcggc ccaacattct 60

tcataatgtt gcgccgaatg atgaaaaggg cgtgcactaa atg gcc att gtt tcc 115
Met Ala Ile Val Ser
1 5

ctc gac aac gtc acc gta tcc att gaa gga aaa aag ctt ctc gac gcc 163
Leu Asp Asn Val Thr Val Ser Ile Glu Gly Lys Lys Leu Leu Asp Ala
10 15 20

gtc tcc ctc aag gcc tac ccc ggg gaa gtg ttg gga ctc atc ggc cca 211
Val Ser Leu Lys Ala Tyr Pro Gly Glu Val Leu Gly Leu Ile Gly Pro
25 30 35

aac ggt gcc gga aaa tcc act ctg ctg agt gtc ctt tca ggc gat cgg 259
Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Val Leu Ser Gly Asp Arg
40 45 50

ctt ccc gat tca ggc gaa gtc aac gtc ggt ggc tta gat ccc gca aca 307
Leu Pro Asp Ser Gly Glu Val Asn Val Gly Gly Leu Asp Pro Ala Thr
55 60 65

gca gcg gca tcc gat atg gcc agg gtg cga gca gtc atg ctt caa gat 355
Ala Ala Ala Ser Asp Met Ala Arg Val Arg Ala Val Met Leu Gln Asp
70 75 80 85

gtc agc gtg gca ttt tcc ttc ctc gtg tgg gac gtc gta gaa atg ggc 403
Val Ser Val Ala Phe Ser Phe Leu Val Trp Asp Val Val Glu Met Gly
90 95 100

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agg cgg ccg tgg cag aag gcg tca acc ccc gaa gag gat cat gaa atc   451
Arg Arg Pro Trp Gln Lys Ala Ser Thr Pro Glu Glu Asp His Glu Ile
            105                 110                 115

atc gaa gca gcg ctt gcc gcc acc tcg gta tcg cac ctt gcc gaa cgt   499
Ile Glu Ala Ala Leu Ala Ala Thr Ser Val Ser His Leu Ala Glu Arg
        120                 125                 130

gaa atc acc aca ctg tca ggc ggc gag cgg gca cgc gtt gcc ttg tcc   547
Glu Ile Thr Thr Leu Ser Gly Gly Glu Arg Ala Arg Val Ala Leu Ser
    135                 140                 145

cgt gtc ctt gct cag caa acc ccc att gtg ctg ttg gac gaa cca aca   595
Arg Val Leu Ala Gln Gln Thr Pro Ile Val Leu Leu Asp Glu Pro Thr
150                 155                 160                 165

gcc gcg atg gat atc agc cac caa gaa caa act ctg ggc aca gcg cga   643
Ala Ala Met Asp Ile Ser His Gln Glu Gln Thr Leu Gly Thr Ala Arg
                170                 175                 180

gca ctg gca gcc gcc ggg gca gca gtg att gtg gtc ctt cat gat ctc   691
Ala Leu Ala Ala Ala Gly Ala Ala Val Ile Val Val Leu His Asp Leu
            185                 190                 195

aat gcg gcc gct gca tat tgc gac agc att gtg tgt ctc agt gat ggt   739
Asn Ala Ala Ala Ala Tyr Cys Asp Ser Ile Val Cys Leu Ser Asp Gly
        200                 205                 210

cga gtg att gcc tcc ggt tct gtt gat cag gtg tat tcc acg gaa acg   787
Arg Val Ile Ala Ser Gly Ser Val Asp Gln Val Tyr Ser Thr Glu Thr
    215                 220                 225

ctg tcc cgt gtt tac ggt tgg cct atc agg gtc gat cat agt gga aaa   835
Leu Ser Arg Val Tyr Gly Trp Pro Ile Arg Val Asp His Ser Gly Lys
230                 235                 240                 245

tat gtt cga gtg gag ccg gac cgt tct gag gcg aat tta ccc tcc gta   883
Tyr Val Arg Val Glu Pro Asp Arg Ser Glu Ala Asn Leu Pro Ser Val
                250                 255                 260

cta cag gtg aaa aat acg gtt tca cca gct tagatacatg actaactaag     933
Leu Gln Val Lys Asn Thr Val Ser Pro Ala
            265                 270

gtt                                                               936
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<210> 208
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 208

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Met Ala Ile Val Ser Leu Asp Asn Val Thr Val Ser Ile Glu Gly Lys
  1               5                  10                  15

Lys Leu Leu Asp Ala Val Ser Leu Lys Ala Tyr Pro Gly Glu Val Leu
             20                  25                  30

Gly Leu Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Val
         35                  40                  45
```

Leu Ser Gly Asp Arg Leu Pro Asp Ser Gly Glu Val Asn Val Gly Gly
50 55 60

Leu Asp Pro Ala Thr Ala Ala Ala Ser Asp Met Ala Arg Val Arg Ala
65 70 75 80

Val Met Leu Gln Asp Val Ser Val Ala Phe Ser Phe Leu Val Trp Asp
85 90 95

Val Val Glu Met Gly Arg Arg Pro Trp Gln Lys Ala Ser Thr Pro Glu
100 105 110

Glu Asp His Glu Ile Ile Glu Ala Ala Leu Ala Ala Thr Ser Val Ser
115 120 125

His Leu Ala Glu Arg Glu Ile Thr Thr Leu Ser Gly Gly Glu Arg Ala
130 135 140

Arg Val Ala Leu Ser Arg Val Leu Ala Gln Gln Thr Pro Ile Val Leu
145 150 155 160

Leu Asp Glu Pro Thr Ala Ala Met Asp Ile Ser His Gln Glu Gln Thr
165 170 175

Leu Gly Thr Ala Arg Ala Leu Ala Ala Ala Gly Ala Ala Val Ile Val
180 185 190

Val Leu His Asp Leu Asn Ala Ala Ala Ala Tyr Cys Asp Ser Ile Val
195 200 205

Cys Leu Ser Asp Gly Arg Val Ile Ala Ser Gly Ser Val Asp Gln Val
210 215 220

Tyr Ser Thr Glu Thr Leu Ser Arg Val Tyr Gly Trp Pro Ile Arg Val
225 230 235 240

Asp His Ser Gly Lys Tyr Val Arg Val Glu Pro Asp Arg Ser Glu Ala
245 250 255

Asn Leu Pro Ser Val Leu Gln Val Lys Asn Thr Val Ser Pro Ala
260 265 270

<210> 209
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)
<223> RXN03080

<400> 209
cttgcaaaca ggcgtggtgg tggcgttcat tggctcacca attttccttt atttactgct 60

cagcatgcgc aagcgacgcg gattggggct gtaaaaactc atg cct caa tta gtt 115
Met Pro Gln Leu Val
1 5

```
gaa att cgt gat ctc aac gtt gaa ttc ccc tct cgc cat gca gtg aaa   163
Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser Arg His Ala Val Lys
                 10                  15                  20

aac gtg tct ttt tct gca cct gct gga aaa gtc acc gca ctg att ggc   211
Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val Thr Ala Leu Ile Gly
             25                  30                  35

cca aat ggt gct ggt aaa agt act gcc ctt tcg gcg att gca gga ttg   259
Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser Ala Ile Ala Gly Leu
         40                  45                  50

gtt gaa tcc acc ggc gag gta atg gtt ggt ggg agt ggg gtt gcg tcg   307
Val Glu Ser Thr Gly Glu Val Met Val Gly Gly Ser Gly Val Ala Ser
     55                  60                  65

aaa agc gct aaa gcc cga gcc cgc ctg ctc tca ctc gtg ccg caa aac   355
Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser Leu Val Pro Gln Asn
 70                  75                  80                  85

acc gag ttg cgc att ggt ttt agt gca cgc gac gtt gtc gcg atg ggc   403
Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp Val Val Ala Met Gly
                 90                  95                 100

cgc tac ccg cat cgt ggc cgc ttc gcc gtg gag acc gac gca gat cga   451
Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu Thr Asp Ala Asp Arg
            105                 110                 115

cgc gcc acc gat gac gcc ctg cgc gcc atc aac gcg ctc gac atc gcc   499
Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn Ala Leu Asp Ile Ala
        120                 125                 130

gag cag ccc gtc aac gaa tta tcg ggc ggc cag cag cag ctc atc cac   547
Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln Gln Gln Leu Ile His
    135                 140                 145

atc ggc cga gcg ctc gcc caa gac acc gcc gtc gtg ctt ctc gac gag   595
Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val Val Leu Leu Asp Glu
150                 155                 160                 165

ccc gtc tcc gcc ctt gat cta cgg cac caa gtt gaa gtc ctt caa ctc   643
Pro Val Ser Ala Leu Asp Leu Arg His Gln Val Glu Val Leu Gln Leu
                170                 175                 180

ctg cgc gcc cga gct aat tcc ggc acc acc gtg atc gtc gtc ctt cac   691
Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val Ile Val Val Leu His
            185                 190                 195

gat ctc aac cac gtt gcc cgt tgg tgc gac cat gca gtg ttg atg gcc   739
Asp Leu Asn His Val Ala Arg Trp Cys Asp His Ala Val Leu Met Ala
        200                 205                 210

gac ggc gaa gtt gtc tcc caa ggt gac atc cgc gag gtg ctc gaa cct   787
Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg Glu Val Leu Glu Pro
    215                 220                 225

gcc aca ctg tcc acc gtg tac gga ctg ccc att gcg gtg cgc gat gat   835
Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile Ala Val Arg Asp Asp
230                 235                 240                 245

ccc gaa acc agc tca ctt cgc gtg atc ccg cat cca aat ccc ttt       880
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Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His Pro Asn Pro Phe
250 255 260

tgattgaaag tttgacttaa aaa 903

<210> 210
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 210
Met Pro Gln Leu Val Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser
1 5 10 15

Arg His Ala Val Lys Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val
20 25 30

Thr Ala Leu Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser
35 40 45

Ala Ile Ala Gly Leu Val Glu Ser Thr Gly Glu Val Met Val Gly Gly
50 55 60

Ser Gly Val Ala Ser Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser
65 70 75 80

Leu Val Pro Gln Asn Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp
85 90 95

Val Val Ala Met Gly Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu
100 105 110

Thr Asp Ala Asp Arg Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn
115 120 125

Ala Leu Asp Ile Ala Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln
130 135 140

Gln Gln Leu Ile His Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val
145 150 155 160

Val Leu Leu Asp Glu Pro Val Ser Ala Leu Asp Leu Arg His Gln Val
165 170 175

Glu Val Leu Gln Leu Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val
180 185 190

Ile Val Val Leu His Asp Leu Asn His Val Ala Arg Trp Cys Asp His
195 200 205

Ala Val Leu Met Ala Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg
210 215 220

Glu Val Leu Glu Pro Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile
225 230 235 240

Ala Val Arg Asp Asp Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His
245 250 255

Pro Asn Pro Phe

260

<210> 211
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)
<223> FRXA02864

<400> 211
cttgcaaaca ggcgtggtgg tggcgttcat tggctcacca attttccttt atttactgct 60

cagcatgcgc aagcgacgcg gattggggct gtaaaaactc atg cct caa tta gtt 115
Met Pro Gln Leu Val
1 5

gaa att cgt gat ctc aac gtt gaa ttc ccc tct cgc cat gca gtg aaa 163
Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser Arg His Ala Val Lys
10 15 20

aac gtg tct ttt tct gca cct gct gga aaa gtc acc gca ctg att ggc 211
Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val Thr Ala Leu Ile Gly
25 30 35

cca aat ggt gct ggt aaa agt act gcc ctt tcg gcg att gca gga ttg 259
Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser Ala Ile Ala Gly Leu
40 45 50

gtt gaa tcc acc ggc gag gta atg gtt ggt ggg agt ggg gtt gcg tcg 307
Val Glu Ser Thr Gly Glu Val Met Val Gly Gly Ser Gly Val Ala Ser
55 60 65

aaa agc gct aaa gcc cga gcc cgc ctg ctc tca ctc gtg ccg caa aac 355
Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser Leu Val Pro Gln Asn
70 75 80 85

acc gag ttg cgc att ggt ttt agt gca cgc gac gtt gtc gcg atg ggc 403
Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp Val Val Ala Met Gly
90 95 100

cgc tac ccg cat cgt ggc cgc ttc gcc gtg gag acc gac gca gat cga 451
Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu Thr Asp Ala Asp Arg
105 110 115

cgc gcc acc gat gac gcc ctg cgc gcc atc aac gcg ctc gac atc gcc 499
Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn Ala Leu Asp Ile Ala
120 125 130

gag cag ccc gtc aac gaa tta tcg ggc ggc cag cag cag ctc atc cac 547
Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln Gln Leu Ile His
135 140 145

atc ggc cga gcg ctc gcc caa gac acc gcc gtc gtg ctt ctc gac gag 595
Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val Val Leu Leu Asp Glu
150 155 160 165

ccc gtc tcc gcc ctt gat cta cgg cac caa gtt gaa gtc ctt caa ctc 643

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Pro Val Ser Ala Leu Asp Leu Arg His Gln Val Glu Val Leu Gln Leu
                  170                 175                 180

ctg cgc gcc cga gct aat tcc ggc acc acc gtg atc gtc gtc ctt cac   691
Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val Ile Val Val Leu His
            185                 190                 195

gat ctc aac cac gtt gcc cgt tgg tgc gac cat gca gtg ttg atg gcc   739
Asp Leu Asn His Val Ala Arg Trp Cys Asp His Ala Val Leu Met Ala
        200                 205                 210

gac ggc gaa gtt gtc tcc caa ggt gac atc cgc gag gtg ctc gaa cct   787
Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg Glu Val Leu Glu Pro
    215                 220                 225

gcc aca ctg tcc acc gtg tac gga ctg ccc att gcg gtg cgc gat gat   835
Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile Ala Val Arg Asp Asp
230                 235                 240                 245

ccc gaa acc agc tca ctt cgc gtg atc ccg cat cca aat ccc ttt       880
Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His Pro Asn Pro Phe
                250                 255                 260

tgattgaaag tttgacttaa aaa                                        903


<210> 212
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 212
Met Pro Gln Leu Val Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser
  1               5                  10                  15

Arg His Ala Val Lys Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val
            20                  25                  30

Thr Ala Leu Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser
        35                  40                  45

Ala Ile Ala Gly Leu Val Glu Ser Thr Gly Glu Val Met Val Gly Gly
    50                  55                  60

Ser Gly Val Ala Ser Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser
65                  70                  75                  80

Leu Val Pro Gln Asn Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp
                85                  90                  95

Val Val Ala Met Gly Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu
            100                 105                 110

Thr Asp Ala Asp Arg Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn
        115                 120                 125

Ala Leu Asp Ile Ala Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln
    130                 135                 140

Gln Gln Leu Ile His Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val
145                 150                 155                 160
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Val Leu Leu Asp Glu Pro Val Ser Ala Leu Asp Leu Arg His Gln Val
                165                 170                 175

Glu Val Leu Gln Leu Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val
            180                 185                 190

Ile Val Val Leu His Asp Leu Asn His Val Ala Arg Trp Cys Asp His
        195                 200                 205

Ala Val Leu Met Ala Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg
    210                 215                 220

Glu Val Leu Glu Pro Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile
225                 230                 235                 240

Ala Val Arg Asp Asp Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His
                245                 250                 255

Pro Asn Pro Phe
            260
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<210> 213
<211> 1149
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1126)
<223> RXN00523

<400> 213

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tggtgactcg tccgagtgaa attgccgtgg gcatcatcat gccgatcatt ggtgcgccac 60

tgtttatttg gattattcgt cgtcagaaag tcaaagagct atg agc ctt agc cat   115
                                          Met Ser Leu Ser His
                                            1               5

caa ctc aag cgc cag cgc gca tcg cgc aac tcc cgc agg tgg ctg att   163
Gln Leu Lys Arg Gln Arg Ala Ser Arg Asn Ser Arg Arg Trp Leu Ile
                10                  15                  20

gtt gcg gca ttg ggc gtc gtc acg ctt ggt att ttt gct ttt tct ttg   211
Val Ala Ala Leu Gly Val Val Thr Leu Gly Ile Phe Ala Phe Ser Leu
            25                  30                  35

atg tgg ggc gag gtg ttt tat ggc cct gct cag gtg ctg aaa gtg ttg   259
Met Trp Gly Glu Val Phe Tyr Gly Pro Ala Gln Val Leu Lys Val Leu
        40                  45                  50

tct gga cag cag gtt ccc ggc gcg agt tat tcc gtt ggc gtg ttg cgt   307
Ser Gly Gln Gln Val Pro Gly Ala Ser Tyr Ser Val Gly Val Leu Arg
    55                  60                  65

ttg ccg cgc gcg gtg atg ggt ttg act gcg ggt ttg gcg ttt ggc gcg   355
Leu Pro Arg Ala Val Met Gly Leu Thr Ala Gly Leu Ala Phe Gly Ala
70                  75                  80                  85

gcg ggc gtg att ttt cag acg gtg ttg cgt aat cag ttg gcg tcg ccg   403
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Ala Gly Val Ile Phe Gln Thr Val Leu Arg Asn Gln Leu Ala Ser Pro
                  90                  95                 100

gat att atc ggc att tct tct ggc gcg tcg gcg gcg ggc gta att tgc   451
Asp Ile Ile Gly Ile Ser Ser Gly Ala Ser Ala Ala Gly Val Ile Cys
             105                 110                 115

att gtg ttt ttc ggg atg tcg cag tct gca gtg tcg gcg att tct ttg   499
Ile Val Phe Phe Gly Met Ser Gln Ser Ala Val Ser Ala Ile Ser Leu
         120                 125                 130

tgt gcg tcc ttg gct gtg gcg ttg ttg att tat ctg gtg gcg tat cgc   547
Cys Ala Ser Leu Ala Val Ala Leu Leu Ile Tyr Leu Val Ala Tyr Arg
     135                 140                 145

ggt ggt ttt tcg gcc acg cgt ctg att ctt acc ggc att ggt att gct   595
Gly Gly Phe Ser Ala Thr Arg Leu Ile Leu Thr Gly Ile Gly Ile Ala
150                 155                 160                 165

gcg atg ctg aat tca tta gtg tcg tat tcg ctg tcc aag gct gat tct   643
Ala Met Leu Asn Ser Leu Val Ser Tyr Ser Leu Ser Lys Ala Asp Ser
                 170                 175                 180

tgg gat ctg ccg acc gcg acg cgc tgg ctt acc ggc tcg ctc aat ggt   691
Trp Asp Leu Pro Thr Ala Thr Arg Trp Leu Thr Gly Ser Leu Asn Gly
             185                 190                 195

gcg acg tgg gat cgt gcg atg ccg ctg att gtc acc act gtg gta ctc   739
Ala Thr Trp Asp Arg Ala Met Pro Leu Ile Val Thr Thr Val Val Leu
         200                 205                 210

att ccg ctg ctg gtg gct aat gcg cgc aat gtg gat ctt atg cgt ttg   787
Ile Pro Leu Leu Val Ala Asn Ala Arg Asn Val Asp Leu Met Arg Leu
     215                 220                 225

ggc aat gat tcc gcg gtg ggt ttg ggc gtt gct act aat cgc acg cgc   835
Gly Asn Asp Ser Ala Val Gly Leu Gly Val Ala Thr Asn Arg Thr Arg
230                 235                 240                 245

gtc att gcg att att gcc gct gtt gcg ctc atc gcc gtt gct acc gct   883
Val Ile Ala Ile Ile Ala Ala Val Ala Leu Ile Ala Val Ala Thr Ala
                 250                 255                 260

gca tgc ggc ccg atc gca ttc gtg gcg ttt gtg tct ggc ccc att gcc   931
Ala Cys Gly Pro Ile Ala Phe Val Ala Phe Val Ser Gly Pro Ile Ala
             265                 270                 275

gcg cgc att tta ggc tcc ggc gga tcg ctc atc atc ccc tcc gca ctc   979
Ala Arg Ile Leu Gly Ser Gly Gly Ser Leu Ile Ile Pro Ser Ala Leu
         280                 285                 290

atc ggc ggg ttg atc gtg ctc atc gcc gac cta att ggc caa tac ttc   1027
Ile Gly Gly Leu Ile Val Leu Ile Ala Asp Leu Ile Gly Gln Tyr Phe
     295                 300                 305

ctc ggc acc cgc tac ccc gtc gga gtt gtc acc ggc gca ttc ggc gcc   1075
Leu Gly Thr Arg Tyr Pro Val Gly Val Val Thr Gly Ala Phe Gly Ala
310                 315                 320                 325

cca ttc ctt atc tat tta ctc att cgt tcc aac cgc gcg gga gta acc   1123
Pro Phe Leu Ile Tyr Leu Leu Ile Arg Ser Asn Arg Ala Gly Val Thr
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330 335 340

ctg tgaccaccaa ccatcaacta tcc 1149
Leu

<210> 214
<211> 342
<212> PRT
<213> Corynebacterium glutamicum

<400> 214

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Met | Ser | Leu | Ser | His | Gln | Leu | Lys | Arg | Gln | Arg | Ala | Ser | Arg | Asn | Ser |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Arg | Arg | Trp | Leu | Ile | Val | Ala | Ala | Leu | Gly | Val | Val | Thr | Leu | Gly | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Ala | Phe | Ser | Leu | Met | Trp | Gly | Glu | Val | Phe | Tyr | Gly | Pro | Ala | Gln |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Leu | Lys | Val | Leu | Ser | Gly | Gln | Gln | Val | Pro | Gly | Ala | Ser | Tyr | Ser |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Gly | Val | Leu | Arg | Leu | Pro | Arg | Ala | Val | Met | Gly | Leu | Thr | Ala | Gly |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Leu | Ala | Phe | Gly | Ala | Ala | Gly | Val | Ile | Phe | Gln | Thr | Val | Leu | Arg | Asn |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gln | Leu | Ala | Ser | Pro | Asp | Ile | Ile | Gly | Ile | Ser | Ser | Gly | Ala | Ser | Ala |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ala | Gly | Val | Ile | Cys | Ile | Val | Phe | Phe | Gly | Met | Ser | Gln | Ser | Ala | Val |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ser | Ala | Ile | Ser | Leu | Cys | Ala | Ser | Leu | Ala | Val | Ala | Leu | Leu | Ile | Tyr |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Leu | Val | Ala | Tyr | Arg | Gly | Gly | Phe | Ser | Ala | Thr | Arg | Leu | Ile | Leu | Thr |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Gly | Ile | Gly | Ile | Ala | Ala | Met | Leu | Asn | Ser | Leu | Val | Ser | Tyr | Ser | Leu |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ser | Lys | Ala | Asp | Ser | Trp | Asp | Leu | Pro | Thr | Ala | Thr | Arg | Trp | Leu | Thr |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Gly | Ser | Leu | Asn | Gly | Ala | Thr | Trp | Asp | Arg | Ala | Met | Pro | Leu | Ile | Val |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Thr | Thr | Val | Val | Leu | Ile | Pro | Leu | Leu | Val | Ala | Asn | Ala | Arg | Asn | Val |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Asp | Leu | Met | Arg | Leu | Gly | Asn | Asp | Ser | Ala | Val | Gly | Leu | Gly | Val | Ala |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Thr | Asn | Arg | Thr | Arg | Val | Ile | Ala | Ile | Ile | Ala | Ala | Val | Ala | Leu | Ile |
| | | | | 245 | | | | | 250 | | | | | 255 | |

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Ala Val Ala Thr Ala Ala Cys Gly Pro Ile Ala Phe Val Ala Phe Val
            260                 265                 270

Ser Gly Pro Ile Ala Ala Arg Ile Leu Gly Ser Gly Gly Ser Leu Ile
        275                 280                 285

Ile Pro Ser Ala Leu Ile Gly Gly Leu Ile Val Leu Ile Ala Asp Leu
    290                 295                 300

Ile Gly Gln Tyr Phe Leu Gly Thr Arg Tyr Pro Val Gly Val Val Thr
305                 310                 315                 320

Gly Ala Phe Gly Ala Pro Phe Leu Ile Tyr Leu Leu Ile Arg Ser Asn
                325                 330                 335

Arg Ala Gly Val Thr Leu
            340
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<210> 215
<211> 802
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (30)..(779)
<223> FRXA00523

<400> 215

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                                   Val Leu Arg Asn Gln Leu Ala Ser
                                     1               5

ccg gat att atc ggc att tct tct ggc gcg tcg gcg gcg ggc gta att   101
Pro Asp Ile Ile Gly Ile Ser Ser Gly Ala Ser Ala Ala Gly Val Ile
     10                  15                  20

tgc att gtg ttt ttc gga atg tcg cag tct gca gtg tcg gcg att tct   149
Cys Ile Val Phe Phe Gly Met Ser Gln Ser Ala Val Ser Ala Ile Ser
 25                  30                  35                  40

ttg tgt gcg tcc ttg gct gtg gcg ttg ttg att tat ctg gtg gcg tat   197
Leu Cys Ala Ser Leu Ala Val Ala Leu Leu Ile Tyr Leu Val Ala Tyr
                45                  50                  55

cgc ggt ggt ttt tcg gcc acg cgt ctg att ctt acc ggc att ggt att   245
Arg Gly Gly Phe Ser Ala Thr Arg Leu Ile Leu Thr Gly Ile Gly Ile
            60                  65                  70

gct gcg atg ctg aat tca tta gtg tcg tat tcg ctg tcc aag gct gat   293
Ala Ala Met Leu Asn Ser Leu Val Ser Tyr Ser Leu Ser Lys Ala Asp
        75                  80                  85

tct tgg gat ctg ccg acc gcg acg cgc tgg ctt acc ggc tcg ctc aat   341
Ser Trp Asp Leu Pro Thr Ala Thr Arg Trp Leu Thr Gly Ser Leu Asn
     90                  95                 100

ggt gcg acg tgg gat cgt gcg atg ccg ctg att gtc acc act gtg gta   389
Gly Ala Thr Trp Asp Arg Ala Met Pro Leu Ile Val Thr Thr Val Val
105                 110                 115                 120
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ctc att ccg ctg ctg gtg gct aat gcg cgc aat gtg gat ctt atg cgt   437
Leu Ile Pro Leu Leu Val Ala Asn Ala Arg Asn Val Asp Leu Met Arg
                125                 130                 135

ttg ggc aat gat tcc gcg gtg ggt ttg ggc gtt gct act aat cgc acg   485
Leu Gly Asn Asp Ser Ala Val Gly Leu Gly Val Ala Thr Asn Arg Thr
            140                 145                 150

cgc gtc att gcg att att gcc gct gtt gcg ctc atc gcc gtt gct acc   533
Arg Val Ile Ala Ile Ile Ala Ala Val Ala Leu Ile Ala Val Ala Thr
        155                 160                 165

gct gca tgc ggc ccg atc gca ttc gtg gcg ttt gtg tct ggc ccc att   581
Ala Ala Cys Gly Pro Ile Ala Phe Val Ala Phe Val Ser Gly Pro Ile
    170                 175                 180

gcc gcg cgc att tta ggc tcc ggc gga tcg ctc atc atc ccc tcc gca   629
Ala Ala Arg Ile Leu Gly Ser Gly Gly Ser Leu Ile Ile Pro Ser Ala
185                 190                 195                 200

ctc atc ggc ggg ttg atc gtg ctc atc gcc gac cta att ggc caa tac   677
Leu Ile Gly Gly Leu Ile Val Leu Ile Ala Asp Leu Ile Gly Gln Tyr
                205                 210                 215

ttc ctc ggc acc cgc tac ccc gtc gga gtt gtc acc ggc gca ttc ggc   725
Phe Leu Gly Thr Arg Tyr Pro Val Gly Val Val Thr Gly Ala Phe Gly
            220                 225                 230

gcc cca ttc ctt atc tat tta ctc att cgt tcc aac cgc gcg gga gta   773
Ala Pro Phe Leu Ile Tyr Leu Leu Ile Arg Ser Asn Arg Ala Gly Val
        235                 240                 245

acc ctg tgaccaccaa ccatcaacta tcc                                 802
Thr Leu
    250
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1336353.seq

<210> 216
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 216

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Val Leu Arg Asn Gln Leu Ala Ser Pro Asp Ile Ile Gly Ile Ser Ser
  1               5                  10                  15

Gly Ala Ser Ala Ala Gly Val Ile Cys Ile Val Phe Phe Gly Met Ser
            20                  25                  30

Gln Ser Ala Val Ser Ala Ile Ser Leu Cys Ala Ser Leu Ala Val Ala
        35                  40                  45

Leu Leu Ile Tyr Leu Val Ala Tyr Arg Gly Gly Phe Ser Ala Thr Arg
    50                  55                  60

Leu Ile Leu Thr Gly Ile Gly Ile Ala Ala Met Leu Asn Ser Leu Val
65                  70                  75                  80

Ser Tyr Ser Leu Ser Lys Ala Asp Ser Trp Asp Leu Pro Thr Ala Thr
                85                  90                  95
```

```
Arg Trp Leu Thr Gly Ser Leu Asn Gly Ala Thr Trp Asp Arg Ala Met
            100                 105                 110

Pro Leu Ile Val Thr Thr Val Val Leu Ile Pro Leu Leu Val Ala Asn
        115                 120                 125

Ala Arg Asn Val Asp Leu Met Arg Leu Gly Asn Asp Ser Ala Val Gly
    130                 135                 140

Leu Gly Val Ala Thr Asn Arg Thr Arg Val Ile Ala Ile Ile Ala Ala
145                 150                 155                 160

Val Ala Leu Ile Ala Val Ala Thr Ala Ala Cys Gly Pro Ile Ala Phe
                165                 170                 175

Val Ala Phe Val Ser Gly Pro Ile Ala Ala Arg Ile Leu Gly Ser Gly
            180                 185                 190

Gly Ser Leu Ile Ile Pro Ser Ala Leu Ile Gly Gly Leu Ile Val Leu
        195                 200                 205

Ile Ala Asp Leu Ile Gly Gln Tyr Phe Leu Gly Thr Arg Tyr Pro Val
    210                 215                 220

Gly Val Val Thr Gly Ala Phe Gly Ala Pro Phe Leu Ile Tyr Leu Leu
225                 230                 235                 240

Ile Arg Ser Asn Arg Ala Gly Val Thr Leu
                245                 250
```

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<210> 217
<211> 1167
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1144)
<223> RXA01289

<400> 217

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ctcacctaag atgttctaag cgttttagtt tcagctagtt ttaaggactt tcgatgtctc 60

atacttttct ttccccctcg atctttagga gtcacgcgat atg acg gcg gtg gcg   115
                                              Met Thr Ala Val Ala
                                                1               5

gta gag aag cag aag gag acg tcg ata agc aaa aac ctc ggc agg cgc   163
Val Glu Lys Gln Lys Glu Thr Ser Ile Ser Lys Asn Leu Gly Arg Arg
                10                  15                  20

cga gcg ctg ggc att ctc gga atc gtc gtg gca ctg ggt gcg ctt att   211
Arg Ala Leu Gly Ile Leu Gly Ile Val Val Ala Leu Gly Ala Leu Ile
            25                  30                  35

gtt tta agt att gct gtg ggt gcg aac cca ctt tct ttt agc tcc gta   259
Val Leu Ser Ile Ala Val Gly Ala Asn Pro Leu Ser Phe Ser Ser Val
        40                  45                  50
```

tgg cag ggt ttt acc gca cac gac agc tct gag gcg tcg att atc gtg 307
Trp Gln Gly Phe Thr Ala His Asp Ser Ser Glu Ala Ser Ile Ile Val
55 60 65

tgg tca atg cgt att ccg cgc acg ctg gtg ggc atc gtg act ggc gct 355
Trp Ser Met Arg Ile Pro Arg Thr Leu Val Gly Ile Val Thr Gly Ala
70 75 80 85

gct ttt ggt gtg gcg ggt gct tta att caa gcg ctg acg cgc aac ccg 403
Ala Phe Gly Val Ala Gly Ala Leu Ile Gln Ala Leu Thr Arg Asn Pro
90 95 100

ctt gcc gat ccc gga att ttg gga gtt aac gcg ggt gca ggt ttc gca 451
Leu Ala Asp Pro Gly Ile Leu Gly Val Asn Ala Gly Ala Gly Phe Ala
105 110 115

gtg acc gta ggt gtc gga ttt ttc gga ctc agc agc gtg acg ggc tac 499
Val Thr Val Gly Val Gly Phe Phe Gly Leu Ser Ser Val Thr Gly Tyr
120 125 130

atc tgg ttc gca ttc ctg ggc gct gcc gcc gct acc ctg ctg gtg tat 547
Ile Trp Phe Ala Phe Leu Gly Ala Ala Ala Ala Thr Leu Leu Val Tyr
135 140 145

ttc att ggt gcg agc acc agc ggc agc gtt aat cct gtt gct ctg gtc 595
Phe Ile Gly Ala Ser Thr Ser Gly Ser Val Asn Pro Val Ala Leu Val
150 155 160 165

ctc gcc ggc gtt gct ctg gcc gcc gtg ctt ggt ggc gtc acg agc ttc 643
Leu Ala Gly Val Ala Leu Ala Ala Val Leu Gly Gly Val Thr Ser Phe
170 175 180

ctc aca ctg att gat cct gag act ttt gaa agc atc cgc aat tgg aat 691
Leu Thr Leu Ile Asp Pro Glu Thr Phe Glu Ser Ile Arg Asn Trp Asn
185 190 195

ctt ggt tct gtt gca cgc acc gac ctc agc gac acc atg acc gta ttg 739
Leu Gly Ser Val Ala Arg Thr Asp Leu Ser Asp Thr Met Thr Val Leu
200 205 210

cca ttc ctg gca gtc gga ctg gcc atc gcg ctc ctg ctg tcg gga gca 787
Pro Phe Leu Ala Val Gly Leu Ala Ile Ala Leu Leu Leu Ser Gly Ala
215 220 225

ctg aac tcc att gcg ctt ggc gat gac ctt gct gca tcc ctg ggc acc 835
Leu Asn Ser Ile Ala Leu Gly Asp Asp Leu Ala Ala Ser Leu Gly Thr
230 235 240 245

aaa gtg atg cgc acc cgc gtg ctc ggc atc att tca gtc acc ttg ttg 883
Lys Val Met Arg Thr Arg Val Leu Gly Ile Ile Ser Val Thr Leu Leu
250 255 260

gcc ggc ggc gcg acc gcc ctt act ggt ggt atc ggc ttc gta ggc ctt 931
Ala Gly Gly Ala Thr Ala Leu Thr Gly Gly Ile Gly Phe Val Gly Leu
265 270 275

atg gtt ccc cac gtt gtg cgc tgg gta gtt ggc ccc gat caa cga tgg 979
Met Val Pro His Val Val Arg Trp Val Val Gly Pro Asp Gln Arg Trp
280 285 290

atc atc acc ttc agc gcc ctg tgc gcc cct gtt ctt gta ctc ggc gca 1027

```
Ile Ile Thr Phe Ser Ala Leu Cys Ala Pro Val Leu Val Leu Gly Ala
    295                 300                 305

gac att ttg gga cgc atc atc gcc cgc ccc ggc gaa att gaa gta ggc   1075
Asp Ile Leu Gly Arg Ile Ile Ala Arg Pro Gly Glu Ile Glu Val Gly
310                 315                 320                 325

att gtt acc gca gtc atc ggc gca cct gtc ctg atc gca cta gtt cga   1123
Ile Val Thr Ala Val Ile Gly Ala Pro Val Leu Ile Ala Leu Val Arg
                330                 335                 340

cgg agg aaa gcc agt ggt ctt taatatcaaa tctagaactg atg             1167
Arg Arg Lys Ala Ser Gly Leu
            345
```

<210> 218
<211> 348
<212> PRT
<213> Corynebacterium glutamicum

<400> 218

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Met Thr Ala Val Ala Val Glu Lys Gln Lys Glu Thr Ser Ile Ser Lys
  1               5                  10                  15

Asn Leu Gly Arg Arg Arg Ala Leu Gly Ile Leu Gly Ile Val Val Ala
            20                  25                  30

Leu Gly Ala Leu Ile Val Leu Ser Ile Ala Val Gly Ala Asn Pro Leu
        35                  40                  45

Ser Phe Ser Ser Val Trp Gln Gly Phe Thr Ala His Asp Ser Ser Glu
    50                  55                  60

Ala Ser Ile Ile Val Trp Ser Met Arg Ile Pro Arg Thr Leu Val Gly
65                  70                  75                  80

Ile Val Thr Gly Ala Ala Phe Gly Val Ala Gly Ala Leu Ile Gln Ala
                85                  90                  95

Leu Thr Arg Asn Pro Leu Ala Asp Pro Gly Ile Leu Gly Val Asn Ala
            100                 105                 110

Gly Ala Gly Phe Ala Val Thr Val Gly Val Gly Phe Phe Gly Leu Ser
        115                 120                 125

Ser Val Thr Gly Tyr Ile Trp Phe Ala Phe Leu Gly Ala Ala Ala Ala
    130                 135                 140

Thr Leu Leu Val Tyr Phe Ile Gly Ala Ser Thr Ser Gly Ser Val Asn
145                 150                 155                 160

Pro Val Ala Leu Val Leu Ala Gly Val Ala Leu Ala Ala Val Leu Gly
                165                 170                 175

Gly Val Thr Ser Phe Leu Thr Leu Ile Asp Pro Glu Thr Phe Glu Ser
            180                 185                 190

Ile Arg Asn Trp Asn Leu Gly Ser Val Ala Arg Thr Asp Leu Ser Asp
        195                 200                 205
```

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```
Thr Met Thr Val Leu Pro Phe Leu Ala Val Gly Leu Ala Ile Ala Leu
    210                 215                 220

Leu Leu Ser Gly Ala Leu Asn Ser Ile Ala Leu Gly Asp Asp Leu Ala
225                 230                 235                 240

Ala Ser Leu Gly Thr Lys Val Met Arg Thr Arg Val Leu Gly Ile Ile
                245                 250                 255

Ser Val Thr Leu Leu Ala Gly Gly Ala Thr Ala Leu Thr Gly Gly Ile
            260                 265                 270

Gly Phe Val Gly Leu Met Val Pro His Val Val Arg Trp Val Val Gly
        275                 280                 285

Pro Asp Gln Arg Trp Ile Ile Thr Phe Ser Ala Leu Cys Ala Pro Val
    290                 295                 300

Leu Val Leu Gly Ala Asp Ile Leu Gly Arg Ile Ile Ala Arg Pro Gly
305                 310                 315                 320

Glu Ile Glu Val Gly Ile Val Thr Ala Val Ile Gly Ala Pro Val Leu
                325                 330                 335

Ile Ala Leu Val Arg Arg Arg Lys Ala Ser Gly Leu
            340                 345
```

<210> 219
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1264)
<223> RXA01290

<400> 219
ggacgcatca tcgcccgccc cggcgaaatt gaagtaggca ttgttaccgc agtcatcggc 60

gcacctgtcc tgatcgcact agttcgacgg aggaaagcca gtg gtc ttt aat atc 115
                                                Val Val Phe Asn Ile
                                                  1               5

aaa tct aga act gat gaa act cct gtt gct gcg tct gag ccg gtg gaa 163
Lys Ser Arg Thr Asp Glu Thr Pro Val Ala Ala Ser Glu Pro Val Glu
                  10                  15                  20

tcc act aga cct gtg tct gaa gct tcg aca agc cct gcg ctt aac ccc 211
Ser Thr Arg Pro Val Ser Glu Ala Ser Thr Ser Pro Ala Leu Asn Pro
              25                  30                  35

ggc tac cac gca gtt tca gtg cag agg cgc cgg ttc tct ttc cgc atc 259
Gly Tyr His Ala Val Ser Val Gln Arg Arg Arg Phe Ser Phe Arg Ile
          40                  45                  50

cca gcc cgc ctc atg gtg gtt agc ctt atc ctt ttc gcc atc gcg cta 307
Pro Ala Arg Leu Met Val Val Ser Leu Ile Leu Phe Ala Ile Ala Leu
      55                  60                  65
```
```

```
tgc agc gcc aca tgg gct atc acg atg ggc gat tac cca ctg tct ttg   355
Cys Ser Ala Thr Trp Ala Ile Thr Met Gly Asp Tyr Pro Leu Ser Leu
 70                  75                  80                  85

ggg cag gtg att aat gca ctt gct ggc acc ggc gag aaa ttc cag ttg   403
Gly Gln Val Ile Asn Ala Leu Ala Gly Thr Gly Glu Lys Phe Gln Leu
                90                  95                 100

ttg gtg gtg cgg gaa tgg cgt cta cct gta gcc att gct gct gtt gtc   451
Leu Val Val Arg Glu Trp Arg Leu Pro Val Ala Ile Ala Ala Val Val
            105                 110                 115

ttc ggc gcg ctg ctt ggc ata ggt gga gcg att ttc cag tcg att act   499
Phe Gly Ala Leu Leu Gly Ile Gly Gly Ala Ile Phe Gln Ser Ile Thr
        120                 125                 130

cga aac ccg ttg ggt tca cct gac gtg att ggt ttc gat gca ggt tct   547
Arg Asn Pro Leu Gly Ser Pro Asp Val Ile Gly Phe Asp Ala Gly Ser
    135                 140                 145

tac acg gcg gtg gtt ctt gtc att ttg gtc ctc ggc aac act cac tac   595
Tyr Thr Ala Val Val Leu Val Ile Leu Val Leu Gly Asn Thr His Tyr
150                 155                 160                 165

tgg agc atc gct ttc gct gcc atc gtc ggt ggc att gtt acc gcc ttt   643
Trp Ser Ile Ala Phe Ala Ala Ile Val Gly Gly Ile Val Thr Ala Phe
                170                 175                 180

gcc gtg tat gtc ctg gcg tgg cgt aaa ggt gtg caa ggt ttc cgc ttg   691
Ala Val Tyr Val Leu Ala Trp Arg Lys Gly Val Gln Gly Phe Arg Leu
            185                 190                 195

atc atc gtg ggc atc ggt gtc tcg gcc atg ctc agt tcc gtt aac gcg   739
Ile Ile Val Gly Ile Gly Val Ser Ala Met Leu Ser Ser Val Asn Ala
        200                 205                 210

tat cta atc acc cgc gcc gat gtg gaa gac gcc atg gtt gtg ggc ttc   787
Tyr Leu Ile Thr Arg Ala Asp Val Glu Asp Ala Met Val Val Gly Phe
    215                 220                 225

tgg agt gcc ggt tcc atc aac cgc att acc tgg caa tct ctg ctc ccc   835
Trp Ser Ala Gly Ser Ile Asn Arg Ile Thr Trp Gln Ser Leu Leu Pro
230                 235                 240                 245

tct ctg gtg atc gct gct gtc atc atc gtg gcc gcc att gtg ctg gca   883
Ser Leu Val Ile Ala Ala Val Ile Ile Val Ala Ala Ile Val Leu Ala
                250                 255                 260

agg tca ctg cgt ttc atg gaa atg ggc gat gac gta gcc acc acc ctc   931
Arg Ser Leu Arg Phe Met Glu Met Gly Asp Asp Val Ala Thr Thr Leu
            265                 270                 275

ggt gtg aaa aca aac tcc acc cgc ttg gca ctc atc gtt gtc ggc gtt   979
Gly Val Lys Thr Asn Ser Thr Arg Leu Ala Leu Ile Val Val Gly Val
        280                 285                 290

gct acc tcc gcg ttg gtt aca gca gct gcc gga ccg atc tcc ttc atc   1027
Ala Thr Ser Ala Leu Val Thr Ala Ala Ala Gly Pro Ile Ser Phe Ile
    295                 300                 305

gcg ttg gtt gcc cca cag ctg gca cgt cgc ctc act aaa acc cct ggt   1075
```

```
Ala Leu Val Ala Pro Gln Leu Ala Arg Arg Leu Thr Lys Thr Pro Gly
310                 315                 320                 325

gtc agc ctg gtt gct gcc gct gca atg ggt tcc gca ctg ctc agc tgc   1123
Val Ser Leu Val Ala Ala Ala Ala Met Gly Ser Ala Leu Leu Ser Cys
                330                 335                 340

gct cac ctc ctt tcc ctg att atc agc tcc ttc tac cgc acc atc ccg   1171
Ala His Leu Leu Ser Leu Ile Ile Ser Ser Phe Tyr Arg Thr Ile Pro
            345                 350                 355

gtt ggc ctg ttg act gta tcc atc ggt ggt tgc tac atg atc tgg ctt   1219
Val Gly Leu Leu Thr Val Ser Ile Gly Gly Cys Tyr Met Ile Trp Leu
        360                 365                 370

ctg ctg cgc gaa acc cgc cgc caa tac cgc acc ggc acc atc cga       1264
Leu Leu Arg Glu Thr Arg Arg Gln Tyr Arg Thr Gly Thr Ile Arg
    375                 380                 385

tagttctttt aaggatccct cat                                        1287
```

<210> 220
<211> 388
<212> PRT
<213> Corynebacterium glutamicum

<400> 220

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Val Val Phe Asn Ile Lys Ser Arg Thr Asp Glu Thr Pro Val Ala Ala
  1               5                  10                  15

Ser Glu Pro Val Glu Ser Thr Arg Pro Val Ser Glu Ala Ser Thr Ser
             20                  25                  30

Pro Ala Leu Asn Pro Gly Tyr His Ala Val Ser Val Gln Arg Arg Arg
         35                  40                  45

Phe Ser Phe Arg Ile Pro Ala Arg Leu Met Val Val Ser Leu Ile Leu
     50                  55                  60

Phe Ala Ile Ala Leu Cys Ser Ala Thr Trp Ala Ile Thr Met Gly Asp
 65                  70                  75                  80

Tyr Pro Leu Ser Leu Gly Gln Val Ile Asn Ala Leu Ala Gly Thr Gly
                 85                  90                  95

Glu Lys Phe Gln Leu Leu Val Val Arg Glu Trp Arg Leu Pro Val Ala
            100                 105                 110

Ile Ala Ala Val Val Phe Gly Ala Leu Leu Gly Ile Gly Gly Ala Ile
        115                 120                 125

Phe Gln Ser Ile Thr Arg Asn Pro Leu Gly Ser Pro Asp Val Ile Gly
    130                 135                 140

Phe Asp Ala Gly Ser Tyr Thr Ala Val Val Leu Val Ile Leu Val Leu
145                 150                 155                 160

Gly Asn Thr His Tyr Trp Ser Ile Ala Phe Ala Ala Ile Val Gly Gly
                165                 170                 175
```

Ile Val Thr Ala Phe Ala Val Tyr Val Leu Ala Trp Arg Lys Gly Val
180 185 190

Gln Gly Phe Arg Leu Ile Ile Val Gly Ile Gly Val Ser Ala Met Leu
195 200 205

Ser Ser Val Asn Ala Tyr Leu Ile Thr Arg Ala Asp Val Glu Asp Ala
210 215 220

Met Val Val Gly Phe Trp Ser Ala Gly Ser Ile Asn Arg Ile Thr Trp
225 230 235 240

Gln Ser Leu Leu Pro Ser Leu Val Ile Ala Ala Val Ile Ile Val Ala
245 250 255

Ala Ile Val Leu Ala Arg Ser Leu Arg Phe Met Glu Met Gly Asp Asp
260 265 270

Val Ala Thr Thr Leu Gly Val Lys Thr Asn Ser Thr Arg Leu Ala Leu
275 280 285

Ile Val Val Gly Val Ala Thr Ser Ala Leu Val Thr Ala Ala Ala Gly
290 295 300

Pro Ile Ser Phe Ile Ala Leu Val Ala Pro Gln Leu Ala Arg Arg Leu
305 310 315 320

Thr Lys Thr Pro Gly Val Ser Leu Val Ala Ala Ala Ala Met Gly Ser
325 330 335

Ala Leu Leu Ser Cys Ala His Leu Leu Ser Leu Ile Ile Ser Ser Phe
340 345 350

Tyr Arg Thr Ile Pro Val Gly Leu Leu Thr Val Ser Ile Gly Gly Cys
355 360 365

Tyr Met Ile Trp Leu Leu Leu Arg Glu Thr Arg Arg Gln Tyr Arg Thr
370 375 380

Gly Thr Ile Arg
385

<210> 221
<211> 605
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(582)
<223> RXA01822

<400> 221
atg gcc aga caa aat agc aat acc ggc ggg ttg cgt ctg gtg ttg gtt 48
Met Ala Arg Gln Asn Ser Asn Thr Gly Gly Leu Arg Leu Val Leu Val
1 5 10 15

ggt atc gga aca ggt gca ttt ttg ggt gct gct cgt gat ttc ttc atg 96
Gly Ile Gly Thr Gly Ala Phe Leu Gly Ala Ala Arg Asp Phe Phe Met
20 25 30

```
gtg cgc gca gat att acg ggt gct tcg acg gta cag ctg tgg tct gcc   144
Val Arg Ala Asp Ile Thr Gly Ala Ser Thr Val Gln Leu Trp Ser Ala
          35                  40                  45

ggt tcg ttg agc ggg cgc gac tgg aat cat gcc ctg ttg gtg ttg att   192
Gly Ser Leu Ser Gly Arg Asp Trp Asn His Ala Leu Leu Val Leu Ile
      50                  55                  60

tcg tgt gca gtg att gtg cca gca ctg tgc att att gtc cgc cgt tta   240
Ser Cys Ala Val Ile Val Pro Ala Leu Cys Ile Ile Val Arg Arg Leu
 65                  70                  75                  80

cgc ctg atg gaa atg ggt gat gat gca gct ggg gca ctt gga att tca   288
Arg Leu Met Glu Met Gly Asp Asp Ala Ala Gly Ala Leu Gly Ile Ser
                 85                  90                  95

gtg gag aga aca cgg ttg ata gcc att ttg ttg gct gtg ctg ctg gtg   336
Val Glu Arg Thr Arg Leu Ile Ala Ile Leu Leu Ala Val Leu Leu Val
            100                 105                 110

ggg atc gcc acc gca gct gca ggt ccc atc gct ttt att gca ctg gca   384
Gly Ile Ala Thr Ala Ala Ala Gly Pro Ile Ala Phe Ile Ala Leu Ala
        115                 120                 125

gca cct cag att gcc cgg gct ctg gcc cgg gag gat gga gtg ctg gtg   432
Ala Pro Gln Ile Ala Arg Ala Leu Ala Arg Glu Asp Gly Val Leu Val
    130                 135                 140

gct gcg tcg ata agc att ggc tct ggg ctg tta gtt gcg gcg gat tgc   480
Ala Ala Ser Ile Ser Ile Gly Ser Gly Leu Leu Val Ala Ala Asp Cys
145                 150                 155                 160

cta gag caa cac gtt gat act gag ctg cac acg ccc gtt ggc ctg gtg   528
Leu Glu Gln His Val Asp Thr Glu Leu His Thr Pro Val Gly Leu Val
                165                 170                 175

acc agt ttg ctg ggc ggg gtg tat ttg atg tgg ctt ttg agc cga aag   576
Thr Ser Leu Leu Gly Gly Val Tyr Leu Met Trp Leu Leu Ser Arg Lys
            180                 185                 190

gag gca taaatgctgc aagcgcatga tct                                 605
Glu Ala
```

<210> 222
<211> 194
<212> PRT
<213> Corynebacterium glutamicum

<400> 222

```
Met Ala Arg Gln Asn Ser Asn Thr Gly Gly Leu Arg Leu Val Leu Val
  1               5                  10                  15

Gly Ile Gly Thr Gly Ala Phe Leu Gly Ala Ala Arg Asp Phe Phe Met
             20                  25                  30

Val Arg Ala Asp Ile Thr Gly Ala Ser Thr Val Gln Leu Trp Ser Ala
         35                  40                  45
```

```
Gly Ser Leu Ser Gly Arg Asp Trp Asn His Ala Leu Leu Val Leu Ile
     50                  55                  60

Ser Cys Ala Val Ile Val Pro Ala Leu Cys Ile Ile Val Arg Arg Leu
 65                  70                  75                  80

Arg Leu Met Glu Met Gly Asp Asp Ala Ala Gly Ala Leu Gly Ile Ser
                 85                  90                  95

Val Glu Arg Thr Arg Leu Ile Ala Ile Leu Leu Ala Val Leu Leu Val
            100                 105                 110

Gly Ile Ala Thr Ala Ala Ala Gly Pro Ile Ala Phe Ile Ala Leu Ala
        115                 120                 125

Ala Pro Gln Ile Ala Arg Ala Leu Ala Arg Glu Asp Gly Val Leu Val
    130                 135                 140

Ala Ala Ser Ile Ser Ile Gly Ser Gly Leu Leu Val Ala Ala Asp Cys
145                 150                 155                 160

Leu Glu Gln His Val Asp Thr Glu Leu His Thr Pro Val Gly Leu Val
                165                 170                 175

Thr Ser Leu Leu Gly Gly Val Tyr Leu Met Trp Leu Leu Ser Arg Lys
            180                 185                 190

Glu Ala
```

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<210> 223
<211> 1119
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXN00466

<400> 223

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tttaaaagcg cactaagagc tcgtcaattc tttaaaacaa gctgagaatg tgaataatag 60

gataggttaa cctgattcga ttagaaaacg gagatttgtc gtg caa tcc cgc ctg   115
                                            Val Gln Ser Arg Leu
                                              1               5

tcc aaa atc ctg cgc agt agc gtc gta ggc gtt gct gtc cta gcc ctg   163
Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val Ala Val Leu Ala Leu
                 10                  15                  20

tta gct ggg tgt tct aac aat gca gat gac acc gac gct gat tca aca   211
Leu Ala Gly Cys Ser Asn Asn Ala Asp Asp Thr Asp Ala Asp Ser Thr
             25                  30                  35

tcc acg gga aac tcc gct ttt cct gtt tcg att gaa cac gag ttc gga   259
Ser Thr Gly Asn Ser Ala Phe Pro Val Ser Ile Glu His Glu Phe Gly
         40                  45                  50

acc acc aca atc gat gat gta ccc gaa aga gtt gtc acc ctt ggc gtt   307
```

```
Thr Thr Thr Ile Asp Asp Val Pro Glu Arg Val Val Thr Leu Gly Val
     55                  60                  65

acc gac gcc gat att gtc ctc gca ttg ggg acc gtc cca gta ggc aac   355
Thr Asp Ala Asp Ile Val Leu Ala Leu Gly Thr Val Pro Val Gly Asn
 70                  75                  80                  85

acc gga tac aaa ttc ttc gaa aac gga ttg gga ccg tgg act gat gag   403
Thr Gly Tyr Lys Phe Phe Glu Asn Gly Leu Gly Pro Trp Thr Asp Glu
                 90                  95                 100

tta gtg gaa ggc aaa gaa tta aca ctg ctt gac tct gat tcc aca cca   451
Leu Val Glu Gly Lys Glu Leu Thr Leu Leu Asp Ser Asp Ser Thr Pro
            105                 110                 115

gat ctt gaa caa gta gca gcc ctg gag cca gac ctg att att gga gtc   499
Asp Leu Glu Gln Val Ala Ala Leu Glu Pro Asp Leu Ile Ile Gly Val
        120                 125                 130

tct gcg ggg ttt gac gac gtt gta tac gag caa cta tct gat atc gca   547
Ser Ala Gly Phe Asp Asp Val Val Tyr Glu Gln Leu Ser Asp Ile Ala
    135                 140                 145

ccg gtg gtc gcc cgt cca gcg gga aca gct gca tac gca gta gct cgc   595
Pro Val Val Ala Arg Pro Ala Gly Thr Ala Ala Tyr Ala Val Ala Arg
150                 155                 160                 165

gag gaa gct acc aac ctt gtt gcc cgt gcg atg ggg caa tca gaa aaa   643
Glu Glu Ala Thr Asn Leu Val Ala Arg Ala Met Gly Gln Ser Glu Lys
                170                 175                 180

gga caa gag ctc aat gag gaa aca gat gct ctg atc caa gct gcg cgt   691
Gly Gln Glu Leu Asn Glu Glu Thr Asp Ala Leu Ile Gln Ala Ala Arg
            185                 190                 195

gat gaa aat cct tct ttt gac ggt aaa aca gga acc gtc atc ttg cca   739
Asp Glu Asn Pro Ser Phe Asp Gly Lys Thr Gly Thr Val Ile Leu Pro
        200                 205                 210

tac cag ggt aaa tac ggt gcc tac ctg cca ggc gat gca cgg gga caa   787
Tyr Gln Gly Lys Tyr Gly Ala Tyr Leu Pro Gly Asp Ala Arg Gly Gln
    215                 220                 225

ttc ctc gat tca ctt ggc att tcg ctg ccg gaa gca gtt ctt tcg cga   835
Phe Leu Asp Ser Leu Gly Ile Ser Leu Pro Glu Ala Val Leu Ser Arg
230                 235                 240                 245

gac acc ggc gac agc ttc ttt gtc gat gtc ccc gct gaa agc gtc aaa   883
Asp Thr Gly Asp Ser Phe Phe Val Asp Val Pro Ala Glu Ser Val Lys
                250                 255                 260

gac gta gac ggt gat gtt ctc ctc gtg ctt tcc aac gac gaa aat ctg   931
Asp Val Asp Gly Asp Val Leu Leu Val Leu Ser Asn Asp Glu Asn Leu
            265                 270                 275

gat atc aca gca gag aat cca ctg ttt gaa aca ctc aac gtt gtg caa   979
Asp Ile Thr Ala Glu Asn Pro Leu Phe Glu Thr Leu Asn Val Val Gln
        280                 285                 290

aaa gac gca gta att gtg gca aca acc gaa gaa cgc ggg gcg att acc   1027
Lys Asp Ala Val Ile Val Ala Thr Thr Glu Glu Arg Gly Ala Ile Thr
```

295 300 305

tac aac tca gtg ctg tct gtt cct ttt gcg ttg gaa cat ctc gca cca 1075
Tyr Asn Ser Val Leu Ser Val Pro Phe Ala Leu Glu His Leu Ala Pro
310 315 320 325

cgt att gct gag gct ttg aag taaaactcaa ctactcgagc aca 1119
Arg Ile Ala Glu Ala Leu Lys
330

<210> 224
<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 224
Val Gln Ser Arg Leu Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val
1 5 10 15

Ala Val Leu Ala Leu Leu Ala Gly Cys Ser Asn Asn Ala Asp Asp Thr
20 25 30

Asp Ala Asp Ser Thr Ser Thr Gly Asn Ser Ala Phe Pro Val Ser Ile
35 40 45

Glu His Glu Phe Gly Thr Thr Thr Ile Asp Asp Val Pro Glu Arg Val
50 55 60

Val Thr Leu Gly Val Thr Asp Ala Asp Ile Val Leu Ala Leu Gly Thr
65 70 75 80

Val Pro Val Gly Asn Thr Gly Tyr Lys Phe Phe Glu Asn Gly Leu Gly
85 90 95

Pro Trp Thr Asp Glu Leu Val Glu Gly Lys Glu Leu Thr Leu Leu Asp
100 105 110

Ser Asp Ser Thr Pro Asp Leu Glu Gln Val Ala Ala Leu Glu Pro Asp
115 120 125

Leu Ile Ile Gly Val Ser Ala Gly Phe Asp Asp Val Val Tyr Glu Gln
130 135 140

Leu Ser Asp Ile Ala Pro Val Val Ala Arg Pro Ala Gly Thr Ala Ala
145 150 155 160

Tyr Ala Val Ala Arg Glu Glu Ala Thr Asn Leu Val Ala Arg Ala Met
165 170 175

Gly Gln Ser Glu Lys Gly Gln Glu Leu Asn Glu Glu Thr Asp Ala Leu
180 185 190

Ile Gln Ala Ala Arg Asp Glu Asn Pro Ser Phe Asp Gly Lys Thr Gly
195 200 205

Thr Val Ile Leu Pro Tyr Gln Gly Lys Tyr Gly Ala Tyr Leu Pro Gly
210 215 220

Asp Ala Arg Gly Gln Phe Leu Asp Ser Leu Gly Ile Ser Leu Pro Glu
225 230 235 240

```
Ala Val Leu Ser Arg Asp Thr Gly Asp Ser Phe Phe Val Asp Val Pro
                245                 250                 255

Ala Glu Ser Val Lys Asp Val Asp Gly Asp Val Leu Leu Val Leu Ser
            260                 265                 270

Asn Asp Glu Asn Leu Asp Ile Thr Ala Glu Asn Pro Leu Phe Glu Thr
        275                 280                 285

Leu Asn Val Val Gln Lys Asp Ala Val Ile Val Ala Thr Thr Glu Glu
    290                 295                 300

Arg Gly Ala Ile Thr Tyr Asn Ser Val Leu Ser Val Pro Phe Ala Leu
305                 310                 315                 320

Glu His Leu Ala Pro Arg Ile Ala Glu Ala Leu Lys
                325                 330
```

<210> 225
<211> 1087
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1087)
<223> FRXA00466

<400> 225

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tttaaaagcg cactaagagc tcgtcaattc tttaaaacaa gctgagaatg tgaataatag 60

gataggttaa cctgattcga ttagaaaacg gagatttgtc gtg caa tcc cgc ctg   115
                                          Val Gln Ser Arg Leu
                                            1               5

tcc aaa atc ctg cgc agt agc gtc gta ggc gtt gct gtc cta gcc ctg   163
Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val Ala Val Leu Ala Leu
                10                  15                  20

tta gct ggg tgt tct aac aat gca gat gac acc gac gct gat tca aca   211
Leu Ala Gly Cys Ser Asn Asn Ala Asp Asp Thr Asp Ala Asp Ser Thr
            25                  30                  35

tcc acg gga aac tcc gct ttt cct gtt tcg att gaa cac gag ttc gga   259
Ser Thr Gly Asn Ser Ala Phe Pro Val Ser Ile Glu His Glu Phe Gly
        40                  45                  50

acc acc aca atc gat gat gta ccc gaa aga gtt gtc acc ctt ggc gtt   307
Thr Thr Thr Ile Asp Asp Val Pro Glu Arg Val Val Thr Leu Gly Val
    55                  60                  65

acc gac gcc gat att gtc ctc gca ttg ggg acc gtc cca gta ggc aac   355
Thr Asp Ala Asp Ile Val Leu Ala Leu Gly Thr Val Pro Val Gly Asn
70                  75                  80                  85

acc gga tac aaa ttc ttc gaa aac gga ttg gga ccg tgg act gat gag   403
Thr Gly Tyr Lys Phe Phe Glu Asn Gly Leu Gly Pro Trp Thr Asp Glu
                90                  95                  100
```

```
tta gtg gaa ggc aaa gaa tta aca ctg ctt gac tct gat tcc aca cca   451
Leu Val Glu Gly Lys Glu Leu Thr Leu Leu Asp Ser Asp Ser Thr Pro
            105                 110                 115

gat ctt gaa caa gta gca gcc ctg gag cca gac ctg att att gga gtc   499
Asp Leu Glu Gln Val Ala Ala Leu Glu Pro Asp Leu Ile Ile Gly Val
        120                 125                 130

tct gcg ggg ttt gac gac gtt gta tac gag caa cta tct gat atc gca   547
Ser Ala Gly Phe Asp Asp Val Val Tyr Glu Gln Leu Ser Asp Ile Ala
    135                 140                 145

ccg gtg gtc gcc cgt cca gcg gga aca gct gca tac gca gta gct cgc   595
Pro Val Val Ala Arg Pro Ala Gly Thr Ala Ala Tyr Ala Val Ala Arg
150                 155                 160                 165

gag gaa gct acc aac ctt gtt gcc cgt gcg atg ggg caa tca gaa aaa   643
Glu Glu Ala Thr Asn Leu Val Ala Arg Ala Met Gly Gln Ser Glu Lys
                170                 175                 180

gga caa gag ctc aat gag gaa aca gat gct ctg atc caa gct gcg cgt   691
Gly Gln Glu Leu Asn Glu Glu Thr Asp Ala Leu Ile Gln Ala Ala Arg
            185                 190                 195

gat gaa aat cct tct ttt gac ggt aaa aca gga acc gtc atc ttg cca   739
Asp Glu Asn Pro Ser Phe Asp Gly Lys Thr Gly Thr Val Ile Leu Pro
        200                 205                 210

tac cag ggt aaa tac ggt gcc tac ctg cca ggc gat gca cgg gga caa   787
Tyr Gln Gly Lys Tyr Gly Ala Tyr Leu Pro Gly Asp Ala Arg Gly Gln
    215                 220                 225

ttc ctc gat tca ctt ggc att tcg ctg ccg gaa gca gtt ctt tcg cga   835
Phe Leu Asp Ser Leu Gly Ile Ser Leu Pro Glu Ala Val Leu Ser Arg
230                 235                 240                 245

gac acc ggc gac agc ttc ttt gtc gat gtc ccc gct gaa agc gtc aaa   883
Asp Thr Gly Asp Ser Phe Phe Val Asp Val Pro Ala Glu Ser Val Lys
                250                 255                 260

gac gta gac ggt gat gtt ctc ctc gtg ctt tcc aac gac gaa aat ctg   931
Asp Val Asp Gly Asp Val Leu Leu Val Leu Ser Asn Asp Glu Asn Leu
            265                 270                 275

gat atc aca gca gag aat cca ctg ttt gaa aca ctc aac gtt gtg caa   979
Asp Ile Thr Ala Glu Asn Pro Leu Phe Glu Thr Leu Asn Val Val Gln
        280                 285                 290

aaa gac gca gta att gtg gca aca acc gaa gaa cgc ggg gcg att acc   1027
Lys Asp Ala Val Ile Val Ala Thr Thr Glu Glu Arg Gly Ala Ile Thr
    295                 300                 305

tac aac tca gtg ctg tct gtt cct ttt gcg ttg gaa cat ctc gca cca   1075
Tyr Asn Ser Val Leu Ser Val Pro Phe Ala Leu Glu His Leu Ala Pro
310                 315                 320                 325

cgt att gct gag                                                  1087
Arg Ile Ala Glu
```

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<210> 226
<211> 329
<212> PRT
<213> Corynebacterium glutamicum

<400> 226

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Val Gln Ser Arg Leu Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val
  1               5                  10                  15

Ala Val Leu Ala Leu Leu Ala Gly Cys Ser Asn Asn Ala Asp Asp Thr
            20                  25                  30

Asp Ala Asp Ser Thr Ser Thr Gly Asn Ser Ala Phe Pro Val Ser Ile
        35                  40                  45

Glu His Glu Phe Gly Thr Thr Thr Ile Asp Asp Val Pro Glu Arg Val
    50                  55                  60

Val Thr Leu Gly Val Thr Asp Ala Asp Ile Val Leu Ala Leu Gly Thr
65                  70                  75                  80

Val Pro Val Gly Asn Thr Gly Tyr Lys Phe Phe Glu Asn Gly Leu Gly
                85                  90                  95

Pro Trp Thr Asp Glu Leu Val Glu Gly Lys Glu Leu Thr Leu Leu Asp
            100                 105                 110

Ser Asp Ser Thr Pro Asp Leu Glu Gln Val Ala Ala Leu Glu Pro Asp
        115                 120                 125

Leu Ile Ile Gly Val Ser Ala Gly Phe Asp Asp Val Val Tyr Glu Gln
    130                 135                 140

Leu Ser Asp Ile Ala Pro Val Val Ala Arg Pro Ala Gly Thr Ala Ala
145                 150                 155                 160

Tyr Ala Val Ala Arg Glu Glu Ala Thr Asn Leu Val Ala Arg Ala Met
                165                 170                 175

Gly Gln Ser Glu Lys Gly Gln Glu Leu Asn Glu Glu Thr Asp Ala Leu
            180                 185                 190

Ile Gln Ala Ala Arg Asp Glu Asn Pro Ser Phe Asp Gly Lys Thr Gly
        195                 200                 205

Thr Val Ile Leu Pro Tyr Gln Gly Lys Tyr Gly Ala Tyr Leu Pro Gly
    210                 215                 220

Asp Ala Arg Gly Gln Phe Leu Asp Ser Leu Gly Ile Ser Leu Pro Glu
225                 230                 235                 240

Ala Val Leu Ser Arg Asp Thr Gly Asp Ser Phe Phe Val Asp Val Pro
                245                 250                 255

Ala Glu Ser Val Lys Asp Val Asp Gly Asp Val Leu Leu Val Leu Ser
            260                 265                 270

Asn Asp Glu Asn Leu Asp Ile Thr Ala Glu Asn Pro Leu Phe Glu Thr
        275                 280                 285

Leu Asn Val Val Gln Lys Asp Ala Val Ile Val Ala Thr Thr Glu Glu
```

```
    290                 295                 300

Arg Gly Ala Ile Thr Tyr Asn Ser Val Leu Ser Val Pro Phe Ala Leu
305                 310                 315                 320

Glu His Leu Ala Pro Arg Ile Ala Glu
                325
```

<210> 227
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> RXN03081

<400> 227

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acggactgcc cattgcggtg cgcgatgatc ccgaaaccag ctcacttcgc gtgatcccgc 60

atccaaatcc cttttgattg aaagtttgac ttaaaaaccc atg aaa aaa tca ctc   115
                                             Met Lys Lys Ser Leu
                                               1               5

atc gcc att gtt gcc agt gcg ctc gtg tta agc ggc tgc acc tct gat   163
Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser Gly Cys Thr Ser Asp
                 10                  15                  20

tct tct gac tct tcc ggc act tcc gga act gtg gaa acc act tcg att   211
Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val Glu Thr Thr Ser Ile
             25                  30                  35

aca acc agc gtt gcc gca gct gac ggc gca ttc cca cgc acc gtc aca   259
Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe Pro Arg Thr Val Thr
         40                  45                  50

ctc gac gat tcc tcc atc acc tta gaa tcc aaa cca gag cgc atc gcc   307
Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys Pro Glu Arg Ile Ala
     55                  60                  65

gta ctc acc cca gag gca gca tcc ttg gtt ctc ccc atc aca ggc gcc   355
Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu Pro Ile Thr Gly Ala
 70                  75                  80                  85

gac cgc gtc gtg atg acc gcc gaa atg gac acc gct gac gaa gaa acc   403
Asp Arg Val Val Met Thr Ala Glu Met Asp Thr Ala Asp Glu Glu Thr
                 90                  95                 100

gca gct ctg gcc tcc caa gtg gaa tac caa gtc aaa aac ggt ggc agg   451
Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val Lys Asn Gly Gly Arg
            105                 110                 115

ctc gac ccc gaa caa gtt gtc gcc ggc gac cca gat ttg gtg atc gtc   499
Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro Asp Leu Val Ile Val
        120                 125                 130

agt gcg cgt ttc gat acc gaa caa ggc acc atc gac att ttg gaa ggc   547
Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile Asp Ile Leu Glu Gly
    135                 140                 145
```

ctc aac gtc ccg tagttaactt cgattcagac gct 582
Leu Asn Val Pro
150

<210> 228
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 228
Met Lys Lys Ser Leu Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser
1 5 10 15

Gly Cys Thr Ser Asp Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val
20 25 30

Glu Thr Thr Ser Ile Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe
35 40 45

Pro Arg Thr Val Thr Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys
50 55 60

Pro Glu Arg Ile Ala Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu
65 70 75 80

Pro Ile Thr Gly Ala Asp Arg Val Val Met Thr Ala Glu Met Asp Thr
85 90 95

Ala Asp Glu Glu Thr Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val
100 105 110

Lys Asn Gly Gly Arg Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro
115 120 125

Asp Leu Val Ile Val Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile
130 135 140

Asp Ile Leu Glu Gly Leu Asn Val Pro
145 150

<210> 229
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1075)
<223> FRXA02863

<400> 229
acggactgcc cattgcggtg cgcgatgatc ccgaaaccag ctcacttcgc gtgatcccgc 60

atccaaatcc cttttgattg aaagtttgac ttaaaaaccc atg aaa aaa tca ctc 115
Met Lys Lys Ser Leu
1 5

atc gcc att gtt gcc agt gcg ctc gtg tta agc ggc tgc acc tct gat 163

```
Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser Gly Cys Thr Ser Asp
                  10                  15                  20

tct tct gac tct tcc ggc act tcc gga act gtg gaa acc act tcg att   211
Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val Glu Thr Thr Ser Ile
            25                  30                  35

aca acc agc gtt gcc gca gct gac ggc gca ttc cca cgc acc gtc aca   259
Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe Pro Arg Thr Val Thr
        40                  45                  50

ctc gac gat tcc tcc atc acc tta gaa tcc aaa cca gag cgc atc gcc   307
Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys Pro Glu Arg Ile Ala
    55                  60                  65

gta ctc acc cca gag gca gca tcc ttg gtt ctc ccc atc aca ggc gcc   355
Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu Pro Ile Thr Gly Ala
70                  75                  80                  85

gac cgc gtc gtg atg acc gcc gaa atg gac acc gct gac gaa gaa acc   403
Asp Arg Val Val Met Thr Ala Glu Met Asp Thr Ala Asp Glu Glu Thr
                90                  95                 100

gca gct ctg gcc tcc caa gtg gaa tac caa gtc aaa aac ggt ggc agc   451
Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val Lys Asn Gly Gly Ser
            105                 110                 115

ctc gac ccc gaa caa gtt gtc gcc ggc gac cca gat ttg gtg atc gtc   499
Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro Asp Leu Val Ile Val
        120                 125                 130

agt gcg cgt ttc gat acc gaa caa ggc acc atc gac att ttg gaa ggc   547
Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile Asp Ile Leu Glu Gly
    135                 140                 145

ctc aac gtc ccc gta gtt aac ttc gat tca gac gct tgg gga gac atc   595
Leu Asn Val Pro Val Val Asn Phe Asp Ser Asp Ala Trp Gly Asp Ile
150                 155                 160                 165

gac gcc atc acc aaa cac cta gaa att gtg ggt gaa ctc gtc ggc gaa   643
Asp Ala Ile Thr Lys His Leu Glu Ile Val Gly Glu Leu Val Gly Glu
                170                 175                 180

gaa gac aaa gcc gca gaa gca atc gca gaa atc gat gca aac cgc atc   691
Glu Asp Lys Ala Ala Glu Ala Ile Ala Glu Ile Asp Ala Asn Arg Ile
            185                 190                 195

gac atc gac aag cct gcc acc tcc ccc act gtg ctc act ttg atg caa   739
Asp Ile Asp Lys Pro Ala Thr Ser Pro Thr Val Leu Thr Leu Met Gln
        200                 205                 210

cgc gga cca cgc caa atg gtc atg cca gaa tct gcc atg ctc aac ggc   787
Arg Gly Pro Arg Gln Met Val Met Pro Glu Ser Ala Met Leu Asn Gly
    215                 220                 225

ctg atc cgc gaa gcc ggc ggc act cca gtg gta gat tct ctc ggc gcg   835
Leu Ile Arg Glu Ala Gly Gly Thr Pro Val Val Asp Ser Leu Gly Ala
230                 235                 240                 245

gta ggc acc atc act gca gac cca gaa caa gtt gtt gcg atg gca cct   883
Val Gly Thr Ile Thr Ala Asp Pro Glu Gln Val Val Ala Met Ala Pro
```

```
                250                 255                 260

gag atc atc atc att cag gac ttc caa ggt aaa ggc cga gag aac ttc   931
Glu Ile Ile Ile Ile Gln Asp Phe Gln Gly Lys Gly Arg Glu Asn Phe
            265                 270                 275

gct aat ttc ctc tcc aac cca gcg cta gcc aac gtt ccc gcc att gaa   979
Ala Asn Phe Leu Ser Asn Pro Ala Leu Ala Asn Val Pro Ala Ile Glu
        280                 285                 290

aac gac aag att ttc tac gcc gac act gtc acc act gga gtt act gca   1027
Asn Asp Lys Ile Phe Tyr Ala Asp Thr Val Thr Thr Gly Val Thr Ala
    295                 300                 305

ggt acc gat atc acc act ggt ctg cag caa gtg gca gaa atg ctg agc   1075
Gly Thr Asp Ile Thr Thr Gly Leu Gln Gln Val Ala Glu Met Leu Ser
310                 315                 320                 325

tagttttgag atgttgaaac tag                                        1098


<210> 230
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 230
Met Lys Lys Ser Leu Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser
  1               5                  10                  15

Gly Cys Thr Ser Asp Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val
            20                  25                  30

Glu Thr Thr Ser Ile Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe
        35                  40                  45

Pro Arg Thr Val Thr Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys
    50                  55                  60

Pro Glu Arg Ile Ala Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu
65                  70                  75                  80

Pro Ile Thr Gly Ala Asp Arg Val Val Met Thr Ala Glu Met Asp Thr
                85                  90                  95

Ala Asp Glu Glu Thr Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val
            100                 105                 110

Lys Asn Gly Gly Ser Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro
        115                 120                 125

Asp Leu Val Ile Val Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile
    130                 135                 140

Asp Ile Leu Glu Gly Leu Asn Val Pro Val Val Asn Phe Asp Ser Asp
145                 150                 155                 160

Ala Trp Gly Asp Ile Asp Ala Ile Thr Lys His Leu Glu Ile Val Gly
                165                 170                 175

Glu Leu Val Gly Glu Glu Asp Lys Ala Ala Glu Ala Ile Ala Glu Ile
```

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```
            180                 185                 190

Asp Ala Asn Arg Ile Asp Ile Asp Lys Pro Ala Thr Ser Pro Thr Val
        195                 200                 205

Leu Thr Leu Met Gln Arg Gly Pro Arg Gln Met Val Met Pro Glu Ser
    210                 215                 220

Ala Met Leu Asn Gly Leu Ile Arg Glu Ala Gly Gly Thr Pro Val Val
225                 230                 235                 240

Asp Ser Leu Gly Ala Val Gly Thr Ile Thr Ala Asp Pro Glu Gln Val
                245                 250                 255

Val Ala Met Ala Pro Glu Ile Ile Ile Ile Gln Asp Phe Gln Gly Lys
            260                 265                 270

Gly Arg Glu Asn Phe Ala Asn Phe Leu Ser Asn Pro Ala Leu Ala Asn
        275                 280                 285

Val Pro Ala Ile Glu Asn Asp Lys Ile Phe Tyr Ala Asp Thr Val Thr
    290                 295                 300

Thr Gly Val Thr Ala Gly Thr Asp Ile Thr Thr Gly Leu Gln Gln Val
305                 310                 315                 320

Ala Glu Met Leu Ser
                325
```

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<210> 231
<211> 776
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXS03221

<400> 231
caaaagtatt caaaaaaagt ttgttatgta cgattgacgg gacatatcgt gtctgccacg 60

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attaaagaca ttggtgatgt gaatcactgc ctactacatc gtg ttt cgt gac cct   115
                                          Val Phe Arg Asp Pro
                                            1               5

gca cct cca agt aag ggc acg aca aac tta gga gac aag atg gct agt   163
Ala Pro Pro Ser Lys Gly Thr Thr Asn Leu Gly Asp Lys Met Ala Ser
                10                  15                  20

acc ttc att cag gcc gac agc cct gaa aaa agt aag aag ctg ccc cca   211
Thr Phe Ile Gln Ala Asp Ser Pro Glu Lys Ser Lys Lys Leu Pro Pro
            25                  30                  35

ctc aca gaa ggt ccg tat aga aag cgg cta ttc tac gtt gca cta gtt   259
Leu Thr Glu Gly Pro Tyr Arg Lys Arg Leu Phe Tyr Val Ala Leu Val
        40                  45                  50

gcg acg ttt ggt ggg ctg ctc ttc gga tat gac acc gga gta atc aac   307
Ala Thr Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly Val Ile Asn
```

```
     55                  60                  65

ggt gca ctc aac cca atg aca cgt gag ctc gga cta acc gcg ttc acc   355
Gly Ala Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr Ala Phe Thr
 70                  75                  80                  85

gag ggt gtt gta act tct tcc ctg ctg ttt ggt gca gca gct ggt gcg   403
Glu Gly Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala Ala Gly Ala
                 90                  95                 100

atg ttt ttc ggt cgc att tcc gac aac tgg ggt cgc cgg aaa aca atc   451
Met Phe Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg Lys Thr Ile
            105                 110                 115

atc tca ctt gca gta gct ttc ttt gtc ggc acc atg atc tgc gtg ttt   499
Ile Ser Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile Cys Val Phe
        120                 125                 130

gct cca tct ttt gca gta atg gtt gtc gga cgt gtg ctt ctt gga ctc   547
Ala Pro Ser Phe Ala Val Met Val Val Gly Arg Val Leu Leu Gly Leu
    135                 140                 145

gca gtt ggt ggc gct tcc act gtt gtc cct gtc tac ctg gct gaa ctt   595
Ala Val Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu Ala Glu Leu
150                 155                 160                 165

gct cct ttt gaa atc cgt ggc tca ctg gct ggc cgt aat gag ttg atg   643
Ala Pro Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn Glu Leu Met
                170                 175                 180

att gtt gtt ggt cag ctc gca gct ttt gtc atc aat gcg att att gga   691
Ile Val Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala Ile Ile Gly
            185                 190                 195

aat gtt ttt gga cac cac gat ggt gtg tgg cgc tac atg ctg gca att   739
Asn Val Phe Gly His His Asp Gly Val Trp Arg Tyr Met Leu Ala Ile
        200                 205                 210

gcc gca atc cca gca att gcc ctc ttc ttt gga atg                   775
Ala Ala Ile Pro Ala Ile Ala Leu Phe Phe Gly Met
    215                 220                 225

c                                                                 776


<210> 232
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 232
Val Phe Arg Asp Pro Ala Pro Pro Ser Lys Gly Thr Thr Asn Leu Gly
  1               5                  10                  15

Asp Lys Met Ala Ser Thr Phe Ile Gln Ala Asp Ser Pro Glu Lys Ser
             20                  25                  30

Lys Lys Leu Pro Pro Leu Thr Glu Gly Pro Tyr Arg Lys Arg Leu Phe
         35                  40                  45

Tyr Val Ala Leu Val Ala Thr Phe Gly Gly Leu Leu Phe Gly Tyr Asp
```

```
     50                  55                  60

Thr Gly Val Ile Asn Gly Ala Leu Asn Pro Met Thr Arg Glu Leu Gly
 65                  70                  75                  80

Leu Thr Ala Phe Thr Glu Gly Val Val Thr Ser Ser Leu Leu Phe Gly
                85                  90                  95

Ala Ala Ala Gly Ala Met Phe Phe Gly Arg Ile Ser Asp Asn Trp Gly
            100                 105                 110

Arg Arg Lys Thr Ile Ile Ser Leu Ala Val Ala Phe Phe Val Gly Thr
        115                 120                 125

Met Ile Cys Val Phe Ala Pro Ser Phe Ala Val Met Val Val Gly Arg
    130                 135                 140

Val Leu Leu Gly Leu Ala Val Gly Gly Ala Ser Thr Val Val Pro Val
145                 150                 155                 160

Tyr Leu Ala Glu Leu Ala Pro Phe Glu Ile Arg Gly Ser Leu Ala Gly
                165                 170                 175

Arg Asn Glu Leu Met Ile Val Val Gly Gln Leu Ala Ala Phe Val Ile
            180                 185                 190

Asn Ala Ile Ile Gly Asn Val Phe Gly His His Asp Gly Val Trp Arg
        195                 200                 205

Tyr Met Leu Ala Ile Ala Ala Ile Pro Ala Ile Ala Leu Phe Phe Gly
    210                 215                 220

Met
225
```

DO NOT ENTER

<210> 233
<211> 718
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(718)
<223> FRXA01986

<400> 233
gccacgatta aagacattgg tgatgtgaat cactgcctac tacatcgtgt ttcgtgaccc 60

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tgcacctcca agtaagggca cgacaaactt aggagacaag atg gct agt acc ttc   115
                                              Met Ala Ser Thr Phe
                                                1               5

att cag gcc gac agc cct gaa aaa agt aag aag ctg ccc cca ctc aca   163
Ile Gln Ala Asp Ser Pro Glu Lys Ser Lys Lys Leu Pro Pro Leu Thr
                  10                  15                  20

gaa ggt ccg tat aga aag cgg cta ttc tac gtt gca cta gtt gcg acg   211
Glu Gly Pro Tyr Arg Lys Arg Leu Phe Tyr Val Ala Leu Val Ala Thr
              25                  30                  35
```

```
ttt ggt ggg ctg ctc ttc gga tat gac acc gga gta atc aac ggt gca   259
Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly Val Ile Asn Gly Ala
          40                  45                  50

ctc aac cca atg aca cgt gag ctc gga cta acc gcg ttc acc gag ggt   307
Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr Ala Phe Thr Glu Gly
     55                  60                  65

gtt gta act tct tcc ctg ctg ttt ggt gca gca gct ggt gcg atg ttt   355
Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala Ala Gly Ala Met Phe
 70                  75                  80                  85

ttc ggt cgc att tcc gac aac tgg ggt cgc cgg aaa aca atc atc tca   403
Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg Lys Thr Ile Ile Ser
                 90                  95                 100

ctt gca gta gct ttc ttt gtc ggc acc atg atc tgc gtg ttt gct cca   451
Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile Cys Val Phe Ala Pro
            105                 110                 115

tct ttt gca gta atg gtt gtc gga cgt gtg ctt ctt gga ctc gca gtt   499
Ser Phe Ala Val Met Val Val Gly Arg Val Leu Leu Gly Leu Ala Val
        120                 125                 130

ggt ggc gct tcc act gtt gtc cct gtc tac ctg gct gaa ctt gct cct   547
Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro
    135                 140                 145

ttt gaa atc cgt ggc tca ctg gct ggc cgt aat gag ttg atg att gtt   595
Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn Glu Leu Met Ile Val
150                 155                 160                 165

gtt ggt cag ctc gca gct ttt gtc atc aat gcg att att gga aat gtt   643
Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala Ile Ile Gly Asn Val
                170                 175                 180

ttt gga cac cac gat ggt gtg tgg cgc tac atg ctg gca att gcc gca   691
Phe Gly His His Asp Gly Val Trp Arg Tyr Met Leu Ala Ile Ala Ala
            185                 190                 195

atc cca gca att gcc ctc ttc ttt gga                              718
Ile Pro Ala Ile Ala Leu Phe Phe Gly
        200                 205
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<210> 234
<211> 206
<212> PRT
<213> Corynebacterium glutamicum

<400> 234

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Met Ala Ser Thr Phe Ile Gln Ala Asp Ser Pro Glu Lys Ser Lys Lys
  1               5                  10                  15

Leu Pro Pro Leu Thr Glu Gly Pro Tyr Arg Lys Arg Leu Phe Tyr Val
             20                  25                  30

Ala Leu Val Ala Thr Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly
         35                  40                  45

Val Ile Asn Gly Ala Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr
```

```
     50                  55                  60

Ala Phe Thr Glu Gly Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala
 65                  70                  75                  80

Ala Gly Ala Met Phe Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg
                 85                  90                  95

Lys Thr Ile Ile Ser Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile
            100                 105                 110

Cys Val Phe Ala Pro Ser Phe Ala Val Met Val Val Gly Arg Val Leu
        115                 120                 125

Leu Gly Leu Ala Val Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu
    130                 135                 140

Ala Glu Leu Ala Pro Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn
145                 150                 155                 160

Glu Leu Met Ile Val Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala
                165                 170                 175

Ile Ile Gly Asn Val Phe Gly His His Asp Gly Val Trp Arg Tyr Met
            180                 185                 190

Leu Ala Ile Ala Ala Ile Pro Ala Ile Ala Leu Phe Phe Gly
        195                 200                 205


<210> 235
<211> 1118
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1095)
<223> RXN02447

<400> 235
aca gta gtt ccg gtg tac ctc gct gaa ctc gca cca cta gaa atc cgc   48
Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg
  1               5                  10                  15

ggc tcc ctg acc ggc cga aac gag ctt gct atc gtc acc ggc cag ctg   96
Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu
             20                  25                  30

ctt gcc ttc gtg atc aac gcg ctt atc gcc gtc acc cta cac gga gtt   144
Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val
         35                  40                  45

att gat gga atc tgg cgc atc atg ttc gcc gtc tgt gcc ctc cct gcc   192
Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala
     50                  55                  60

gtc gcc ctc ttc ctc ggc atg ctg cgg atg ccg gaa tca cca cgc tgg   240
Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp
 65                  70                  75                  80
```

```
ctg gtc aac cag ggg cgt tac gac gac gcc cgc cgc gtc atg gag acc   288
Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr
                85                  90                  95

gtc cgt acc cct gag cgt gcg aaa gcc gaa atg gat gaa atc atc gcg   336
Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala
            100                 105                 110

gtg cac tct gaa aac aat gcg gca ctt cct ggt gtt aag cag tct tcg   384
Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser
        115                 120                 125

ggc cag gct tca ggc cag gtt tct agc aag cac acc cac atg tcc atc   432
Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile
    130                 135                 140

ggc gaa gtc ctc agc aac aaa tgg ctg gtt cgt ctg ctc atc gcc ggc   480
Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly
145                 150                 155                 160

atc ggt gtt gca gtt gcc cag cag ctc acc ggc atc aac gcc atc atg   528
Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met
                165                 170                 175

tac tac gga acc cgc gtc ctc gag gaa tcc ggc atg agc gca gaa atg   576
Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met
            180                 185                 190

gct gtg gtt gcc aac att gct ttc ggt gcc gtt gcc gtc atc ggt gga   624
Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly
        195                 200                 205

ctg atc gca ctg cgc aac atg gac cgc ctg gat cgc cgc acc acc ttc   672
Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe
    210                 215                 220

atc atc ggc ctg tca ctg acc acc acc ttc cac ctt ttg atc gca gct   720
Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu Ile Ala Ala
225                 230                 235                 240

gcc ggc act ctc ctt cca gaa ggt aac tcc att cga cca ttc gcc atc   768
Ala Gly Thr Leu Leu Pro Glu Gly Asn Ser Ile Arg Pro Phe Ala Ile
                245                 250                 255

atg atc ctt gtt gtt ggg ttc gtg ctc tcc atg cag act ttc ctc aac   816
Met Ile Leu Val Val Gly Phe Val Leu Ser Met Gln Thr Phe Leu Asn
            260                 265                 270

gtt gca gtg tgg gtg tgg ctg gcg gaa atc ttc cca gtc cga atg aag   864
Val Ala Val Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys
        275                 280                 285

ggt atc ggc acc ggt att tcg gta ttc tgc ggt tgg ggc atc aat ggc   912
Gly Ile Gly Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly
    290                 295                 300

gtc cta gcg ttg ttc ttc cca gca ctg gtc tcc ggc gtg ggt atc acc   960
Val Leu Ala Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr
305                 310                 315                 320

ttc tcc ttc ctt atc ttc gca gtc gtc gga gtc att gcc ctg gcg ttc  1008
```

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Phe Ser Phe Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe
                325                 330                 335

gtc acc aag ttt gtt cct gaa acc cgt ggc cgc tca ctt gaa gaa ctc   1056
Val Thr Lys Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu
            340                 345                 350

gat cac gca gca ttc acc ggc cag atc ttc aag aag gct taaacccccc    1105
Asp His Ala Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala
        355                 360                 365

ccgatctctt tgg                                                   1118


<210> 236
<211> 365
<212> PRT
<213> Corynebacterium glutamicum

<400> 236
Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg
  1               5                  10                  15

Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu
             20                  25                  30

Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val
         35                  40                  45

Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala
     50                  55                  60

Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp
 65                  70                  75                  80

Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr
                 85                  90                  95

Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala
            100                 105                 110

Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser
        115                 120                 125

Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile
    130                 135                 140

Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly
145                 150                 155                 160

Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met
                165                 170                 175

Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met
            180                 185                 190

Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly
        195                 200                 205

Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe
    210                 215                 220
```

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Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu Ile Ala Ala
225                 230                 235                 240

Ala Gly Thr Leu Leu Pro Glu Gly Asn Ser Ile Arg Pro Phe Ala Ile
                245                 250                 255

Met Ile Leu Val Val Gly Phe Val Leu Ser Met Gln Thr Phe Leu Asn
            260                 265                 270

Val Ala Val Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys
        275                 280                 285

Gly Ile Gly Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly
    290                 295                 300

Val Leu Ala Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr
305                 310                 315                 320

Phe Ser Phe Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe
                325                 330                 335

Val Thr Lys Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu
            340                 345                 350

Asp His Ala Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala
        355                 360                 365
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<210> 237
<211> 293
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(270)
<223> FRXA02447

<400> 237

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tgg gtg tgg ctg gcg gaa atc ttc cca gtc cga atg aag ggt atc ggc   48
Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys Gly Ile Gly
  1               5                  10                  15

acc ggt att tcg gta ttc tgc ggt tgg ggc atc aat ggc gtc cta gcg   96
Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly Val Leu Ala
             20                  25                  30

ttg ttc ttc cca gca ctg gtc tcc ggc gtg ggt atc acc ttc tcc ttc  144
Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr Phe Ser Phe
         35                  40                  45

ctt atc ttc gca gtc gtc gga gtc att gcc ctg gcg ttc gtc acc aag  192
Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe Val Thr Lys
     50                  55                  60

ttt gtt cct gaa acc cgt ggc cgc tca ctt gaa gaa ctc gat cac gca  240
Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu Asp His Ala
 65                  70                  75                  80

gca ttc acc ggc cag atc ttc aag aag gct taaacccccc ccgatctctt     290
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Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala
85 90

tgg 293

<210> 238
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 238
Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys Gly Ile Gly
1 5 10 15

Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly Val Leu Ala
20 25 30

Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr Phe Ser Phe
35 40 45

Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe Val Thr Lys
50 55 60

Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu Asp His Ala
65 70 75 80

Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala
85 90

<210> 239
<211> 711
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(711)
<223> FRXA02769

<400> 239
aca gta gtt ccg gtg tac ctc gct gaa ctc gca cca cta gaa atc cgc 48
Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg
1 5 10 15

ggc tcc ctg acc ggc cga aac gag ctt gct atc gtc acc ggc cag ctg 96
Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu
20 25 30

ctt gcc ttc gtg atc aac gcg ctt atc gcc gtc acc cta cac gga gtt 144
Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val
35 40 45

att gat gga atc tgg cgc atc atg ttc gcc gtc tgt gcc ctc cct gcc 192
Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala
50 55 60

gtc gcc ctc ttc ctc ggc atg ctg cgg atg ccg gaa tca cca cgc tgg 240
Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp
65 70 75 80

```
ctg gtc aac cag ggg cgt tac gac gac gcc cgc cgc gtc atg gag acc   288
Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr
                  85                  90                  95

gtc cgt acc cct gag cgt gcg aaa gcc gaa atg gat gaa atc atc gcg   336
Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala
            100                 105                 110

gtg cac tct gaa aac aat gcg gca ctt cct ggt gtt aag cag tct tcg   384
Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser
        115                 120                 125

ggc cag gct tca ggc cag gtt tct agc aag cac acc cac atg tcc atc   432
Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile
    130                 135                 140

ggc gaa gtc ctc agc aac aaa tgg ctg gtt cgt ctg ctc atc gcc ggc   480
Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly
145                 150                 155                 160

atc ggt gtt gca gtt gcc cag cag ctc acc ggc atc aac gcc atc atg   528
Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met
                165                 170                 175

tac tac gga acc cgc gtc ctc gag gaa tcc ggc atg agc gca gaa atg   576
Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met
            180                 185                 190

gct gtg gtt gcc aac att gct ttc ggt gcc gtt gcc gtc atc ggt gga   624
Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly
        195                 200                 205

ctg atc gca ctg cgc aac atg gac cgc ctg gat cgc cgc acc acc ttc   672
Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe
    210                 215                 220

atc atc ggc ctg tca ctg acc acc acc ttc cac ctt ttg               711
Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu
225                 230                 235
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<210> 240
<211> 237
<212> PRT
<213> Corynebacterium glutamicum

<400> 240

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Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg
  1               5                  10                  15

Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu
            20                  25                  30

Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val
        35                  40                  45

Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala
    50                  55                  60

Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp
```

```
 65                  70                  75                  80

Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr
                 85                  90                  95

Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala
            100                 105                 110

Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser
        115                 120                 125

Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile
    130                 135                 140

Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly
145                 150                 155                 160

Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met
                165                 170                 175

Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met
            180                 185                 190

Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly
        195                 200                 205

Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe
    210                 215                 220

Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu
225                 230                 235
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<210> 241
<211> 725
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (3)..(695)
<223> RXS03220

<400> 241

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ccatg ggc tta agg gaa att ttg tcc agc aag tgg ctt gtg cgc atc ctc 50
  Met Gly Leu Arg Glu Ile Leu Ser Ser Lys Trp Leu Val Arg Ile Leu
    1               5                  10                  15

ctg gta ggt atc gga ttg ggt gtc gca cag cag ctg acc ggc atc aac   98
Leu Val Gly Ile Gly Leu Gly Val Ala Gln Gln Leu Thr Gly Ile Asn
             20                  25                  30

tcc atc atg tac tac ggc cag gtt gtt ctc att gag gct ggt ttc tcc   146
Ser Ile Met Tyr Tyr Gly Gln Val Val Leu Ile Glu Ala Gly Phe Ser
         35                  40                  45

gag aat gca gct ctg atc gcc aac gtg gcg cca gga gtg atc gca gtt   194
Glu Asn Ala Ala Leu Ile Ala Asn Val Ala Pro Gly Val Ile Ala Val
     50                  55                  60

gtc ggt gca ttc atc gca ctg tgg atg atg gat ggt atc aac cgc cgt   242
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Val Gly Ala Phe Ile Ala Leu Trp Met Met Asp Gly Ile Asn Arg Arg
65 70 75 80

acc acc ctc att acc ggt tat tct ctc acc acc att agc cac gta ttg 290
Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser His Val Leu
85 90 95

atc ggt atc gca tcc gta gca ttc cca gtc ggc gat cct ctt cgc ccc 338
Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro Leu Arg Pro
100 105 110

tac gtt atc ttg act ctg gtt gtg gtc ttc gtg gga tcc atg cag acc 386
Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser Met Gln Thr
115 120 125

ttc ctc aac gta gct acc tgg gtt atg ctc tct gag ctc ttc ccg ctg 434
Phe Leu Asn Val Ala Thr Trp Val Met Leu Ser Glu Leu Phe Pro Leu
130 135 140

gca atg cgc ggt ttc gca atc ggt atc tca gtg ttc ttc ctc tgg atc 482
Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe Leu Trp Ile
145 150 155 160

gca aac gcg ttc ctc gga ttg ttc ttc cca acc atc atg gaa gca gta 530
Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met Glu Ala Val
165 170 175

gga cta acc gga acc ttc ttc atg ttc gcc gga atc ggt gtg gtt gcc 578
Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly Val Val Ala
180 185 190

ttg atc ttc atc tac acc cag gtt cct gaa act cgt gga cgt acc ttg 626
Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly Arg Thr Leu
195 200 205

gag gag att gat gag gat gtt act tcc ggt gtc att ttc aac aag gac 674
Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe Asn Lys Asp
210 215 220

atc cga aaa gga aag gtg cac taaaaaccca gacactgcat agataacacg 725
Ile Arg Lys Gly Lys Val His
225 230

<210> 242
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 242
Met Gly Leu Arg Glu Ile Leu Ser Ser Lys Trp Leu Val Arg Ile Leu
1 5 10 15

Leu Val Gly Ile Gly Leu Gly Val Ala Gln Gln Leu Thr Gly Ile Asn
20 25 30

Ser Ile Met Tyr Tyr Gly Gln Val Val Leu Ile Glu Ala Gly Phe Ser
35 40 45

Glu Asn Ala Ala Leu Ile Ala Asn Val Ala Pro Gly Val Ile Ala Val
50 55 60

Val Gly Ala Phe Ile Ala Leu Trp Met Met Asp Gly Ile Asn Arg Arg
65 70 75 80

Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser His Val Leu
85 90 95

Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro Leu Arg Pro
100 105 110

Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser Met Gln Thr
115 120 125

Phe Leu Asn Val Ala Thr Trp Val Met Leu Ser Glu Leu Phe Pro Leu
130 135 140

Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe Leu Trp Ile
145 150 155 160

Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met Glu Ala Val
165 170 175

Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly Val Val Ala
180 185 190

Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly Arg Thr Leu
195 200 205

Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe Asn Lys Asp
210 215 220

Ile Arg Lys Gly Lys Val His
225 230

<210> 243
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> FRXA02762

<400> 243
ttcccagtcg gcgatcctct tcgcccctac gttatcttga ctctggttgt ggtcttcgtg 60

ggatccatgc agaccttcct caacggtagc tacctgggtt atg ctc tct gag ctc 115
Met Leu Ser Glu Leu
1 5

ttc ccg ctg gca atg cgc ggt ttc gca atc ggt atc tca gtg ttc ttc 163
Phe Pro Leu Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe
10 15 20

ctc tgg atc gca aac gcg ttc ctc gga ttg ttc ttc cca acc atc atg 211
Leu Trp Ile Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met
25 30 35

gaa gca gta gga cta acc gga acc ttc ttc atg ttc gcc gga atc ggt 259

Glu Ala Val Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly
40 45 50

gtg gtt gcc ttg atc ttc atc tac acc cag gtt cct gaa act cgt gga 307
Val Val Ala Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly
55 60 65

cgt acc ttg gag gag att gat gag gat gtt act tcc ggt gtc att ttc 355
Arg Thr Leu Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe
70 75 80 85

aac aag gac atc cga aaa gga aag gtg cac taaaaaccca gacactgcat 405
Asn Lys Asp Ile Arg Lys Gly Lys Val His
90 95

aga 408

<210> 244
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 244
Met Leu Ser Glu Leu Phe Pro Leu Ala Met Arg Gly Phe Ala Ile Gly
1 5 10 15

Ile Ser Val Phe Phe Leu Trp Ile Ala Asn Ala Phe Leu Gly Leu Phe
20 25 30

Phe Pro Thr Ile Met Glu Ala Val Gly Leu Thr Gly Thr Phe Phe Met
35 40 45

Phe Ala Gly Ile Gly Val Val Ala Leu Ile Phe Ile Tyr Thr Gln Val
50 55 60

Pro Glu Thr Arg Gly Arg Thr Leu Glu Glu Ile Asp Glu Asp Val Thr
65 70 75 80

Ser Gly Val Ile Phe Asn Lys Asp Ile Arg Lys Gly Lys Val His
85 90 95

<210> 245
<211> 324
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(301)
<223> FRXA02761

<400> 245
caggttgttc tcattgaggt ggtttctccg agaatgcagc tttgatcgcc aacgtggcgc 60

cagaagtgat cgcagttgtc gggcattcat cgcactgtgg atg atg gat ggt atc 115
Met Met Asp Gly Ile
1 5

aac cgc cgt acc acc ctc att acc ggt tat tct ctc acc acc att agc 163

Asn Arg Arg Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser
10 15 20

cac gta ttg atc ggt atc gca tcc gta gca ttc cca gtc ggc gat cct 211
His Val Leu Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro
25 30 35

ctt cgc ccc tac gtt atc ttg act ctg gtt gtg gtc ttc gtg gga tcc 259
Leu Arg Pro Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser
40 45 50

atg cag acc ttc ctc aac ggt agc tac ctg ggt tat gct ctc 301
Met Gln Thr Phe Leu Asn Gly Ser Tyr Leu Gly Tyr Ala Leu
55 60 65

tgagctcttc ccgctggcaa tgc 324

<210> 246
<211> 67
<212> PRT
<213> Corynebacterium glutamicum

<400> 246
Met Met Asp Gly Ile Asn Arg Arg Thr Thr Leu Ile Thr Gly Tyr Ser
1 5 10 15

Leu Thr Thr Ile Ser His Val Leu Ile Gly Ile Ala Ser Val Ala Phe
20 25 30

Pro Val Gly Asp Pro Leu Arg Pro Tyr Val Ile Leu Thr Leu Val Val
35 40 45

Val Phe Val Gly Ser Met Gln Thr Phe Leu Asn Gly Ser Tyr Leu Gly
50 55 60

Tyr Ala Leu
65

<210> 247
<211> 1242
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1219)
<223> RXA00123

<400> 247
gaaggatcgt cagaatagct ctcgaatagg ccatttctta cttcatcggc aatactgact 60

tagtagaaat tgctgtccag aactgttgaa ggagttgaaa atg cca aag aat tac 115
Met Pro Lys Asn Tyr
1 5

gac atc aac ggg gcg atc cgc aga cgg gat atg ctc aga cgt cgg tac 163
Asp Ile Asn Gly Ala Ile Arg Arg Arg Asp Met Leu Arg Arg Arg Tyr
10 15 20

```
ctt cct gat tcg gca aat tca act cct gta cct gaa gag gtt tct ccg   211
Leu Pro Asp Ser Ala Asn Ser Thr Pro Val Pro Glu Glu Val Ser Pro
            25                  30                  35

ctg acc cgc tat gtc acc gac ggc atc ccg aag cgc cca ccg ctg ggt   259
Leu Thr Arg Tyr Val Thr Asp Gly Ile Pro Lys Arg Pro Pro Leu Gly
        40                  45                  50

gcc act gtt gct gac ggt tta aaa ttc gcc gaa ggc gcc tcc aac cgc   307
Ala Thr Val Ala Asp Gly Leu Lys Phe Ala Glu Gly Ala Ser Asn Arg
    55                  60                  65

atg gtc atg tcg ctg tac cct gcg cca tcc aag ccc gca atc gag gaa   355
Met Val Met Ser Leu Tyr Pro Ala Pro Ser Lys Pro Ala Ile Glu Glu
70                  75                  80                  85

ttg gca gag gcc tgg gac ctc cac ccc acc atc gta gaa gac ttg ctc   403
Leu Ala Glu Ala Trp Asp Leu His Pro Thr Ile Val Glu Asp Leu Leu
                90                  95                  100

ctt ggt cag cag cgc cca aaa cta gac cgc tac gaa gac atc att ttt   451
Leu Gly Gln Gln Arg Pro Lys Leu Asp Arg Tyr Glu Asp Ile Ile Phe
            105                 110                 115

atc gcg atc cgc tcc gcg cgc tac atc gac tcc cgc gaa gag gtg gac   499
Ile Ala Ile Arg Ser Ala Arg Tyr Ile Asp Ser Arg Glu Glu Val Asp
        120                 125                 130

ttc tcc gaa ttc cac atc ctc atg aag cct cag gcc ata gcc att ttg   547
Phe Ser Glu Phe His Ile Leu Met Lys Pro Gln Ala Ile Ala Ile Leu
    135                 140                 145

tgc cag gat aac caa tgg att gac ggc acc agc gcc gcc agc ttc agc   595
Cys Gln Asp Asn Gln Trp Ile Asp Gly Thr Ser Ala Ala Ser Phe Ser
150                 155                 160                 165

aac ccc gag gag atc gat aag cgc ata aaa aca ttg ctt gcc gac gcc   643
Asn Pro Glu Glu Ile Asp Lys Arg Ile Lys Thr Leu Leu Ala Asp Ala
                170                 175                 180

gag tta ctc tcg tcc ggc ccc cgc gcc gcg gcc tat agg ctt ctc gac   691
Glu Leu Leu Ser Ser Gly Pro Arg Ala Ala Ala Tyr Arg Leu Leu Asp
            185                 190                 195

gcc atc gtc gac ggc ttc tcc ccc gtt ctt aga ggc atc gcc atc gac   739
Ala Ile Val Asp Gly Phe Ser Pro Val Leu Arg Gly Ile Ala Ile Asp
        200                 205                 210

cag gaa cag att gag cgc cag gtg ttc tcc ggc gac gcc gcc gtc gcc   787
Gln Glu Gln Ile Glu Arg Gln Val Phe Ser Gly Asp Ala Ala Val Ala
    215                 220                 225

gaa cgt att tac aac ctg tcc caa gaa atc atc gac atg cag cac acc   835
Glu Arg Ile Tyr Asn Leu Ser Gln Glu Ile Ile Asp Met Gln His Thr
230                 235                 240                 245

acc agc tca gtt acc gaa gtg gtg caa cgc ctc aac aaa gac ttc atc   883
Thr Ser Ser Val Thr Glu Val Val Gln Arg Leu Asn Lys Asp Phe Ile
                250                 255                 260

cga agt ggc atg tcc gaa gaa ctc cgc gcc tac ctc gac gac gtc gcc   931
```

```
Arg Ser Gly Met Ser Glu Glu Leu Arg Ala Tyr Leu Asp Asp Val Ala
            265                 270                 275

gac cac ctc acc cgc gac aac acc cgc gtc tcc gaa tac cgc gaa tcc   979
Asp His Leu Thr Arg Asp Asn Thr Arg Val Ser Glu Tyr Arg Glu Ser
        280                 285                 290

cta tcc caa att ttg aac gtc aac gcc acc ctt gta gcc caa cgc caa   1027
Leu Ser Gln Ile Leu Asn Val Asn Ala Thr Leu Val Ala Gln Arg Gln
    295                 300                 305

aac gaa gac atg aag aaa atc tcc gga tgg gcc gcc atc atc ttc gcc   1075
Asn Glu Asp Met Lys Lys Ile Ser Gly Trp Ala Ala Ile Ile Phe Ala
310                 315                 320                 325

cca acc ctc gtg tcc tcc atc tac ggc atg aac ttc gac atc atg cca   1123
Pro Thr Leu Val Ser Ser Ile Tyr Gly Met Asn Phe Asp Ile Met Pro
                330                 335                 340

gaa ctt cac tgg gcg ttt ggc tac ccg ttg gct ctc tta gca atg ctc   1171
Glu Leu His Trp Ala Phe Gly Tyr Pro Leu Ala Leu Leu Ala Met Leu
            345                 350                 355

gga ttc acc ctc ctt ttg tac tgg atc ttc aaa cgc agt aag tgg atg   1219
Gly Phe Thr Leu Leu Leu Tyr Trp Ile Phe Lys Arg Ser Lys Trp Met
        360                 365                 370

tgagacaaaa accgaaaaac caa                                        1242


<210> 248
<211> 373
<212> PRT
<213> Corynebacterium glutamicum

<400> 248
Met Pro Lys Asn Tyr Asp Ile Asn Gly Ala Ile Arg Arg Arg Asp Met
  1               5                  10                  15

Leu Arg Arg Arg Tyr Leu Pro Asp Ser Ala Asn Ser Thr Pro Val Pro
             20                  25                  30

Glu Glu Val Ser Pro Leu Thr Arg Tyr Val Thr Asp Gly Ile Pro Lys
         35                  40                  45

Arg Pro Pro Leu Gly Ala Thr Val Ala Asp Gly Leu Lys Phe Ala Glu
     50                  55                  60

Gly Ala Ser Asn Arg Met Val Met Ser Leu Tyr Pro Ala Pro Ser Lys
 65                  70                  75                  80

Pro Ala Ile Glu Glu Leu Ala Glu Ala Trp Asp Leu His Pro Thr Ile
                 85                  90                  95

Val Glu Asp Leu Leu Leu Gly Gln Gln Arg Pro Lys Leu Asp Arg Tyr
            100                 105                 110

Glu Asp Ile Ile Phe Ile Ala Ile Arg Ser Ala Arg Tyr Ile Asp Ser
        115                 120                 125

Arg Glu Glu Val Asp Phe Ser Glu Phe His Ile Leu Met Lys Pro Gln
```

```
    130                 135                 140

Ala Ile Ala Ile Leu Cys Gln Asp Asn Gln Trp Ile Asp Gly Thr Ser
145                 150                 155                 160

Ala Ala Ser Phe Ser Asn Pro Glu Glu Ile Asp Lys Arg Ile Lys Thr
                165                 170                 175

Leu Leu Ala Asp Ala Glu Leu Leu Ser Ser Gly Pro Arg Ala Ala Ala
            180                 185                 190

Tyr Arg Leu Leu Asp Ala Ile Val Asp Gly Phe Ser Pro Val Leu Arg
        195                 200                 205

Gly Ile Ala Ile Asp Gln Glu Gln Ile Glu Arg Gln Val Phe Ser Gly
    210                 215                 220

Asp Ala Ala Val Ala Glu Arg Ile Tyr Asn Leu Ser Gln Glu Ile Ile
225                 230                 235                 240

Asp Met Gln His Thr Thr Ser Ser Val Thr Glu Val Val Gln Arg Leu
                245                 250                 255

Asn Lys Asp Phe Ile Arg Ser Gly Met Ser Glu Glu Leu Arg Ala Tyr
            260                 265                 270

Leu Asp Asp Val Ala Asp His Leu Thr Arg Asp Asn Thr Arg Val Ser
        275                 280                 285

Glu Tyr Arg Glu Ser Leu Ser Gln Ile Leu Asn Val Asn Ala Thr Leu
    290                 295                 300

Val Ala Gln Arg Gln Asn Glu Asp Met Lys Lys Ile Ser Gly Trp Ala
305                 310                 315                 320

Ala Ile Ile Phe Ala Pro Thr Leu Val Ser Ser Ile Tyr Gly Met Asn
                325                 330                 335

Phe Asp Ile Met Pro Glu Leu His Trp Ala Phe Gly Tyr Pro Leu Ala
            340                 345                 350

Leu Leu Ala Met Leu Gly Phe Thr Leu Leu Leu Tyr Trp Ile Phe Lys
        355                 360                 365

Arg Ser Lys Trp Met
    370
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<210> 249
<211> 780
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(757)
<223> RXA02441

<400> 249
ccggcgacca gggcgcggga gatgaatgaa acgtcaaaag gcactatgag ggcgtcagta 60

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aaaaacttca tttgaaaatg ataaccgtta tcattaagga atg gca gaa ctc agc   115
                                              Met Ala Glu Leu Ser
                                                1               5

gtc cgg aat ctc aca tgc aca tac ggc aat cac atc gcg ctc aac aac   163
Val Arg Asn Leu Thr Cys Thr Tyr Gly Asn His Ile Ala Leu Asn Asn
                   10                  15                  20

atc acg gca cgc ttc cca acc gga aaa ata act gcc ctc atc ggc agc   211
Ile Thr Ala Arg Phe Pro Thr Gly Lys Ile Thr Ala Leu Ile Gly Ser
               25                  30                  35

aac ggc tcc gga aaa tcc aca ctg ttg gaa act ttg gcg ggc atg ctg   259
Asn Gly Ser Gly Lys Ser Thr Leu Leu Glu Thr Leu Ala Gly Met Leu
           40                  45                  50

gca ccc cgc agc gga agc att aac aac ctt gtg cca gaa atc gcg ttc   307
Ala Pro Arg Ser Gly Ser Ile Asn Asn Leu Val Pro Glu Ile Ala Phe
       55                  60                  65

gtc ccc caa cgc agc cac gtc tcc cat aat ttg ccc atc acg atc aga   355
Val Pro Gln Arg Ser His Val Ser His Asn Leu Pro Ile Thr Ile Arg
   70                  75                  80                  85

caa aca gtc agc atg ggg cga tgg tca gcc aag aaa aac tgg caa cga   403
Gln Thr Val Ser Met Gly Arg Trp Ser Ala Lys Lys Asn Trp Gln Arg
                   90                  95                 100

ctc act gcc gca gat tgc aac atc gtg gac agc tgc ctc gac cgg ctc   451
Leu Thr Ala Ala Asp Cys Asn Ile Val Asp Ser Cys Leu Asp Arg Leu
               105                 110                 115

gaa atc tcc ggc ctc gcc gac cgc ccc ctc ggc gaa gta tca ggc ggg   499
Glu Ile Ser Gly Leu Ala Asp Arg Pro Leu Gly Glu Val Ser Gly Gly
           120                 125                 130

cag cgc caa cgc gcc ctc ata gcg caa ggt tta gcg caa cag gcg ccc   547
Gln Arg Gln Arg Ala Leu Ile Ala Gln Gly Leu Ala Gln Gln Ala Pro
       135                 140                 145

tta ttg ctt ctc gac gaa ccc ctc gcc gcc gtg gac tcc cac gcg gca   595
Leu Leu Leu Leu Asp Glu Pro Leu Ala Ala Val Asp Ser His Ala Ala
   150                 155                 160                 165

agt ctt atc gaa gat gtc att aac caa caa cgc aac caa gga acc aca   643
Ser Leu Ile Glu Asp Val Ile Asn Gln Gln Arg Asn Gln Gly Thr Thr
                   170                 175                 180

att att ctt gcg act cac gat ctt gat caa gca cat caa gca gat cag   691
Ile Ile Leu Ala Thr His Asp Leu Asp Gln Ala His Gln Ala Asp Gln
               185                 190                 195

att atc gcc ttg gaa aaa gga atc ata aag cca cag cgc aaa gcc act   739
Ile Ile Ala Leu Glu Lys Gly Ile Ile Lys Pro Gln Arg Lys Ala Thr
           200                 205                 210

gaa tca ata aag aag cgt taataaagtt tgacttgtgc ctc                 780
Glu Ser Ile Lys Lys Arg
       215
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<210> 250
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 250
Met Ala Glu Leu Ser Val Arg Asn Leu Thr Cys Thr Tyr Gly Asn His
1 5 10 15

Ile Ala Leu Asn Asn Ile Thr Ala Arg Phe Pro Thr Gly Lys Ile Thr
20 25 30

Ala Leu Ile Gly Ser Asn Gly Ser Gly Lys Ser Thr Leu Leu Glu Thr
35 40 45

Leu Ala Gly Met Leu Ala Pro Arg Ser Gly Ser Ile Asn Asn Leu Val
50 55 60

Pro Glu Ile Ala Phe Val Pro Gln Arg Ser His Val Ser His Asn Leu
65 70 75 80

Pro Ile Thr Ile Arg Gln Thr Val Ser Met Gly Arg Trp Ser Ala Lys
85 90 95

Lys Asn Trp Gln Arg Leu Thr Ala Ala Asp Cys Asn Ile Val Asp Ser
100 105 110

Cys Leu Asp Arg Leu Glu Ile Ser Gly Leu Ala Asp Arg Pro Leu Gly
115 120 125

Glu Val Ser Gly Gly Gln Arg Gln Arg Ala Leu Ile Ala Gln Gly Leu
130 135 140

Ala Gln Gln Ala Pro Leu Leu Leu Leu Asp Glu Pro Leu Ala Ala Val
145 150 155 160

Asp Ser His Ala Ala Ser Leu Ile Glu Asp Val Ile Asn Gln Gln Arg
165 170 175

Asn Gln Gly Thr Thr Ile Ile Leu Ala Thr His Asp Leu Asp Gln Ala
180 185 190

His Gln Ala Asp Gln Ile Ile Ala Leu Glu Lys Gly Ile Ile Lys Pro
195 200 205

Gln Arg Lys Ala Thr Glu Ser Ile Lys Lys Arg
210 215

<210> 251
<211> 972
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(949)
<223> RXN02442

<400> 251
gccgtgatgt tgttgagcgc gatgtgattg ccgtatgtgc atgtgagatt ccggacgctg 60

09540130 - 20050630

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agttctgcca ttccttaatg ataacggtta tcattttcaa atg aag ttt ttt act   115
                                              Met Lys Phe Phe Thr
                                                1               5

gac gcc ctc ata gtg cct ttt gac gtt tca ttc atc tcc cgc gcc ctg   163
Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe Ile Ser Arg Ala Leu
                   10                  15                  20

gtc gcc gga tgc ctg gcc gca att tta tgc tca ctc att gga acg tgg   211
Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser Leu Ile Gly Thr Trp
               25                  30                  35

gtt att ttg cgc agg cta acc ttt ttc ggc gac gct atg tcg cac ggc   259
Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp Ala Met Ser His Gly
           40                  45                  50

ttg ctc ccc gga gta gcc acg gca tca cta ttg ggc gga aat ctc atg   307
Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu Gly Gly Asn Leu Met
       55                  60                  65

ttc ggc gca gca atc agc gca tta atc atg tca gcc gga gtg gtg tgg   355
Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser Ala Gly Val Val Trp
   70                  75                  80                  85

acc agc aga aaa tcc agc ctc tcc caa gac gtc agc att ggc ctg caa   403
Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val Ser Ile Gly Leu Gln
                   90                  95                 100

ttt att acc atg ctt tcc ctc ggc gtg gtt att gtg tcc cac tcc gat   451
Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile Val Ser His Ser Asp
               105                 110                 115

tcc cac gcc gta gac ctc acc agt ttc ctt ttt gga gac att ctt ggc   499
Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe Gly Asp Ile Leu Gly
           120                 125                 130

gtg cga ccc tcg gat ata ttc atc atc gcc att gca aca gtg ttg ggt   547
Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile Ala Thr Val Leu Gly
       135                 140                 145

gga ttg act att ttt ctc ttc cac cga cag ttc act gca ctc gct ttc   595
Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe Thr Ala Leu Ala Phe
   150                 155                 160                 165

gac gag cgt aaa gct cac acc tta gga ctc aat ccc cgc ttt gca cac   643
Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn Pro Arg Phe Ala His
                   170                 175                 180

cta ctc atg ctg gca ctg atc gca tta gct acg gtg gtg tcg ttt cag   691
Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr Val Val Ser Phe Gln
               185                 190                 195

gtg gtg gga acg ctt tta gtg ttt gga ctt ctc att ggt ccg ccc gcc   739
Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu Ile Gly Pro Pro Ala
           200                 205                 210

acg gct gca ctt tta gtg caa gac aaa gca agt att tca ctg atc atg   787
Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser Ile Ser Leu Ile Met
       215                 220                 225
```

```
atc gtc gcg tcg ctt ctt gga tgc gcg gaa att tac ctc ggg ctt tta   835
Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile Tyr Leu Gly Leu Leu
230                 235                 240                 245

atc agc tgg cac gca agc act gcc gcg gga gcc act atc act ttg tta   883
Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala Thr Ile Thr Leu Leu
                250                 255                 260

agt gct gcg ata ttt ttt gcc acc tta ttg aca aag agt gcc att agt   931
Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr Lys Ser Ala Ile Ser
            265                 270                 275

agg tta aac ttc acc gcg tgatactgaa agacattttc aat                 972
Arg Leu Asn Phe Thr Ala
        280
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<210> 252
<211> 283
<212> PRT
<213> Corynebacterium glutamicum

<400> 252

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Met Lys Phe Phe Thr Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe
  1               5                  10                  15

Ile Ser Arg Ala Leu Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser
            20                  25                  30

Leu Ile Gly Thr Trp Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp
        35                  40                  45

Ala Met Ser His Gly Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu
    50                  55                  60

Gly Gly Asn Leu Met Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser
65                  70                  75                  80

Ala Gly Val Val Trp Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val
                85                  90                  95

Ser Ile Gly Leu Gln Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile
            100                 105                 110

Val Ser His Ser Asp Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe
        115                 120                 125

Gly Asp Ile Leu Gly Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile
    130                 135                 140

Ala Thr Val Leu Gly Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe
145                 150                 155                 160

Thr Ala Leu Ala Phe Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn
                165                 170                 175

Pro Arg Phe Ala His Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr
            180                 185                 190

Val Val Ser Phe Gln Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu
        195                 200                 205
```

```
Ile Gly Pro Pro Ala Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser
    210                 215                 220

Ile Ser Leu Ile Met Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile
225                 230                 235                 240

Tyr Leu Gly Leu Leu Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala
                245                 250                 255

Thr Ile Thr Leu Leu Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr
            260                 265                 270

Lys Ser Ala Ile Ser Arg Leu Asn Phe Thr Ala
        275                 280
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<210> 253
<211> 972
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(949)
<223> FRXA02442

<400> 253

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gccgtgatgt tgttgagcgc gatgtgattg ccgtatgtgc atgtgagatt ccggacgctg 60

agttctgcca ttccttaatg ataacggtta tcattttcaa atg aag ttt ttt act   115
                                              Met Lys Phe Phe Thr
                                                1               5

gac gcc ctc ata gtg cct ttt gac gtt tca ttc atc tcc cgc gcc ctg   163
Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe Ile Ser Arg Ala Leu
                10                  15                  20

gtc gcc gga tgc ctg gcc gca att tta tgc tca ctc att gga acg tgg   211
Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser Leu Ile Gly Thr Trp
            25                  30                  35

gtt att ttg cgc agg cta acc ttt ttc ggc gac gct atg tcg cac ggc   259
Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp Ala Met Ser His Gly
        40                  45                  50

ttg ctc ccc gga gta gcc acg gca tca cta ttg ggc gga aat ctc atg   307
Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu Gly Gly Asn Leu Met
    55                  60                  65

ttc ggc gca gca atc agc gca tta atc atg tca gcc gga gtg gtg tgg   355
Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser Ala Gly Val Val Trp
70                  75                  80                  85

acc agc aga aaa tcc agc ctc tcc caa gac gtc agc att ggc ctg caa   403
Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val Ser Ile Gly Leu Gln
                90                  95                  100

ttt att acc atg ctt tcc ctc ggc gtg gtt att gtg tcc cac tcc gat   451
Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile Val Ser His Ser Asp
            105                 110                 115
```

```
tcc cac gcc gta gac ctc acc agt ttc ctt ttt gga gac att ctt ggc   499
Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe Gly Asp Ile Leu Gly
        120                 125                 130

gtg cga ccc tcg gat ata ttc atc atc gcc att gca aca gtg ttg ggt   547
Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile Ala Thr Val Leu Gly
    135                 140                 145

gga ttg act att ttt ctc ttc cac cga cag ttc act gca ctc gct ttc   595
Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe Thr Ala Leu Ala Phe
150                 155                 160                 165

gac gag cgt aaa gct cac acc tta gga ctc aat ccc cgc ttt gca cac   643
Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn Pro Arg Phe Ala His
                170                 175                 180

cta ctc atg ctg gca ctg atc gca tta gct acg gtg gtg tcg ttt cag   691
Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr Val Val Ser Phe Gln
            185                 190                 195

gtg gtg gga acg ctt tta gtg ttt gga ctt ctc att ggt ccg ccc gcc   739
Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu Ile Gly Pro Pro Ala
        200                 205                 210

acg gct gca ctt tta gtg caa gac aaa gca agt att tca ctg atc atg   787
Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser Ile Ser Leu Ile Met
    215                 220                 225

atc gtc gcg tcg ctt ctt gga tgc gcg gaa att tac ctc ggg ctt tta   835
Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile Tyr Leu Gly Leu Leu
230                 235                 240                 245

atc agc tgg cac gca agc act gcc gcg gga gcc act atc act ttg tta   883
Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala Thr Ile Thr Leu Leu
                250                 255                 260

agt gct gcg ata ttt ttt gcc acc tta ttg aca aag agt gcc att agt   931
Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr Lys Ser Ala Ile Ser
            265                 270                 275

agg tta aac ttc acc gcg tgatactgaa agacattttc aat                972
Arg Leu Asn Phe Thr Ala
        280
```

<210> 254
<211> 283
<212> PRT
<213> Corynebacterium glutamicum

<400> 254

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Met Lys Phe Phe Thr Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe
  1               5                  10                  15

Ile Ser Arg Ala Leu Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser
             20                  25                  30

Leu Ile Gly Thr Trp Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp
         35                  40                  45
```

```
Ala Met Ser His Gly Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu
     50                  55                  60

Gly Gly Asn Leu Met Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser
 65                  70                  75                  80

Ala Gly Val Val Trp Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val
                 85                  90                  95

Ser Ile Gly Leu Gln Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile
            100                 105                 110

Val Ser His Ser Asp Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe
        115                 120                 125

Gly Asp Ile Leu Gly Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile
    130                 135                 140

Ala Thr Val Leu Gly Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe
145                 150                 155                 160

Thr Ala Leu Ala Phe Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn
                165                 170                 175

Pro Arg Phe Ala His Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr
            180                 185                 190

Val Val Ser Phe Gln Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu
        195                 200                 205

Ile Gly Pro Pro Ala Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser
    210                 215                 220

Ile Ser Leu Ile Met Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile
225                 230                 235                 240

Tyr Leu Gly Leu Leu Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala
                245                 250                 255

Thr Ile Thr Leu Leu Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr
            260                 265                 270

Lys Ser Ala Ile Ser Arg Leu Asn Phe Thr Ala
        275                 280
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<210> 255
<211> 1431
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1408)
<223> RXA01756

<400> 255
gcttcaaaca ggatttaatc taaaatctta aacctcgtat tttccctgat aggctcagat 60

gcgcctgaaa tcgggcttgt tgaggggaga ggtgtgtgac atg aaa gag ttg gaa 115
                                                Met Lys Glu Leu Glu

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                                                    1               5

ctg ggc gag gcg agg gac gtc gct gca acg ttg gaa gcg atg ccg atc   163
Leu Gly Glu Ala Arg Asp Val Ala Ala Thr Leu Glu Ala Met Pro Ile
                10                  15                  20

cag gag gtt att gat cag gtt gag cga act tct ata act aaa ggt gcg   211
Gln Glu Val Ile Asp Gln Val Glu Arg Thr Ser Ile Thr Lys Gly Ala
            25                  30                  35

gta ctg ctg cgt ctg ctc agt aaa gat cga tcg ttg ttg gtc ttc gat   259
Val Leu Leu Arg Leu Leu Ser Lys Asp Arg Ser Leu Leu Val Phe Asp
        40                  45                  50

gct ctt ggt ccg cga ctc cag gct gat ctc att ggt gct ttt cag gat   307
Ala Leu Gly Pro Arg Leu Gln Ala Asp Leu Ile Gly Ala Phe Gln Asp
    55                  60                  65

gcg gaa gtg ctg gat tat ttc gct gac ctt gac cct gat gac cgc gtt   355
Ala Glu Val Leu Asp Tyr Phe Ala Asp Leu Asp Pro Asp Asp Arg Val
70                  75                  80                  85

tca ctg ctt gat gag ctg ccg gcg tcg atc gct gac gag ttg ctt cgc   403
Ser Leu Leu Asp Glu Leu Pro Ala Ser Ile Ala Asp Glu Leu Leu Arg
                90                  95                  100

agt ctc gat ccg cag gaa aag cag gtc acg gag ctg gtc ttg ggt tac   451
Ser Leu Asp Pro Gln Glu Lys Gln Val Thr Glu Leu Val Leu Gly Tyr
            105                 110                 115

gca aag ggg tcg gtt gga cgt tgg atg tcg ccc cag gtt tta ttg ctt   499
Ala Lys Gly Ser Val Gly Arg Trp Met Ser Pro Gln Val Leu Leu Leu
        120                 125                 130

ttc gac gac atg tcc gtc gcc gaa gtc tta gat ttt gtg cgc aat cat   547
Phe Asp Asp Met Ser Val Ala Glu Val Leu Asp Phe Val Arg Asn His
    135                 140                 145

gct gct gag gct gag acg att tat gcc tta cct att gtg aac cgt gct   595
Ala Ala Glu Ala Glu Thr Ile Tyr Ala Leu Pro Ile Val Asn Arg Ala
150                 155                 160                 165

cgc caa gtg atg ggc gtg gtg tcg ttg cga aag ctg ttc atc gca gat   643
Arg Gln Val Met Gly Val Val Ser Leu Arg Lys Leu Phe Ile Ala Asp
                170                 175                 180

ccc act cta aaa gtc tcg gaa atc atg gtg cgt cct gtt tcg gtg ttg   691
Pro Thr Leu Lys Val Ser Glu Ile Met Val Arg Pro Val Ser Val Leu
            185                 190                 195

gcg tcc gcg gat att gaa gaa acc gcc cgc tgg ttc cta cag ttg gac   739
Ala Ser Ala Asp Ile Glu Glu Thr Ala Arg Trp Phe Leu Gln Leu Asp
        200                 205                 210

ctc gtt gcg atg ccc gtt gtg gat gaa tcg aac atg ctc tta gga gtg   787
Leu Val Ala Met Pro Val Val Asp Glu Ser Asn Met Leu Leu Gly Val
    215                 220                 225

ctg acc ttc gat gat gcg caa gac atc gtg gag caa gcc gac tct gag   835
Leu Thr Phe Asp Asp Ala Gln Asp Ile Val Glu Gln Ala Asp Ser Glu
230                 235                 240                 245
```

```
gac tcc gct cgc agt ggt ggt tcg gaa cct ctc cag cag ccg tat cta   883
Asp Ser Ala Arg Ser Gly Gly Ser Glu Pro Leu Gln Gln Pro Tyr Leu
                250                 255                 260

tcc acg ccg att cgg aaa ctg gtg aag tcc cgc atc gta tgg ctt ctg   931
Ser Thr Pro Ile Arg Lys Leu Val Lys Ser Arg Ile Val Trp Leu Leu
            265                 270                 275

gtt ttg gca gtg tca gca att ttg acg gtt caa gtt ctt gat att ttc   979
Val Leu Ala Val Ser Ala Ile Leu Thr Val Gln Val Leu Asp Ile Phe
        280                 285                 290

gaa gcc acc ttg gtt gaa gcc gtg gta ctg gca ttg ttc att cct ttg   1027
Glu Ala Thr Leu Val Glu Ala Val Val Leu Ala Leu Phe Ile Pro Leu
    295                 300                 305

ctc act ggt act ggc gga aac acc gga aac caa gct gca aca acc gtg   1075
Leu Thr Gly Thr Gly Gly Asn Thr Gly Asn Gln Ala Ala Thr Thr Val
310                 315                 320                 325

acc cgt gcg ctc gca ttg ggt gac gtc cga aaa tca gat gtc ttc cgc   1123
Thr Arg Ala Leu Ala Leu Gly Asp Val Arg Lys Ser Asp Val Phe Arg
                330                 335                 340

gtc ttg ggc aga gaa atc cga gtc ggc ctc atg ctc ggg gca ttg ttg   1171
Val Leu Gly Arg Glu Ile Arg Val Gly Leu Met Leu Gly Ala Leu Leu
            345                 350                 355

ggt gcc gtt gga ttt gtg atc gca tcg ctt gtt tac ggc atg ccc gta   1219
Gly Ala Val Gly Phe Val Ile Ala Ser Leu Val Tyr Gly Met Pro Val
        360                 365                 370

ggc act gtc atc ggt ctg aca ttg ttg gcg gtg tgc acg atg gcc gca   1267
Gly Thr Val Ile Gly Leu Thr Leu Leu Ala Val Cys Thr Met Ala Ala
    375                 380                 385

tca gtt ggc gga gta atg cca att att gcc aag gcg atc gga gcg gac   1315
Ser Val Gly Gly Val Met Pro Ile Ile Ala Lys Ala Ile Gly Ala Asp
390                 395                 400                 405

cca gcg gtg ttc tct aat cct ttt att tca acc ttc tgt gat gca aca   1363
Pro Ala Val Phe Ser Asn Pro Phe Ile Ser Thr Phe Cys Asp Ala Thr
                410                 415                 420

ggt ttg atc atc tac ttt gca att gcc aag ttg gtg ctc gga atc       1408
Gly Leu Ile Ile Tyr Phe Ala Ile Ala Lys Leu Val Leu Gly Ile
            425                 430                 435

taaaagattt ttgcttttcg acg                                       1431


<210> 256
<211> 436
<212> PRT
<213> Corynebacterium glutamicum

<400> 256
Met Lys Glu Leu Glu Leu Gly Glu Ala Arg Asp Val Ala Ala Thr Leu
  1               5                  10                  15
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Glu Ala Met Pro Ile Gln Glu Val Ile Asp Gln Val Glu Arg Thr Ser
20 25 30

Ile Thr Lys Gly Ala Val Leu Leu Arg Leu Leu Ser Lys Asp Arg Ser
35 40 45

Leu Leu Val Phe Asp Ala Leu Gly Pro Arg Leu Gln Ala Asp Leu Ile
50 55 60

Gly Ala Phe Gln Asp Ala Glu Val Leu Asp Tyr Phe Ala Asp Leu Asp
65 70 75 80

Pro Asp Asp Arg Val Ser Leu Leu Asp Glu Leu Pro Ala Ser Ile Ala
85 90 95

Asp Glu Leu Leu Arg Ser Leu Asp Pro Gln Glu Lys Gln Val Thr Glu
100 105 110

Leu Val Leu Gly Tyr Ala Lys Gly Ser Val Gly Arg Trp Met Ser Pro
115 120 125

Gln Val Leu Leu Leu Phe Asp Asp Met Ser Val Ala Glu Val Leu Asp
130 135 140

Phe Val Arg Asn His Ala Ala Glu Ala Glu Thr Ile Tyr Ala Leu Pro
145 150 155 160

Ile Val Asn Arg Ala Arg Gln Val Met Gly Val Val Ser Leu Arg Lys
165 170 175

Leu Phe Ile Ala Asp Pro Thr Leu Lys Val Ser Glu Ile Met Val Arg
180 185 190

Pro Val Ser Val Leu Ala Ser Ala Asp Ile Glu Glu Thr Ala Arg Trp
195 200 205

Phe Leu Gln Leu Asp Leu Val Ala Met Pro Val Val Asp Glu Ser Asn
210 215 220

Met Leu Leu Gly Val Leu Thr Phe Asp Asp Ala Gln Asp Ile Val Glu
225 230 235 240

Gln Ala Asp Ser Glu Asp Ser Ala Arg Ser Gly Gly Ser Glu Pro Leu
245 250 255

Gln Gln Pro Tyr Leu Ser Thr Pro Ile Arg Lys Leu Val Lys Ser Arg
260 265 270

Ile Val Trp Leu Leu Val Leu Ala Val Ser Ala Ile Leu Thr Val Gln
275 280 285

Val Leu Asp Ile Phe Glu Ala Thr Leu Val Glu Ala Val Val Leu Ala
290 295 300

Leu Phe Ile Pro Leu Leu Thr Gly Thr Gly Gly Asn Thr Gly Asn Gln
305 310 315 320

Ala Ala Thr Thr Val Thr Arg Ala Leu Ala Leu Gly Asp Val Arg Lys
325 330 335

Ser Asp Val Phe Arg Val Leu Gly Arg Glu Ile Arg Val Gly Leu Met

```
            340                 345                 350

Leu Gly Ala Leu Leu Gly Ala Val Gly Phe Val Ile Ala Ser Leu Val
        355                 360                 365

Tyr Gly Met Pro Val Gly Thr Val Ile Gly Leu Thr Leu Leu Ala Val
    370                 375                 380

Cys Thr Met Ala Ala Ser Val Gly Gly Val Met Pro Ile Ile Ala Lys
385                 390                 395                 400

Ala Ile Gly Ala Asp Pro Ala Val Phe Ser Asn Pro Phe Ile Ser Thr
                405                 410                 415

Phe Cys Asp Ala Thr Gly Leu Ile Ile Tyr Phe Ala Ile Ala Lys Leu
            420                 425                 430

Val Leu Gly Ile
        435
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<210> 257
<211> 1142
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1119)
<223> RXA02068

<400> 257

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att ttt gtc ccc atg ttg cgt atc gct gcc att gaa ccg aaa gac att   48
Ile Phe Val Pro Met Leu Arg Ile Ala Ala Ile Glu Pro Lys Asp Ile
  1               5                  10                  15

act ttg gtt acc ggt tct gta tca ctt cga acc ttt cgc gtg cgc acc   96
Thr Leu Val Thr Gly Ser Val Ser Leu Arg Thr Phe Arg Val Arg Thr
             20                  25                  30

ggt gaa ttg cag gtc atg ggc gat att gtg ggt gca aaa gta cat acc   144
Gly Glu Leu Gln Val Met Gly Asp Ile Val Gly Ala Lys Val His Thr
         35                  40                  45

gat gat cca gag ctg caa caa ttc cac ggt cgc gcg gta gaa atc gcc   192
Asp Asp Pro Glu Leu Gln Gln Phe His Gly Arg Ala Val Glu Ile Ala
     50                  55                  60

gat gtg gag ctg gag tta tcg cgc act cgc gat tgg atc atc acg cgc   240
Asp Val Glu Leu Glu Leu Ser Arg Thr Arg Asp Trp Ile Ile Thr Arg
 65                  70                  75                  80

gtg gcg gtg ctg ggt gag cgc cct aaa ttt ggc cgg cgc cca gtg ctg   288
Val Ala Val Leu Gly Glu Arg Pro Lys Phe Gly Arg Arg Pro Val Leu
                 85                  90                  95

cac aca gtg ccg tgg agt cat atc cac ggc atc acc gca ggt ggt gtc   336
His Thr Val Pro Trp Ser His Ile His Gly Ile Thr Ala Gly Gly Val
            100                 105                 110

ggc gag tcc aat cac acc gcc gaa ctc atc gca ggg ttt gag gat atg   384
```

```
Gly Glu Ser Asn His Thr Ala Glu Leu Ile Ala Gly Phe Glu Asp Met
        115                 120                 125

agg cct gcg gac gtc gca aag cag ctt tat cag ctg cct acg gct cag   432
Arg Pro Ala Asp Val Ala Lys Gln Leu Tyr Gln Leu Pro Thr Ala Gln
    130                 135                 140

cgt acc gaa gtg acg gaa gag ctt gac gac gaa aag ctg gcg gat atc   480
Arg Thr Glu Val Thr Glu Glu Leu Asp Asp Glu Lys Leu Ala Asp Ile
145                 150                 155                 160

ctg cag gaa ttg tcc gag gac cgc caa gcc gag ttg att gaa gaa tta   528
Leu Gln Glu Leu Ser Glu Asp Arg Gln Ala Glu Leu Ile Glu Glu Leu
                165                 170                 175

gac atc gaa cgt gcc gcg gac att ctg gag gaa atg gat cca gat gat   576
Asp Ile Glu Arg Ala Ala Asp Ile Leu Glu Glu Met Asp Pro Asp Asp
            180                 185                 190

gct gca gac ttg ttg ggt gag ctg cct gat gac aaa gct gat gtg ttg   624
Ala Ala Asp Leu Leu Gly Glu Leu Pro Asp Asp Lys Ala Asp Val Leu
        195                 200                 205

ttg gat ctg atg gac cct gag gaa tct gcg ccg gtg cgt cgt ttg atg   672
Leu Asp Leu Met Asp Pro Glu Glu Ser Ala Pro Val Arg Arg Leu Met
    210                 215                 220

gat ttc tcc ccg gac acc gtt ggt gcg ctg atg act cct gag cca tta   720
Asp Phe Ser Pro Asp Thr Val Gly Ala Leu Met Thr Pro Glu Pro Leu
225                 230                 235                 240

att atg gat cct tcc acc aca gtc gct gaa gcg ttg gcg atg gcc aga   768
Ile Met Asp Pro Ser Thr Thr Val Ala Glu Ala Leu Ala Met Ala Arg
                245                 250                 255

aac ccc gac ctt cct act tct ttg gca tcg ttg atc ttt gtg gtg cgc   816
Asn Pro Asp Leu Pro Thr Ser Leu Ala Ser Leu Ile Phe Val Val Arg
            260                 265                 270

cca ccc acg gcc acg cct act gga aaa tac ctc ggc tgc gtg cat ctg   864
Pro Pro Thr Ala Thr Pro Thr Gly Lys Tyr Leu Gly Cys Val His Leu
        275                 280                 285

cag aaa ctg ctt cgg gag cct cca tca agt ttg att ggt ggc atc ctc   912
Gln Lys Leu Leu Arg Glu Pro Pro Ser Ser Leu Ile Gly Gly Ile Leu
    290                 295                 300

gac ccc gat ctg cca ccg ctc tac gct gat gat tct caa gaa acc gca   960
Asp Pro Asp Leu Pro Pro Leu Tyr Ala Asp Asp Ser Gln Glu Thr Ala
305                 310                 315                 320

gct cga ttc ttt gcc acc tac aac ttg gtg tgc ggc ccc gtc ttg gat  1008
Ala Arg Phe Phe Ala Thr Tyr Asn Leu Val Cys Gly Pro Val Leu Asp
                325                 330                 335

gaa aac cgc cat ctg ctt ggt gcc gta gct gtc gat gac ttg ctc gac  1056
Glu Asn Arg His Leu Leu Gly Ala Val Ala Val Asp Asp Leu Leu Asp
            340                 345                 350

cac atg ctg cca gaa gac tgg cgc gac gcc gga atc cga cca gga aag  1104
His Met Leu Pro Glu Asp Trp Arg Asp Ala Gly Ile Arg Pro Gly Lys
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355 360 365

gag cac acc cat ggc tgatttcaac cgctctgaat tag 1142
Glu His Thr His Gly
370

<210> 258
<211> 373
<212> PRT
<213> Corynebacterium glutamicum

<400> 258
Ile Phe Val Pro Met Leu Arg Ile Ala Ala Ile Glu Pro Lys Asp Ile
1 5 10 15

Thr Leu Val Thr Gly Ser Val Ser Leu Arg Thr Phe Arg Val Arg Thr
20 25 30

Gly Glu Leu Gln Val Met Gly Asp Ile Val Gly Ala Lys Val His Thr
35 40 45

Asp Asp Pro Glu Leu Gln Gln Phe His Gly Arg Ala Val Glu Ile Ala
50 55 60

Asp Val Glu Leu Glu Leu Ser Arg Thr Arg Asp Trp Ile Ile Thr Arg
65 70 75 80

Val Ala Val Leu Gly Glu Arg Pro Lys Phe Gly Arg Arg Pro Val Leu
85 90 95

His Thr Val Pro Trp Ser His Ile His Gly Ile Thr Ala Gly Gly Val
100 105 110

Gly Glu Ser Asn His Thr Ala Glu Leu Ile Ala Gly Phe Glu Asp Met
115 120 125

Arg Pro Ala Asp Val Ala Lys Gln Leu Tyr Gln Leu Pro Thr Ala Gln
130 135 140

Arg Thr Glu Val Thr Glu Glu Leu Asp Asp Glu Lys Leu Ala Asp Ile
145 150 155 160

Leu Gln Glu Leu Ser Glu Asp Arg Gln Ala Glu Leu Ile Glu Glu Leu
165 170 175

Asp Ile Glu Arg Ala Ala Asp Ile Leu Glu Glu Met Asp Pro Asp Asp
180 185 190

Ala Ala Asp Leu Leu Gly Glu Leu Pro Asp Asp Lys Ala Asp Val Leu
195 200 205

Leu Asp Leu Met Asp Pro Glu Glu Ser Ala Pro Val Arg Arg Leu Met
210 215 220

Asp Phe Ser Pro Asp Thr Val Gly Ala Leu Met Thr Pro Glu Pro Leu
225 230 235 240

Ile Met Asp Pro Ser Thr Thr Val Ala Glu Ala Leu Ala Met Ala Arg
245 250 255

US13/45,045

```
Asn Pro Asp Leu Pro Thr Ser Leu Ala Ser Leu Ile Phe Val Val Arg
            260                 265                 270

Pro Pro Thr Ala Thr Pro Thr Gly Lys Tyr Leu Gly Cys Val His Leu
        275                 280                 285

Gln Lys Leu Leu Arg Glu Pro Pro Ser Ser Leu Ile Gly Gly Ile Leu
    290                 295                 300

Asp Pro Asp Leu Pro Pro Leu Tyr Ala Asp Asp Ser Gln Glu Thr Ala
305                 310                 315                 320

Ala Arg Phe Phe Ala Thr Tyr Asn Leu Val Cys Gly Pro Val Leu Asp
                325                 330                 335

Glu Asn Arg His Leu Leu Gly Ala Val Ala Val Asp Asp Leu Leu Asp
            340                 345                 350

His Met Leu Pro Glu Asp Trp Arg Asp Ala Gly Ile Arg Pro Gly Lys
        355                 360                 365

Glu His Thr His Gly
    370
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<210> 259
<211> 538
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> RXA00665

<400> 259

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accaaacact tctgtgcgtg acacgcgcca ccttatactc ccacaagcaa cacagaacac 60

tcgggatctc aaagtttcga gaaacacaga aagggcagca atg agc agc tca aca   115
                                              Met Ser Ser Ser Thr
                                                1               5

ctt ctc ctg gct tca gga caa gtc acg gca tta gcc gct gac tac acg   163
Leu Leu Leu Ala Ser Gly Gln Val Thr Ala Leu Ala Ala Asp Tyr Thr
                  10                  15                  20

ctc agc cac acc ccc tca gat ggc atc ctg gta gtc ctt ggc ttc gcc   211
Leu Ser His Thr Pro Ser Asp Gly Ile Leu Val Val Leu Gly Phe Ala
              25                  30                  35

atg atc ctc acc ttc atg acc ctg atc atg ctg ggt cga ctc acc cca   259
Met Ile Leu Thr Phe Met Thr Leu Ile Met Leu Gly Arg Leu Thr Pro
          40                  45                  50

atg gtg gcc atg ctg ttg gtc ccc acc atc ttc ggt ctc atc gcc ggc   307
Met Val Ala Met Leu Leu Val Pro Thr Ile Phe Gly Leu Ile Ala Gly
      55                  60                  65

gca gga ctc ggc ctt ggt gac atg gcg ctt gac gcc atc aag gac atg   355
Ala Gly Leu Gly Leu Gly Asp Met Ala Leu Asp Ala Ile Lys Asp Met
  70                  75                  80                  85
```

```
gcg cct acc gcg gca ctc ctg atg ttc gcg att atg ttc ttc gga atc   403
Ala Pro Thr Ala Ala Leu Leu Met Phe Ala Ile Met Phe Phe Gly Ile
                 90                  95                 100

atg atc gac gtc gga ctc ttc gac ccc ctg atc cgc gtg atc acc cgc   451
Met Ile Asp Val Gly Leu Phe Asp Pro Leu Ile Arg Val Ile Thr Arg
            105                 110                 115

gtt ctt cac gat gac ccc gca aag gtc gtc atc ggc acc gca gta ctt   499
Val Leu His Asp Asp Pro Ala Lys Val Val Ile Gly Thr Ala Val Leu
        120                 125                 130

gca ggt gtt gtc tcc ctc gac ggc gac ggc tcc acc acc               538
Ala Gly Val Val Ser Leu Asp Gly Asp Gly Ser Thr Thr
    135                 140                 145
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<210> 260
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 260

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Met Ser Ser Ser Thr Leu Leu Leu Ala Ser Gly Gln Val Thr Ala Leu
  1               5                  10                  15

Ala Ala Asp Tyr Thr Leu Ser His Thr Pro Ser Asp Gly Ile Leu Val
             20                  25                  30

Val Leu Gly Phe Ala Met Ile Leu Thr Phe Met Thr Leu Ile Met Leu
         35                  40                  45

Gly Arg Leu Thr Pro Met Val Ala Met Leu Leu Val Pro Thr Ile Phe
     50                  55                  60

Gly Leu Ile Ala Gly Ala Gly Leu Gly Leu Gly Asp Met Ala Leu Asp
 65                  70                  75                  80

Ala Ile Lys Asp Met Ala Pro Thr Ala Ala Leu Leu Met Phe Ala Ile
                 85                  90                  95

Met Phe Phe Gly Ile Met Ile Asp Val Gly Leu Phe Asp Pro Leu Ile
            100                 105                 110

Arg Val Ile Thr Arg Val Leu His Asp Asp Pro Ala Lys Val Val Ile
        115                 120                 125

Gly Thr Ala Val Leu Ala Gly Val Val Ser Leu Asp Gly Asp Gly Ser
    130                 135                 140

Thr Thr
145
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<210> 261
<211> 281
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (1)..(258)
<223> RXA02808

<400> 261
ttt tac ttc ggc atc ctc cca gtc ctt gca gaa agt gct tcc cac ttc 48
Phe Tyr Phe Gly Ile Leu Pro Val Leu Ala Glu Ser Ala Ser His Phe
1 5 10 15

ggc atc gag cct gtg gaa atg gcc cgc gca tcc atc act ggc cag ccc 96
Gly Ile Glu Pro Val Glu Met Ala Arg Ala Ser Ile Thr Gly Gln Pro
20 25 30

gtt cac atg caa agc ccg ctg gtc cca gcg atc ctc ctg ctg gtt tcc 144
Val His Met Gln Ser Pro Leu Val Pro Ala Ile Leu Leu Leu Val Ser
35 40 45

ctc gcc aac gtc aac ctt ggc gac cac cac aag aag gtt ctg tgg cgc 192
Leu Ala Asn Val Asn Leu Gly Asp His His Lys Lys Val Leu Trp Arg
50 55 60

gcc tgc atc gtg tcc atc gcg atg ctc gcc gta gcc ctc ttc atc ggc 240
Ala Cys Ile Val Ser Ile Ala Met Leu Ala Val Ala Leu Phe Ile Gly
65 70 75 80

gtc gtg cca ctc agc gca taaaatagct tttcgacgcc aaa 281
Val Val Pro Leu Ser Ala
85

<210> 262
<211> 86
<212> PRT
<213> Corynebacterium glutamicum

<400> 262
Phe Tyr Phe Gly Ile Leu Pro Val Leu Ala Glu Ser Ala Ser His Phe
1 5 10 15

Gly Ile Glu Pro Val Glu Met Ala Arg Ala Ser Ile Thr Gly Gln Pro
20 25 30

Val His Met Gln Ser Pro Leu Val Pro Ala Ile Leu Leu Leu Val Ser
35 40 45

Leu Ala Asn Val Asn Leu Gly Asp His His Lys Lys Val Leu Trp Arg
50 55 60

Ala Cys Ile Val Ser Ile Ala Met Leu Ala Val Ala Leu Phe Ile Gly
65 70 75 80

Val Val Pro Leu Ser Ala
85

<210> 263
<211> 960
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(937)
<223> RXN00444

<400> 263
tacccaatgg cattgaccac caccggtgaa gacaacgagg tagcgaaggc tttcgcagag 60

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ttcctcagca gcgatcgtgc caaggagatc cttgccagct atg gtt ttg gca caa   115
                                              Met Val Leu Ala Gln
                                                1               5

act aaa aag gct cgt cga agc gag aat cat atc ctc cca ggg tgg ttg   163
Thr Lys Lys Ala Arg Arg Ser Glu Asn His Ile Leu Pro Gly Trp Leu
                   10                  15                  20

ctc atc cca gcc acc ctg gcc atg ctg ctg atc att gga cct att ttt   211
Leu Ile Pro Ala Thr Leu Ala Met Leu Leu Ile Ile Gly Pro Ile Phe
               25                  30                  35

gct ttg ctg ttg cag atc ccc tgg gat cgg tct tgg gag ttg ctt acc   259
Ala Leu Leu Leu Gln Ile Pro Trp Asp Arg Ser Trp Glu Leu Leu Thr
           40                  45                  50

gcg ccg gaa tct tta gga acc gca cgg tta tct atc gga act gct ctg   307
Ala Pro Glu Ser Leu Gly Thr Ala Arg Leu Ser Ile Gly Thr Ala Leu
       55                  60                  65

ttt tct acc gcg cta tgc gca att gtg ggt ttc ccg cta gcg ttg gcg   355
Phe Ser Thr Ala Leu Cys Ala Ile Val Gly Phe Pro Leu Ala Leu Ala
   70                  75                  80                  85

ctg cat tta tat gag cgt tcg cac ccc agg gtg aca tca gtt ttg acg   403
Leu His Leu Tyr Glu Arg Ser His Pro Arg Val Thr Ser Val Leu Thr
                   90                  95                 100

gtg ctg gtt tat gcg cct ttg gtg ttg tcg ccg gtg gtg tct ggt ttg   451
Val Leu Val Tyr Ala Pro Leu Val Leu Ser Pro Val Val Ser Gly Leu
               105                 110                 115

gcg ctg act ttt ctg tgg ggc agg cgt ggt ttt tta ggt tct tgg ctt   499
Ala Leu Thr Phe Leu Trp Gly Arg Arg Gly Phe Leu Gly Ser Trp Leu
           120                 125                 130

gat cag gtt gga ttg ccg att gca ttt acc acc acg gct gtg gtg ttt   547
Asp Gln Val Gly Leu Pro Ile Ala Phe Thr Thr Thr Ala Val Val Phe
       135                 140                 145

gcc cag gtg ttt gta gcg ttg cca ttt ttc att tcc act gtg act act   595
Ala Gln Val Phe Val Ala Leu Pro Phe Phe Ile Ser Thr Val Thr Thr
   150                 155                 160                 165

gca ctg cgt ggc att cca aaa cag ttt gag gaa atc gca gct act gaa   643
Ala Leu Arg Gly Ile Pro Lys Gln Phe Glu Glu Ile Ala Ala Thr Glu
                   170                 175                 180

ggc gca acc cgc tgg gag atc atg cac aag atg atc att ccg ctg gcg   691
Gly Ala Thr Arg Trp Glu Ile Met His Lys Met Ile Ile Pro Leu Ala
               185                 190                 195

atg cct gga att ttc acc ggt atg att ttg gga ttc gcc agg gcc ttg   739
Met Pro Gly Ile Phe Thr Gly Met Ile Leu Gly Phe Ala Arg Ala Leu
```

```
        200                 205                 210

ggc gag tat ggt gcg aca ctg act ttt gct gga aat att gca ggt gtt   787
Gly Glu Tyr Gly Ala Thr Leu Thr Phe Ala Gly Asn Ile Ala Gly Val
    215                 220                 225

acc cgc acc att ccg ttg cat att gag ctt ggt ttg agt tcc aat gac   835
Thr Arg Thr Ile Pro Leu His Ile Glu Leu Gly Leu Ser Ser Asn Asp
230                 235                 240                 245

atg gat aaa gcc ttg gga gcg gtg att atg ctt ttg gct gtc tat gtc   883
Met Asp Lys Ala Leu Gly Ala Val Ile Met Leu Leu Ala Val Tyr Val
                250                 255                 260

ctc atc att gga gcc atc gga gcg tta cga ttg ttt tcc aag gtg aga   931
Leu Ile Ile Gly Ala Ile Gly Ala Leu Arg Leu Phe Ser Lys Val Arg
            265                 270                 275

aag gtt taattgatgt ctcgttcgcc gga                                 960
Lys Val
```

US-09-942-050-264

<210> 264
<211> 279
<212> PRT
<213> Corynebacterium glutamicum

<400> 264

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Met Val Leu Ala Gln Thr Lys Lys Ala Arg Arg Ser Glu Asn His Ile
  1               5                  10                  15

Leu Pro Gly Trp Leu Leu Ile Pro Ala Thr Leu Ala Met Leu Leu Ile
             20                  25                  30

Ile Gly Pro Ile Phe Ala Leu Leu Leu Gln Ile Pro Trp Asp Arg Ser
         35                  40                  45

Trp Glu Leu Leu Thr Ala Pro Glu Ser Leu Gly Thr Ala Arg Leu Ser
     50                  55                  60

Ile Gly Thr Ala Leu Phe Ser Thr Ala Leu Cys Ala Ile Val Gly Phe
 65                  70                  75                  80

Pro Leu Ala Leu Ala Leu His Leu Tyr Glu Arg Ser His Pro Arg Val
                 85                  90                  95

Thr Ser Val Leu Thr Val Leu Val Tyr Ala Pro Leu Val Leu Ser Pro
            100                 105                 110

Val Val Ser Gly Leu Ala Leu Thr Phe Leu Trp Gly Arg Arg Gly Phe
        115                 120                 125

Leu Gly Ser Trp Leu Asp Gln Val Gly Leu Pro Ile Ala Phe Thr Thr
    130                 135                 140

Thr Ala Val Val Phe Ala Gln Val Phe Val Ala Leu Pro Phe Phe Ile
145                 150                 155                 160

Ser Thr Val Thr Thr Ala Leu Arg Gly Ile Pro Lys Gln Phe Glu Glu
                165                 170                 175
```

```
Ile Ala Ala Thr Glu Gly Ala Thr Arg Trp Glu Ile Met His Lys Met
            180                 185                 190

Ile Ile Pro Leu Ala Met Pro Gly Ile Phe Thr Gly Met Ile Leu Gly
        195                 200                 205

Phe Ala Arg Ala Leu Gly Glu Tyr Gly Ala Thr Leu Thr Phe Ala Gly
    210                 215                 220

Asn Ile Ala Gly Val Thr Arg Thr Ile Pro Leu His Ile Glu Leu Gly
225                 230                 235                 240

Leu Ser Ser Asn Asp Met Asp Lys Ala Leu Gly Ala Val Ile Met Leu
                245                 250                 255

Leu Ala Val Tyr Val Leu Ile Ile Gly Ala Ile Gly Ala Leu Arg Leu
            260                 265                 270

Phe Ser Lys Val Arg Lys Val
        275
```

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<210> 265
<211> 900
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(877)
<223> FRXA00444

<400> 265

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gatcgtgcca aggagatcct tgccagcnnn nnnnntnnna ntggttttgg cacaaactaa 60

aaaggctcgt cgaagcgaga atcatatcct cccagggtgg ttg ctc atc cca gcc   115
                                          Leu Leu Ile Pro Ala
                                            1               5

acc ctg gcc atg ctg ctg atc att gga cct att ttt gct ttg ctg ttg   163
Thr Leu Ala Met Leu Leu Ile Ile Gly Pro Ile Phe Ala Leu Leu Leu
                10                  15                  20

cag atc ccc tgg gat cgg tct tgg gag ttg ctt acc gcg ccg gaa tct   211
Gln Ile Pro Trp Asp Arg Ser Trp Glu Leu Leu Thr Ala Pro Glu Ser
            25                  30                  35

tta gga acc gca cgg tta tct atc gga act gct ctg ttt tct acc gcg   259
Leu Gly Thr Ala Arg Leu Ser Ile Gly Thr Ala Leu Phe Ser Thr Ala
        40                  45                  50

cta tgc gca att gtg ggt ttc ccg cta gcg ttg gcg ctg cat tta tat   307
Leu Cys Ala Ile Val Gly Phe Pro Leu Ala Leu Ala Leu His Leu Tyr
    55                  60                  65

gag cgt tcg cac ccc agg gtg aca tca gtt ttg acg gtg ctg gtt tat   355
Glu Arg Ser His Pro Arg Val Thr Ser Val Leu Thr Val Leu Val Tyr
70                  75                  80                  85

gcg cct ttg gtg ttg tcg ccg gtg gtg tct ggt ttg gcg ctg act ttt   403
```

```
Ala Pro Leu Val Leu Ser Pro Val Val Ser Gly Leu Ala Leu Thr Phe
                 90                  95                 100

ctg tgg ggc agg cgt ggt ttt tta ggt tct tgg ctt gat cag gtt gga   451
Leu Trp Gly Arg Arg Gly Phe Leu Gly Ser Trp Leu Asp Gln Val Gly
            105                 110                 115

ttg ccg att gca ttt acc acc acg gct gtg gtg ttt gcc cag gtg ttt   499
Leu Pro Ile Ala Phe Thr Thr Thr Ala Val Val Phe Ala Gln Val Phe
        120                 125                 130

gta gcg ttg cca ttt ttc att tcc act gtg act act gca ctg cgt ggc   547
Val Ala Leu Pro Phe Phe Ile Ser Thr Val Thr Thr Ala Leu Arg Gly
    135                 140                 145

att cca aaa cag ttt gag gaa atc gca gct act gaa ggc gca acc cgc   595
Ile Pro Lys Gln Phe Glu Glu Ile Ala Ala Thr Glu Gly Ala Thr Arg
150                 155                 160                 165

tgg gag atc atg cac aag atg atc att ccg ctg gcg atg cct gga att   643
Trp Glu Ile Met His Lys Met Ile Ile Pro Leu Ala Met Pro Gly Ile
                170                 175                 180

ttc acc ggt atg att ttg gga ttc gcc agg gcc ttg ggc gag tat ggt   691
Phe Thr Gly Met Ile Leu Gly Phe Ala Arg Ala Leu Gly Glu Tyr Gly
            185                 190                 195

gcg aca ctg act ttt gct gga aat att gca ggt gtt acc cgc acc att   739
Ala Thr Leu Thr Phe Ala Gly Asn Ile Ala Gly Val Thr Arg Thr Ile
        200                 205                 210

ccg ttg cat att gag ctt ggt ttg agt tcc aat gac atg gat aaa gcc   787
Pro Leu His Ile Glu Leu Gly Leu Ser Ser Asn Asp Met Asp Lys Ala
    215                 220                 225

ttg gga gcg gtg att atg ctt ttg gct gtc tat gtc ctc atc att gga   835
Leu Gly Ala Val Ile Met Leu Leu Ala Val Tyr Val Leu Ile Ile Gly
230                 235                 240                 245

gcc atc gga gcg tta cga ttg ttt tcc aag gtg aga aag gtt           877
Ala Ile Gly Ala Leu Arg Leu Phe Ser Lys Val Arg Lys Val
                250                 255

taattgatgt ctcgttcgcc gga                                        900
```

<210> 266
<211> 259
<212> PRT
<213> Corynebacterium glutamicum

<400> 266

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Leu Leu Ile Pro Ala Thr Leu Ala Met Leu Leu Ile Ile Gly Pro Ile
  1               5                  10                  15

Phe Ala Leu Leu Leu Gln Ile Pro Trp Asp Arg Ser Trp Glu Leu Leu
            20                  25                  30

Thr Ala Pro Glu Ser Leu Gly Thr Ala Arg Leu Ser Ile Gly Thr Ala
        35                  40                  45
```

Leu Phe Ser Thr Ala Leu Cys Ala Ile Val Gly Phe Pro Leu Ala Leu
50 55 60

Ala Leu His Leu Tyr Glu Arg Ser His Pro Arg Val Thr Ser Val Leu
65 70 75 80

Thr Val Leu Val Tyr Ala Pro Leu Val Leu Ser Pro Val Val Ser Gly
85 90 95

Leu Ala Leu Thr Phe Leu Trp Gly Arg Arg Gly Phe Leu Gly Ser Trp
100 105 110

Leu Asp Gln Val Gly Leu Pro Ile Ala Phe Thr Thr Thr Ala Val Val
115 120 125

Phe Ala Gln Val Phe Val Ala Leu Pro Phe Phe Ile Ser Thr Val Thr
130 135 140

Thr Ala Leu Arg Gly Ile Pro Lys Gln Phe Glu Glu Ile Ala Ala Thr
145 150 155 160

Glu Gly Ala Thr Arg Trp Glu Ile Met His Lys Met Ile Ile Pro Leu
165 170 175

Ala Met Pro Gly Ile Phe Thr Gly Met Ile Leu Gly Phe Ala Arg Ala
180 185 190

Leu Gly Glu Tyr Gly Ala Thr Leu Thr Phe Ala Gly Asn Ile Ala Gly
195 200 205

Val Thr Arg Thr Ile Pro Leu His Ile Glu Leu Gly Leu Ser Ser Asn
210 215 220

Asp Met Asp Lys Ala Leu Gly Ala Val Ile Met Leu Leu Ala Val Tyr
225 230 235 240

Val Leu Ile Ile Gly Ala Ile Gly Ala Leu Arg Leu Phe Ser Lys Val
245 250 255

Arg Lys Val

<210> 267
<211> 852
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(829)
<223> RXN02614

<400> 267
tcattgtata cgccaccctc ggtctgctgt ctgaagcgct gatcagagct tgggaacgtc 60

acaccttccg ctaccgaaac gcataagaaa gttgctcgcc atg act gcc aca ttg 115
Met Thr Ala Thr Leu
1 5

tca ctc aaa ccc gca gcc act gtc cgt gga ttg cgc aaa tca tac gga 163

```
Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu Arg Lys Ser Tyr Gly
                10                  15                  20

act aaa gaa gtc ctc caa gga atc gac ctc acc atc aac tgc ggc gaa   211
Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr Ile Asn Cys Gly Glu
            25                  30                  35

gta acc gcg ctg atc gga cgc tca ggt tca gga aaa tcc acc atc ctg   259
Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly Lys Ser Thr Ile Leu
        40                  45                  50

cgc gtg ttg gcg ggc cta tct aaa gag cat tcc ggc tct gta gaa att   307
Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser Gly Ser Val Glu Ile
    55                  60                  65

tcc gga aac ccg gcc gtt gcc ttc caa gag cct cgc ctg ttg ccg tgg   355
Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro Arg Leu Leu Pro Trp
70                  75                  80                  85

aaa acg gtg ctc gat aat gtg acc ttt ggc ctc aac cgc act gat att   403
Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu Asn Arg Thr Asp Ile
                90                  95                  100

tcc tgg tca gaa gca caa gaa cgc gcc tcg gca ctg ctt gca gaa gtc   451
Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala Leu Leu Ala Glu Val
            105                 110                 115

aaa ctt ccc gac tcc gac gcc gcc tgg ccc ctc acg ctc tcc ggc ggc   499
Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu Thr Leu Ser Gly Gly
        120                 125                 130

caa gcc cag cgc gtc tcc ctt gcg cga gcg ctc atc tcc gag cca gag   547
Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu Ile Ser Glu Pro Glu
    135                 140                 145

ctt ttg ctt ctc gac gaa ccc ttc ggc gcc ctc gat gct ctg aca aga   595
Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg
150                 155                 160                 165

ctg aca gcc caa gac ctg ctg ctc aaa acc gtg aac acc cga aac ttg   643
Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val Asn Thr Arg Asn Leu
                170                 175                 180

gga gtt ctg ctg gtc acc cat gat gtt tcc gag gcc atc gcc ctg gcc   691
Gly Val Leu Leu Val Thr His Asp Val Ser Glu Ala Ile Ala Leu Ala
            185                 190                 195

gac cac gtc ctt ctt ctt gac gac ggc gcc atc aca cac agt ttg act   739
Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile Thr His Ser Leu Thr
        200                 205                 210

gta gat atc ccc ggc gat cgc cgc acc cac ccc tcc ttt gcc tcc tac   787
Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro Ser Phe Ala Ser Tyr
    215                 220                 225

acc gct caa ctc ctt gag tgg ctc gaa atc acc aca cct gcc           829
Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr Thr Pro Ala
230                 235                 240

tagaaagaaa tcatgaaatt taa                                        852
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<210> 268
<211> 243
<212> PRT
<213> Corynebacterium glutamicum

<400> 268

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Met Thr Ala Thr Leu Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu
  1               5                  10                  15

Arg Lys Ser Tyr Gly Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr
             20                  25                  30

Ile Asn Cys Gly Glu Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly
         35                  40                  45

Lys Ser Thr Ile Leu Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser
     50                  55                  60

Gly Ser Val Glu Ile Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro
 65                  70                  75                  80

Arg Leu Leu Pro Trp Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu
                 85                  90                  95

Asn Arg Thr Asp Ile Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala
            100                 105                 110

Leu Leu Ala Glu Val Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu
        115                 120                 125

Thr Leu Ser Gly Gly Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu
    130                 135                 140

Ile Ser Glu Pro Glu Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu
145                 150                 155                 160

Asp Ala Leu Thr Arg Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val
                165                 170                 175

Asn Thr Arg Asn Leu Gly Val Leu Leu Val Thr His Asp Val Ser Glu
            180                 185                 190

Ala Ile Ala Leu Ala Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile
        195                 200                 205

Thr His Ser Leu Thr Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro
    210                 215                 220

Ser Phe Ala Ser Tyr Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr
225                 230                 235                 240

Thr Pro Ala
```

<210> 269
<211> 852
<212> DNA
<213> Corynebacterium glutamicum

US20050196749A1

<220>
<221> CDS
<222> (101)..(829)
<223> FRXA02614

<400> 269
tcattgtata cgccaccctc ggtctgctgt ctgaagcgct gatcagagct tgggaacgtc 60

acaccttccg ctaccgaaac gcataagaaa gttgctcgcc atg act gcc aca ttg 115
Met Thr Ala Thr Leu
1 5

tca ctc aaa ccc gca gcc act gtc cgt gga ttg cgc aaa tca tac gga 163
Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu Arg Lys Ser Tyr Gly
10 15 20

act aaa gaa gtc ctc caa gga atc gac ctc acc atc aac tgc ggc gaa 211
Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr Ile Asn Cys Gly Glu
25 30 35

gta acc gcg ctg atc gga cgc tca ggt tca gga aaa tcc acc atc ctg 259
Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly Lys Ser Thr Ile Leu
40 45 50

cgc gtg ttg gcg ggc cta tct aaa gag cat tcc ggc tct gta gaa att 307
Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser Gly Ser Val Glu Ile
55 60 65

tcc gga aac ccg gcc gtt gcc ttc caa gag cct cgc ctg ttg ccg tgg 355
Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro Arg Leu Leu Pro Trp
70 75 80 85

aaa acg gtg ctc gat aat gtg acc ttt ggc ctc aac cgc act gat att 403
Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu Asn Arg Thr Asp Ile
90 95 100

tcc tgg tca gaa gca caa gaa cgc gcc tcg gca ctg ctt gca gaa gtc 451
Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala Leu Leu Ala Glu Val
105 110 115

aaa ctt ccc gac tcc gac gcc gcc tgg ccc ctc acg ctc tcc ggc ggc 499
Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu Thr Leu Ser Gly Gly
120 125 130

caa gcc cag cgc gtc tcc ctt gcg cga gcg ctc atc tcc gag cca gag 547
Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu Ile Ser Glu Pro Glu
135 140 145

ctt ttg ctt ctc gac gaa ccc ttc ggc gcc ctc gat gct ctg aca aga 595
Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg
150 155 160 165

ctg aca gcc caa gac ctg ctg ctc aaa acc gtg aac acc cga aac ttg 643
Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val Asn Thr Arg Asn Leu
170 175 180

gga gtt ctg ctg gtc acc cat gat gtt tcc gag gcc atc gcc ctg gcc 691
Gly Val Leu Leu Val Thr His Asp Val Ser Glu Ala Ile Ala Leu Ala
185 190 195

gac cac gtc ctt ctt ctt gac gac ggc gcc atc aca cac agt ttg act 739

US 2013/0345058 A1

```
Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile Thr His Ser Leu Thr
        200                 205                 210

gta gat atc ccc ggc gat cgc cgc acc cac ccc tcc ttt gcc tcc tac   787
Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro Ser Phe Ala Ser Tyr
    215                 220                 225

acc gct caa ctc ctt gag tgg ctc gaa atc acc aca cct gcc           829
Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr Thr Pro Ala
230                 235                 240

tagaaagaaa tcatgaaatt taa                                        852
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<210> 270
<211> 243
<212> PRT
<213> Corynebacterium glutamicum

<400> 270

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Met Thr Ala Thr Leu Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu
  1               5                  10                  15

Arg Lys Ser Tyr Gly Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr
             20                  25                  30

Ile Asn Cys Gly Glu Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly
         35                  40                  45

Lys Ser Thr Ile Leu Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser
     50                  55                  60

Gly Ser Val Glu Ile Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro
 65                  70                  75                  80

Arg Leu Leu Pro Trp Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu
                 85                  90                  95

Asn Arg Thr Asp Ile Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala
            100                 105                 110

Leu Leu Ala Glu Val Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu
        115                 120                 125

Thr Leu Ser Gly Gly Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu
    130                 135                 140

Ile Ser Glu Pro Glu Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu
145                 150                 155                 160

Asp Ala Leu Thr Arg Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val
                165                 170                 175

Asn Thr Arg Asn Leu Gly Val Leu Leu Val Thr His Asp Val Ser Glu
            180                 185                 190

Ala Ile Ala Leu Ala Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile
        195                 200                 205

Thr His Ser Leu Thr Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro
    210                 215                 220
```

```
Ser Phe Ala Ser Tyr Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr
225                 230                 235                 240

Thr Pro Ala
```

<210> 271
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(598)
<223> RXN01142

<400> 271

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ctccccatcc accggcacag tcagcgcagg caacgaagaa attaaaggac caggacctga 60

ccgaggcatg gttttccaag accacgccct cctgccctga ttg acc gca cgc ggc   115
                                              Leu Thr Ala Arg Gly
                                                1               5

aac atc gac ttc ggg ctc cgc tcc gcg cgc ccc tcc ttg agc aaa acc   163
Asn Ile Asp Phe Gly Leu Arg Ser Ala Arg Pro Ser Leu Ser Lys Thr
                10                  15                  20

gaa cgc gcc gac atc acc cgc acc cac ctc gaa caa gta ggc ctc acc   211
Glu Arg Ala Asp Ile Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr
            25                  30                  35

gac gcc gcc gaa cgg cgc ccc gcc cgc ctc tcc ggc ggc atg caa cag   259
Asp Ala Ala Glu Arg Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln
        40                  45                  50

cga gtc ggc atc gca cgc gcc ttc gcc atc gac cca cca atc atg ctt   307
Arg Val Gly Ile Ala Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu
    55                  60                  65

ctc gac gaa ccc ttc ggc gcc ctc gac gcc ctc acc cgc cgc gaa ctc   355
Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu
70                  75                  80                  85

cag ctc caa cta ctc aac att tgg gaa gcc tcc cgc cgc acc gtc gtc   403
Gln Leu Gln Leu Leu Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val
                90                  95                  100

atg gtc acc cac gac gtc gac gag gcc atc ctg ctc tcc gac cga gtt   451
Met Val Thr His Asp Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val
            105                 110                 115

ctc gtg atg tcc aag agc ccc gaa gcc acc atc atc acc gat att cca   499
Leu Val Met Ser Lys Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro
        120                 125                 130

gtg aat ctt ccc cgc ccc aga cac gag ctg agt gaa gac gct tct gtt   547
Val Asn Leu Pro Arg Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val
    135                 140                 145
```

```
gaa gcc gag acc aca gcc ctg cgt aag cgg atg ctg cat ctg ctg gag   595
Glu Ala Glu Thr Thr Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu
150                 155                 160                 165

cac tagtttctaa cacgtctttt aaa                                   621
His
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<210> 272
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 272

```
Leu Thr Ala Arg Gly Asn Ile Asp Phe Gly Leu Arg Ser Ala Arg Pro
  1               5                  10                  15

Ser Leu Ser Lys Thr Glu Arg Ala Asp Ile Thr Arg Thr His Leu Glu
            20                  25                  30

Gln Val Gly Leu Thr Asp Ala Ala Glu Arg Arg Pro Ala Arg Leu Ser
        35                  40                  45

Gly Gly Met Gln Gln Arg Val Gly Ile Ala Arg Ala Phe Ala Ile Asp
    50                  55                  60

Pro Pro Ile Met Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu
65                  70                  75                  80

Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu Asn Ile Trp Glu Ala Ser
                85                  90                  95

Arg Arg Thr Val Val Met Val Thr His Asp Val Asp Glu Ala Ile Leu
            100                 105                 110

Leu Ser Asp Arg Val Leu Val Met Ser Lys Ser Pro Glu Ala Thr Ile
        115                 120                 125

Ile Thr Asp Ile Pro Val Asn Leu Pro Arg Pro Arg His Glu Leu Ser
    130                 135                 140

Glu Asp Ala Ser Val Glu Ala Glu Thr Thr Ala Leu Arg Lys Arg Met
145                 150                 155                 160

Leu His Leu Leu Glu His
                165
```

<210> 273
<211> 443
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(420)
<223> FRXA01142

<400> 273

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acc cgc acc cac ctc gaa caa gta ggc ctc acc gac gcc gcc gaa cgg   48
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```
Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr Asp Ala Ala Glu Arg
  1               5                  10                  15

cgc ccc gcc cgc ctc tcc ggc ggc atg caa cag cga gtc ggc atc gca   96
Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln Arg Val Gly Ile Ala
            20                  25                  30

cgc gcc ttc gcc atc gac cca cca atc atg ctt ctc gac gaa ccc ttc   144
Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu Leu Asp Glu Pro Phe
        35                  40                  45

gga gcc ctc gac gcc ctc acc cgc cgc gaa ctc cag ctc caa cta ctc   192
Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu
    50                  55                  60

aac att tgg gaa gcc tcc cgc cgc acc gtc gtc atg gtc acc cac gac   240
Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val Met Val Thr His Asp
65                  70                  75                  80

gtc gac gag gcc atc ctg ctc tcc gac cga gtt ctc gtg atg tcc aag   288
Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val Leu Val Met Ser Lys
                85                  90                  95

agc ccc gaa gcc acc atc atc acc gat att cca gtg aat ctt ccc cgc   336
Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro Val Asn Leu Pro Arg
            100                 105                 110

ccc aga cac gag ctg agt gaa gac gct tct gtt gaa gcc gag acc aca   384
Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val Glu Ala Glu Thr Thr
        115                 120                 125

gcc ctg cgt aag cgg atg ctg cat ctg ctg gag cac tagtttctaa        430
Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu His
    130                 135                 140

cacgtctttt aaa                                                   443
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GUID:20040050950

<210> 274
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

```
<400> 274
Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr Asp Ala Ala Glu Arg
  1               5                  10                  15

Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln Arg Val Gly Ile Ala
            20                  25                  30

Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu Leu Asp Glu Pro Phe
        35                  40                  45

Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu
    50                  55                  60

Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val Met Val Thr His Asp
65                  70                  75                  80

Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val Leu Val Met Ser Lys
                85                  90                  95
```

```
Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro Val Asn Leu Pro Arg
            100                 105                 110

Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val Glu Ala Glu Thr Thr
        115                 120                 125

Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu His
    130                 135                 140
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<210> 275
<211> 948
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(925)
<223> RXN01141

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<400> 275

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aaagaacact cggtatggca cctgatttaa ggatgctgca atcgtgacac atatcctctt 60

cgacagcagg cgttttctgc aactgggcgc ttttgcgtcc ttg agc acc gca ttg   115
                                              Leu Ser Thr Ala Leu
                                                1               5

gcc gga gcg gcc cgc tac gtg acg tcg aca agc aat aat gaa cct gcg   163
Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser Asn Asn Glu Pro Ala
                  10                  15                  20

gat aac act ccc ctg acc att ggc tac gtg cct att gcg ggc tcg gcg   211
Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro Ile Ala Gly Ser Ala
              25                  30                  35

ccg att gct atc gca gat gcg cta ggg ctg ttt aag aaa cac ggc gtg   259
Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe Lys Lys His Gly Val
          40                  45                  50

aat gtc acg ttg aag aag tac tca ggc tgg tcc gac ctg tgg acc gcc   307
Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser Asp Leu Trp Thr Ala
      55                  60                  65

tat gca aca gag cag ctt gat gtt gcg cac atg ctg tcg ccg atg act   355
Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met Leu Ser Pro Met Thr
  70                  75                  80                  85

gtg gcg att aat gct gga gtg acc aac gcg tcg cgc ccg acg gag ctg   403
Val Ala Ile Asn Ala Gly Val Thr Asn Ala Ser Arg Pro Thr Glu Leu
                  90                  95                 100

tcg ttt acc cag aac acc aat ggg caa gca att acc ttg gcg tca aag   451
Ser Phe Thr Gln Asn Thr Asn Gly Gln Ala Ile Thr Leu Ala Ser Lys
              105                 110                 115

cac tat ggt tcc gtc aat tca gcg gcg gat ctt aaa ggc atg gtg ctg   499
His Tyr Gly Ser Val Asn Ser Ala Ala Asp Leu Lys Gly Met Val Leu
          120                 125                 130

gga att cct ttt gaa tat tca gtc cat gcg ctg ctc ctg cgc gat tat   547
```

```
Gly Ile Pro Phe Glu Tyr Ser Val His Ala Leu Leu Leu Arg Asp Tyr
    135                 140                 145

ctc gtc tca aac gca gtt gat ccc atc gcc gat ctt gag ctt cgc ctg   595
Leu Val Ser Asn Ala Val Asp Pro Ile Ala Asp Leu Glu Leu Arg Leu
150                 155                 160                 165

ctc cga cct gcc gat atg gtc gca caa ttg aca gtt gag ggc atc gat   643
Leu Arg Pro Ala Asp Met Val Ala Gln Leu Thr Val Glu Gly Ile Asp
                170                 175                 180

gga ttc att ggg cct ggg ccg ttt aat gaa cgc gcc atc agc aat ggc   691
Gly Phe Ile Gly Pro Gly Pro Phe Asn Glu Arg Ala Ile Ser Asn Gly
            185                 190                 195

tcc ggc cgg att tgg ctg ctg acc aaa caa ctg tgg gac aaa cat cca   739
Ser Gly Arg Ile Trp Leu Leu Thr Lys Gln Leu Trp Asp Lys His Pro
        200                 205                 210

tgc tgc gcc gtg gcg atg gcc aaa gag tgg aaa gct gaa cac ccc acg   787
Cys Cys Ala Val Ala Met Ala Lys Glu Trp Lys Ala Glu His Pro Thr
    215                 220                 225

gcg gct cag ggt gtg ctt aat gcg ctg gag gaa gcc tcc gca att ttg   835
Ala Ala Gln Gly Val Leu Asn Ala Leu Glu Glu Ala Ser Ala Ile Leu
230                 235                 240                 245

agc aat ccg gca caa ttt gat tcc tcg gca cgc acg ctg tcg cag gaa   883
Ser Asn Pro Ala Gln Phe Asp Ser Ser Ala Arg Thr Leu Ser Gln Glu
                250                 255                 260

aaa tac ctc aac cag cct gcc acg ttg ctg gat gga ccg tcg           925
Lys Tyr Leu Asn Gln Pro Ala Thr Leu Leu Asp Gly Pro Ser
            265                 270                 275

taatcatcgg catcaccggc tta                                        948
```

<210> 276
<211> 275
<212> PRT
<213> Corynebacterium glutamicum

<400> 276

```
Leu Ser Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser
  1               5                  10                  15

Asn Asn Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro
            20                  25                  30

Ile Ala Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe
        35                  40                  45

Lys Lys His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser
    50                  55                  60

Asp Leu Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met
65                  70                  75                  80

Leu Ser Pro Met Thr Val Ala Ile Asn Ala Gly Val Thr Asn Ala Ser
                85                  90                  95
```

Arg Pro Thr Glu Leu Ser Phe Thr Gln Asn Thr Asn Gly Gln Ala Ile
100 105 110

Thr Leu Ala Ser Lys His Tyr Gly Ser Val Asn Ser Ala Ala Asp Leu
115 120 125

Lys Gly Met Val Leu Gly Ile Pro Phe Glu Tyr Ser Val His Ala Leu
130 135 140

Leu Leu Arg Asp Tyr Leu Val Ser Asn Ala Val Asp Pro Ile Ala Asp
145 150 155 160

Leu Glu Leu Arg Leu Leu Arg Pro Ala Asp Met Val Ala Gln Leu Thr
165 170 175

Val Glu Gly Ile Asp Gly Phe Ile Gly Pro Gly Pro Phe Asn Glu Arg
180 185 190

Ala Ile Ser Asn Gly Ser Gly Arg Ile Trp Leu Leu Thr Lys Gln Leu
195 200 205

Trp Asp Lys His Pro Cys Cys Ala Val Ala Met Ala Lys Glu Trp Lys
210 215 220

Ala Glu His Pro Thr Ala Ala Gln Gly Val Leu Asn Ala Leu Glu Glu
225 230 235 240

Ala Ser Ala Ile Leu Ser Asn Pro Ala Gln Phe Asp Ser Ser Ala Arg
245 250 255

Thr Leu Ser Gln Glu Lys Tyr Leu Asn Gln Pro Ala Thr Leu Leu Asp
260 265 270

Gly Pro Ser
275

<210> 277
<211> 424
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(424)
<223> FRXA01135

<400> 277
catttactaa tctcacaaga catcgcctaa tgaatacaga ctagcctatt caaattcaaa 60

gaacactcgg tatggcacct gatttaagga tgctgcaatc gtg aca cat atc ctc 115
Val Thr His Ile Leu
1 5

ttc gac agc agg cgt ttt ctg caa ctg ggc gct ttt gcg tcc ttg agc 163
Phe Asp Ser Arg Arg Phe Leu Gln Leu Gly Ala Phe Ala Ser Leu Ser
10 15 20

acc gca ttg gcc gga gcg gcc cgc tac gtg acg tcg aca agc aat aat 211
Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser Asn Asn

```
                25                  30                  35

gaa cct gcg gat aac act ccc ctg acc att ggc tac gtg cct att gcg   259
Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro Ile Ala
          40                  45                  50

ggc tcg gcg ccg att gct atc gca gat gcg cta ggg ctg ttt aag aaa   307
Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe Lys Lys
      55                  60                  65

cac ggc gtg aat gtc acg ttg aag aag tac tca ggc tgg tcc gac ctg   355
His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser Asp Leu
 70                  75                  80                  85

tgg acc gcc tat gca aca gag cag ctt gat gtt gcg cac atg ctg tcg   403
Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met Leu Ser
                 90                  95                 100

ccg atg act gtg gcg att aat                                      424
Pro Met Thr Val Ala Ile Asn
            105
```

<210> 278
<211> 108
<212> PRT
<213> Corynebacterium glutamicum

<400> 278

```
Val Thr His Ile Leu Phe Asp Ser Arg Arg Phe Leu Gln Leu Gly Ala
  1               5                  10                  15

Phe Ala Ser Leu Ser Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr
             20                  25                  30

Ser Thr Ser Asn Asn Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly
         35                  40                  45

Tyr Val Pro Ile Ala Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu
     50                  55                  60

Gly Leu Phe Lys Lys His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser
 65                  70                  75                  80

Gly Trp Ser Asp Leu Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val
                 85                  90                  95

Ala His Met Leu Ser Pro Met Thr Val Ala Ile Asn
            100                 105
```

<210> 279
<211> 485
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(462)
<223> FRXA01141

<400> 279

```
gtc aat tca gcg gcg gat ctt aaa ggc atg gtg ctg gga att cct ttt   48
Val Asn Ser Ala Ala Asp Leu Lys Gly Met Val Leu Gly Ile Pro Phe
  1               5                  10                  15

gaa tat tca gtc cat gcg ctg ctc ctg cgc gat tat ctc gtc tca aac   96
Glu Tyr Ser Val His Ala Leu Leu Leu Arg Asp Tyr Leu Val Ser Asn
             20                  25                  30

gca gtt gat ccc atc gcc gat ctt gag ctt cgc ctg ctc cga cct gcc   144
Ala Val Asp Pro Ile Ala Asp Leu Glu Leu Arg Leu Leu Arg Pro Ala
         35                  40                  45

gat atg gtc gca caa ttg aca gtt gag ggc atc gat gga ttc att ggg   192
Asp Met Val Ala Gln Leu Thr Val Glu Gly Ile Asp Gly Phe Ile Gly
     50                  55                  60

cct ggg ccg ttt aat gaa cgc gcc atc agc aat ggc tcc ggc cgg att   240
Pro Gly Pro Phe Asn Glu Arg Ala Ile Ser Asn Gly Ser Gly Arg Ile
 65                  70                  75                  80

tgg ctg ctg acc aaa caa ctg tgg gac aaa cat cca tgc tgc gcc gtg   288
Trp Leu Leu Thr Lys Gln Leu Trp Asp Lys His Pro Cys Cys Ala Val
                 85                  90                  95

gcg atg gcc aaa gag tgg aaa gct gaa cac ccc acg gcg gct cag ggt   336
Ala Met Ala Lys Glu Trp Lys Ala Glu His Pro Thr Ala Ala Gln Gly
            100                 105                 110

gtg ctt aat gcg ctg gag gaa gcc tcc gca att ttg agc aat ccg gca   384
Val Leu Asn Ala Leu Glu Glu Ala Ser Ala Ile Leu Ser Asn Pro Ala
        115                 120                 125

caa ttt gat tcc tcg gca cgc acg ctg tcg cag gaa aaa tac ctc aac   432
Gln Phe Asp Ser Ser Ala Arg Thr Leu Ser Gln Glu Lys Tyr Leu Asn
    130                 135                 140

cag cct gcc acg ttg ctg gat gga ccg tcg taatcatcgg catcaccggc     482
Gln Pro Ala Thr Leu Leu Asp Gly Pro Ser
145                 150

tta                                                               485
```

<210> 280
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 280

```
Val Asn Ser Ala Ala Asp Leu Lys Gly Met Val Leu Gly Ile Pro Phe
  1               5                  10                  15

Glu Tyr Ser Val His Ala Leu Leu Leu Arg Asp Tyr Leu Val Ser Asn
             20                  25                  30

Ala Val Asp Pro Ile Ala Asp Leu Glu Leu Arg Leu Leu Arg Pro Ala
         35                  40                  45

Asp Met Val Ala Gln Leu Thr Val Glu Gly Ile Asp Gly Phe Ile Gly
     50                  55                  60
```

```
Pro Gly Pro Phe Asn Glu Arg Ala Ile Ser Asn Gly Ser Gly Arg Ile
 65                  70                  75                  80

Trp Leu Leu Thr Lys Gln Leu Trp Asp Lys His Pro Cys Cys Ala Val
                 85                  90                  95

Ala Met Ala Lys Glu Trp Lys Ala Glu His Pro Thr Ala Ala Gln Gly
            100                 105                 110

Val Leu Asn Ala Leu Glu Glu Ala Ser Ala Ile Leu Ser Asn Pro Ala
        115                 120                 125

Gln Phe Asp Ser Ser Ala Arg Thr Leu Ser Gln Glu Lys Tyr Leu Asn
    130                 135                 140

Gln Pro Ala Thr Leu Leu Asp Gly Pro Ser
145                 150
```

<210> 281
<211> 892
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(892)
<223> RXA00728

<400> 281

```
gattacttca cagatgtcag atcttaatca agggcctgga gcttcaacgg cccaaccgaa 60

accgattgaa gccaagccac tacgccaccc tggccggtgg gtg gca gcc gct atc   115
                                            Val Ala Ala Ala Ile
                                              1               5

atc gtg gca ctg ctc gca tgg ttt atc atc agc gcg ctc aac aat gag   163
Ile Val Ala Leu Leu Ala Trp Phe Ile Ile Ser Ala Leu Asn Asn Glu
                 10                  15                  20

gcc tac ggt tgg gat acc tac cgc tcg tat ctt ttt gac acc cgc att   211
Ala Tyr Gly Trp Asp Thr Tyr Arg Ser Tyr Leu Phe Asp Thr Arg Ile
             25                  30                  35

gcc acc gcg gca ctt cac acc att gcg ctg acc ttg ctg tcc atg atc   259
Ala Thr Ala Ala Leu His Thr Ile Ala Leu Thr Leu Leu Ser Met Ile
         40                  45                  50

ttg ggt gtg gtt ctc ggc gca atc ttg gcc gtc atg cgt atg tcc ggc   307
Leu Gly Val Val Leu Gly Ala Ile Leu Ala Val Met Arg Met Ser Gly
     55                  60                  65

aac cct gtc atg cag ggc gta gcg tgg ctg tac ctg tgg att ttc cgc   355
Asn Pro Val Met Gln Gly Val Ala Trp Leu Tyr Leu Trp Ile Phe Arg
 70                  75                  80                  85

ggc acc cca att tat gtg cag ttg gtg ttc tgg ggc ctg ctg ggt tcc   403
Gly Thr Pro Ile Tyr Val Gln Leu Val Phe Trp Gly Leu Leu Gly Ser
                 90                  95                 100
```

```
ttg tac cag tcg atc aac ctc ggt ttc gca gag atc gat ctg caa agc   451
Leu Tyr Gln Ser Ile Asn Leu Gly Phe Ala Glu Ile Asp Leu Gln Ser
            105                 110                 115

ttg ctg tct aat atg ttc ctg ctc gcg gtg atc ggt ctg ggt ctc aac   499
Leu Leu Ser Asn Met Phe Leu Leu Ala Val Ile Gly Leu Gly Leu Asn
        120                 125                 130

gag gct gcg tac atg gcg gaa atc gtg cgc tcg ggc atc caa gcg gtg   547
Glu Ala Ala Tyr Met Ala Glu Ile Val Arg Ser Gly Ile Gln Ala Val
    135                 140                 145

cct gag ggc cag atg gag gcg tcg aaa gct ttg ggt atg aac tgg tca   595
Pro Glu Gly Gln Met Glu Ala Ser Lys Ala Leu Gly Met Asn Trp Ser
150                 155                 160                 165

atg acc atg cgt cgc acc atc ttg ccg cag gcc atg cgc atc atc att   643
Met Thr Met Arg Arg Thr Ile Leu Pro Gln Ala Met Arg Ile Ile Ile
                170                 175                 180

ccg cca acc ggc aat gaa ctg atc tcc atg ctc aag acc acc tct ctg   691
Pro Pro Thr Gly Asn Glu Leu Ile Ser Met Leu Lys Thr Thr Ser Leu
            185                 190                 195

gtt gtt gcg att cct tat tct ctc gag ctg tac ggc cgc agc atg gat   739
Val Val Ala Ile Pro Tyr Ser Leu Glu Leu Tyr Gly Arg Ser Met Asp
        200                 205                 210

att gcg tac tcc ctc ttc gag cca gtt cca atg ctt ctg gtt gct gcg   787
Ile Ala Tyr Ser Leu Phe Glu Pro Val Pro Met Leu Leu Val Ala Ala
    215                 220                 225

agc tgg tac ttg gtc atc acc tct att ctt atg gtt ggt cag tac tac   835
Ser Trp Tyr Leu Val Ile Thr Ser Ile Leu Met Val Gly Gln Tyr Tyr
230                 235                 240                 245

ctg gag aag cac ttc gaa aag ggc agc acc cgc acc ctg acc gca cgt   883
Leu Glu Lys His Phe Glu Lys Gly Ser Thr Arg Thr Leu Thr Ala Arg
                250                 255                 260

cag ctc gct                                                      892
Gln Leu Ala
```

<210> 282
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 282

```
Val Ala Ala Ala Ile Ile Val Ala Leu Leu Ala Trp Phe Ile Ile Ser
  1               5                  10                  15

Ala Leu Asn Asn Glu Ala Tyr Gly Trp Asp Thr Tyr Arg Ser Tyr Leu
            20                  25                  30

Phe Asp Thr Arg Ile Ala Thr Ala Ala Leu His Thr Ile Ala Leu Thr
        35                  40                  45

Leu Leu Ser Met Ile Leu Gly Val Val Leu Gly Ala Ile Leu Ala Val
```

50 55 60

Met Arg Met Ser Gly Asn Pro Val Met Gln Gly Val Ala Trp Leu Tyr
65 70 75 80

Leu Trp Ile Phe Arg Gly Thr Pro Ile Tyr Val Gln Leu Val Phe Trp
85 90 95

Gly Leu Leu Gly Ser Leu Tyr Gln Ser Ile Asn Leu Gly Phe Ala Glu
100 105 110

Ile Asp Leu Gln Ser Leu Leu Ser Asn Met Phe Leu Leu Ala Val Ile
115 120 125

Gly Leu Gly Leu Asn Glu Ala Ala Tyr Met Ala Glu Ile Val Arg Ser
130 135 140

Gly Ile Gln Ala Val Pro Glu Gly Gln Met Glu Ala Ser Lys Ala Leu
145 150 155 160

Gly Met Asn Trp Ser Met Thr Met Arg Arg Thr Ile Leu Pro Gln Ala
165 170 175

Met Arg Ile Ile Ile Pro Pro Thr Gly Asn Glu Leu Ile Ser Met Leu
180 185 190

Lys Thr Thr Ser Leu Val Val Ala Ile Pro Tyr Ser Leu Glu Leu Tyr
195 200 205

Gly Arg Ser Met Asp Ile Ala Tyr Ser Leu Phe Glu Pro Val Pro Met
210 215 220

Leu Leu Val Ala Ala Ser Trp Tyr Leu Val Ile Thr Ser Ile Leu Met
225 230 235 240

Val Gly Gln Tyr Tyr Leu Glu Lys His Phe Glu Lys Gly Ser Thr Arg
245 250 255

Thr Leu Thr Ala Arg Gln Leu Ala
260

<210> 283
<211> 1518
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1495)
<223> RXA02663

<400> 283
gtgcaaatat ctgtccagtt cgtgagacta cgtcaatgct tccaaggtca ttggcgcatc 60

aaccgctcac atcttgatca agcacgttgc ccgaaactgc atg gct ccg att ctg 115
Met Ala Pro Ile Leu
1 5

gtg ttc gcc acc gtc ctg gtc gcc gat gcg att gtc ttc gaa gca tcc 163
Val Phe Ala Thr Val Leu Val Ala Asp Ala Ile Val Phe Glu Ala Ser

```
                    10                  15                  20

ctg tcc ttc atc aac gct ggt gtg aaa cca cca tca cct tca tgg ggc   211
Leu Ser Phe Ile Asn Ala Gly Val Lys Pro Pro Ser Pro Ser Trp Gly
                25                  30                  35

aac atc ctt gcc gat ggt aaa gcc ctg ctg ctt agc ggc gca tgg tgg   259
Asn Ile Leu Ala Asp Gly Lys Ala Leu Leu Leu Ser Gly Ala Trp Trp
            40                  45                  50

cca acc ttc ttc cca ggt ttg atg atc ctg ctg acc gtt ctc tgc ttg   307
Pro Thr Phe Phe Pro Gly Leu Met Ile Leu Leu Thr Val Leu Cys Leu
        55                  60                  65

aac atc ctt tct gaa ggc ctc acc gac acc ctg gcc agc cct aag cca   355
Asn Ile Leu Ser Glu Gly Leu Thr Asp Thr Leu Ala Ser Pro Lys Pro
    70                  75                  80                  85

aag cct gtt tca gct tct gca aag aag gca ctg aag aag gaa gaa tcc   403
Lys Pro Val Ser Ala Ser Ala Lys Lys Ala Leu Lys Lys Glu Glu Ser
                90                  95                  100

ggt gaa aag gaa ggc tcc gga atc gtg ctt ggg cac acc aca cgt gaa   451
Gly Glu Lys Glu Gly Ser Gly Ile Val Leu Gly His Thr Thr Arg Glu
            105                 110                 115

gaa gcc aac gcc tca ctg ctc gca tca ctt gct gcg cta tcc acc agc   499
Glu Ala Asn Ala Ser Leu Leu Ala Ser Leu Ala Ala Leu Ser Thr Ser
        120                 125                 130

gaa aac aat tcc aat aac cgg ctt ata ttt gat ggc aac ccc act cct   547
Glu Asn Asn Ser Asn Asn Arg Leu Ile Phe Asp Gly Asn Pro Thr Pro
    135                 140                 145

ctg ttg gaa gtt cgc gat cta aag atc tcc ttc ccc aat gct cac gga   595
Leu Leu Glu Val Arg Asp Leu Lys Ile Ser Phe Pro Asn Ala His Gly
150                 155                 160                 165

gat atc aat att gtc gac ggc gtg aac ttc acc gtc gcc cca ggc caa   643
Asp Ile Asn Ile Val Asp Gly Val Asn Phe Thr Val Ala Pro Gly Gln
                170                 175                 180

acc atg ggt ctt gtc ggt gaa tcc ggc tgt ggt aaa tcg att acc gca   691
Thr Met Gly Leu Val Gly Glu Ser Gly Cys Gly Lys Ser Ile Thr Ala
            185                 190                 195

atg tcg atc atg ggt ctg ctg cct cca aca gca aag atc gaa ggc gag   739
Met Ser Ile Met Gly Leu Leu Pro Pro Thr Ala Lys Ile Glu Gly Glu
        200                 205                 210

atc ctt ttc gac gga aag aac ctc ctt gat ctg aaa cca gac gag ctc   787
Ile Leu Phe Asp Gly Lys Asn Leu Leu Asp Leu Lys Pro Asp Glu Leu
    215                 220                 225

aat gca ctg cgt gga cat gaa atc gcc atg atc tac caa gat gca ctc   835
Asn Ala Leu Arg Gly His Glu Ile Ala Met Ile Tyr Gln Asp Ala Leu
230                 235                 240                 245

tcc tca ctc aac cca tcc atg ctg atc agc gcc caa atg aag cag ctg   883
Ser Ser Leu Asn Pro Ser Met Leu Ile Ser Ala Gln Met Lys Gln Leu
                250                 255                 260
```

```
acc cgc cgc ggt gga aag cgc agt gcc gaa gaa ctc ctg gaa ctt gta   931
Thr Arg Arg Gly Gly Lys Arg Ser Ala Glu Glu Leu Leu Glu Leu Val
            265                 270                 275

ggc ctt gat cca aag cgc acc ctg cag tcc tac ccg cat gag ctt tca   979
Gly Leu Asp Pro Lys Arg Thr Leu Gln Ser Tyr Pro His Glu Leu Ser
        280                 285                 290

ggt ggc cag cgc cag cga gtt ctc atc gca atg gca ctg acc aga aac   1027
Gly Gly Gln Arg Gln Arg Val Leu Ile Ala Met Ala Leu Thr Arg Asn
    295                 300                 305

cca cgc ctc ctc atc gcc gac gag cca acc acc gcg cta gac gtc act   1075
Pro Arg Leu Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp Val Thr
310                 315                 320                 325

gtt cag cag cag gtt gtc gat ctg ctt aat gaa ctg cgt gaa aag ctc   1123
Val Gln Gln Gln Val Val Asp Leu Leu Asn Glu Leu Arg Glu Lys Leu
                330                 335                 340

gga ttc gcc atg atc ttt gta tcc cac gac ttg gct ctt gtc gcc cgc   1171
Gly Phe Ala Met Ile Phe Val Ser His Asp Leu Ala Leu Val Ala Arg
            345                 350                 355

ctg gtg cac aag ctc acc gtc atg tac gca ggt cag gtt gtt gag caa   1219
Leu Val His Lys Leu Thr Val Met Tyr Ala Gly Gln Val Val Glu Gln
        360                 365                 370

gga acc acc cgc gaa atc ctt atc gat cct cga cac gaa tac acc cgc   1267
Gly Thr Thr Arg Glu Ile Leu Ile Asp Pro Arg His Glu Tyr Thr Arg
    375                 380                 385

ggt ttg ctc gga tcc gtg ctc tcc atc gaa gct ggt gtg gac cgc ctc   1315
Gly Leu Leu Gly Ser Val Leu Ser Ile Glu Ala Gly Val Asp Arg Leu
390                 395                 400                 405

tac cag gtc cca ggc act gtt cca tca cca aag gaa ttc gtg gca ggc   1363
Tyr Gln Val Pro Gly Thr Val Pro Ser Pro Lys Glu Phe Val Ala Gly
                410                 415                 420

gac cgc ttt gca cca cga tca gaa ttc cca gaa ctt ggc ctt gac caa   1411
Asp Arg Phe Ala Pro Arg Ser Glu Phe Pro Glu Leu Gly Leu Asp Gln
            425                 430                 435

aag cca gta ctt cgc ccc atc acg ggc aca gag cat gca tac gca gca   1459
Lys Pro Val Leu Arg Pro Ile Thr Gly Thr Glu His Ala Tyr Ala Ala
        440                 445                 450

acc gat gaa ctt ctt gcc gca aag gga gaa caa cga tgacctcgac        1505
Thr Asp Glu Leu Leu Ala Ala Lys Gly Glu Gln Arg
    455                 460                 465

aatcgacacc agg                                                   1518
```

<210> 284
<211> 465
<212> PRT
<213> Corynebacterium glutamicum

<400> 284

```
Met Ala Pro Ile Leu Val Phe Ala Thr Val Leu Val Ala Asp Ala Ile
 1               5                  10                  15

Val Phe Glu Ala Ser Leu Ser Phe Ile Asn Ala Gly Val Lys Pro Pro
            20                  25                  30

Ser Pro Ser Trp Gly Asn Ile Leu Ala Asp Gly Lys Ala Leu Leu Leu
        35                  40                  45

Ser Gly Ala Trp Trp Pro Thr Phe Phe Pro Gly Leu Met Ile Leu Leu
    50                  55                  60

Thr Val Leu Cys Leu Asn Ile Leu Ser Glu Gly Leu Thr Asp Thr Leu
65                  70                  75                  80

Ala Ser Pro Lys Pro Lys Pro Val Ser Ala Ser Ala Lys Lys Ala Leu
                85                  90                  95

Lys Lys Glu Glu Ser Gly Glu Lys Glu Gly Ser Gly Ile Val Leu Gly
            100                 105                 110

His Thr Thr Arg Glu Glu Ala Asn Ala Ser Leu Leu Ala Ser Leu Ala
        115                 120                 125

Ala Leu Ser Thr Ser Glu Asn Asn Ser Asn Asn Arg Leu Ile Phe Asp
    130                 135                 140

Gly Asn Pro Thr Pro Leu Leu Glu Val Arg Asp Leu Lys Ile Ser Phe
145                 150                 155                 160

Pro Asn Ala His Gly Asp Ile Asn Ile Val Asp Gly Val Asn Phe Thr
                165                 170                 175

Val Ala Pro Gly Gln Thr Met Gly Leu Val Gly Glu Ser Gly Cys Gly
            180                 185                 190

Lys Ser Ile Thr Ala Met Ser Ile Met Gly Leu Leu Pro Pro Thr Ala
        195                 200                 205

Lys Ile Glu Gly Glu Ile Leu Phe Asp Gly Lys Asn Leu Leu Asp Leu
    210                 215                 220

Lys Pro Asp Glu Leu Asn Ala Leu Arg Gly His Glu Ile Ala Met Ile
225                 230                 235                 240

Tyr Gln Asp Ala Leu Ser Ser Leu Asn Pro Ser Met Leu Ile Ser Ala
                245                 250                 255

Gln Met Lys Gln Leu Thr Arg Arg Gly Gly Lys Arg Ser Ala Glu Glu
            260                 265                 270

Leu Leu Glu Leu Val Gly Leu Asp Pro Lys Arg Thr Leu Gln Ser Tyr
        275                 280                 285

Pro His Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Leu Ile Ala Met
    290                 295                 300

Ala Leu Thr Arg Asn Pro Arg Leu Leu Ile Ala Asp Glu Pro Thr Thr
305                 310                 315                 320
```

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Ala Leu Asp Val Thr Val Gln Gln Gln Val Val Asp Leu Leu Asn Glu
325 330 335

Leu Arg Glu Lys Leu Gly Phe Ala Met Ile Phe Val Ser His Asp Leu
340 345 350

Ala Leu Val Ala Arg Leu Val His Lys Leu Thr Val Met Tyr Ala Gly
355 360 365

Gln Val Val Glu Gln Gly Thr Thr Arg Glu Ile Leu Ile Asp Pro Arg
370 375 380

His Glu Tyr Thr Arg Gly Leu Leu Gly Ser Val Leu Ser Ile Glu Ala
385 390 395 400

Gly Val Asp Arg Leu Tyr Gln Val Pro Gly Thr Val Pro Ser Pro Lys
405 410 415

Glu Phe Val Ala Gly Asp Arg Phe Ala Pro Arg Ser Glu Phe Pro Glu
420 425 430

Leu Gly Leu Asp Gln Lys Pro Val Leu Arg Pro Ile Thr Gly Thr Glu
435 440 445

His Ala Tyr Ala Ala Thr Asp Glu Leu Leu Ala Ala Lys Gly Glu Gln
450 455 460

Arg
465

<210> 285
<211> 783
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(760)
<223> RXA02664

<400> 285
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catcaacttc aaggcctacc gcgatgaagt aatcggcatc gtg ggt gaa tct ggt 115
Val Gly Glu Ser Gly
1 5

tgc gga aaa tct acc ctt gcc cgc gtt atg gtt ggc ctg caa ccg gtc 163
Cys Gly Lys Ser Thr Leu Ala Arg Val Met Val Gly Leu Gln Pro Val
10 15 20

acc tcc ggc gaa gtg ctg ttc aaa ggc aag ccc atg aag cct cgt ggt 211
Thr Ser Gly Glu Val Leu Phe Lys Gly Lys Pro Met Lys Pro Arg Gly
25 30 35

gcg cag cgc aaa gaa ctc ggc agc tca gta tcc gtc gtg ttc cag gat 259
Ala Gln Arg Lys Glu Leu Gly Ser Ser Val Ser Val Val Phe Gln Asp
40 45 50

cct gcc acc tcg tta aac cca cga atg acc gtg cgc gaa cag ctc ctc 307

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Pro Ala Thr Ser Leu Asn Pro Arg Met Thr Val Arg Glu Gln Leu Leu
     55                  60                  65

gat cca ctt cga gta cac aaa gtt ggc gat gaa gca tcc cgc aac cag   355
Asp Pro Leu Arg Val His Lys Val Gly Asp Glu Ala Ser Arg Asn Gln
 70                  75                  80                  85

tgg gtt tca gag ctg atc tcc atg gtt ggc ctc ccg caa tcc gcg ttg   403
Trp Val Ser Glu Leu Ile Ser Met Val Gly Leu Pro Gln Ser Ala Leu
                 90                  95                 100

gaa gta ctc ccc cga cag gtt tcc ggt ggc caa cgc caa cgc gtg gcc   451
Glu Val Leu Pro Arg Gln Val Ser Gly Gly Gln Arg Gln Arg Val Ala
            105                 110                 115

att gct cga gca ctt gcg ctg aaa cct gac atc atc gtt gcc gac gaa   499
Ile Ala Arg Ala Leu Ala Leu Lys Pro Asp Ile Ile Val Ala Asp Glu
        120                 125                 130

cca acc tcc gcg ctg gat gta tcc gtt cgt gcg cag gtc ctc aac ctt   547
Pro Thr Ser Ala Leu Asp Val Ser Val Arg Ala Gln Val Leu Asn Leu
    135                 140                 145

ctg ctg gat ctg aaa act gaa ctc ggc ctg gga ttg gta ttc atc tcc   595
Leu Leu Asp Leu Lys Thr Glu Leu Gly Leu Gly Leu Val Phe Ile Ser
150                 155                 160                 165

cac gac atc aac act gtt cgc tac gtt tct gat cgc atc gca gtc atg   643
His Asp Ile Asn Thr Val Arg Tyr Val Ser Asp Arg Ile Ala Val Met
                170                 175                 180

ctg gct gga gaa atc att gag gaa aac acc acc tca gag atc ttc aac   691
Leu Ala Gly Glu Ile Ile Glu Glu Asn Thr Thr Ser Glu Ile Phe Asn
            185                 190                 195

aat gcg cag cag gac tac acc cgc act ctg ctc gaa gcg aca cca tcg   739
Asn Ala Gln Gln Asp Tyr Thr Arg Thr Leu Leu Glu Ala Thr Pro Ser
        200                 205                 210

ctg ctg aac aaa act cgt ttg tagtctccaa ccctttattc cct            783
Leu Leu Asn Lys Thr Arg Leu
    215                 220
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<210> 286
<211> 220
<212> PRT
<213> Corynebacterium glutamicum

<400> 286

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Val Gly Glu Ser Gly Cys Gly Lys Ser Thr Leu Ala Arg Val Met Val
  1               5                  10                  15

Gly Leu Gln Pro Val Thr Ser Gly Glu Val Leu Phe Lys Gly Lys Pro
             20                  25                  30

Met Lys Pro Arg Gly Ala Gln Arg Lys Glu Leu Gly Ser Ser Val Ser
         35                  40                  45

Val Val Phe Gln Asp Pro Ala Thr Ser Leu Asn Pro Arg Met Thr Val
     50                  55                  60
```

```
Arg Glu Gln Leu Leu Asp Pro Leu Arg Val His Lys Val Gly Asp Glu
 65                  70                  75                  80

Ala Ser Arg Asn Gln Trp Val Ser Glu Leu Ile Ser Met Val Gly Leu
                85                  90                  95

Pro Gln Ser Ala Leu Glu Val Leu Pro Arg Gln Val Ser Gly Gly Gln
            100                 105                 110

Arg Gln Arg Val Ala Ile Ala Arg Ala Leu Ala Leu Lys Pro Asp Ile
        115                 120                 125

Ile Val Ala Asp Glu Pro Thr Ser Ala Leu Asp Val Ser Val Arg Ala
    130                 135                 140

Gln Val Leu Asn Leu Leu Leu Asp Leu Lys Thr Glu Leu Gly Leu Gly
145                 150                 155                 160

Leu Val Phe Ile Ser His Asp Ile Asn Thr Val Arg Tyr Val Ser Asp
                165                 170                 175

Arg Ile Ala Val Met Leu Ala Gly Glu Ile Ile Glu Glu Asn Thr Thr
            180                 185                 190

Ser Glu Ile Phe Asn Asn Ala Gln Gln Asp Tyr Thr Arg Thr Leu Leu
        195                 200                 205

Glu Ala Thr Pro Ser Leu Leu Asn Lys Thr Arg Leu
    210                 215                 220
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<210> 287
<211> 1155
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1132)
<223> RXA00760

<400> 287

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accacggttg tctccattgt cactgtgctg gtcatcgtct acatcatcgc caaccttctc 60

gtggacttga tctacgccgt tctcgatccg aggatccgct atg cct aat aat gaa   115
                                               Met Pro Asn Asn Glu
                                                 1               5

ttc cac aca aac cac tcg ttg ggc caa gat gat caa acc cca gat cag   163
Phe His Thr Asn His Ser Leu Gly Gln Asp Asp Gln Thr Pro Asp Gln
                10                  15                  20

gct cat ttc ttc cca caa gga cga ggc gag gct cta gtt cga cca ggt   211
Ala His Phe Phe Pro Gln Gly Arg Gly Glu Ala Leu Val Arg Pro Gly
            25                  30                  35

caa gag cac ttc atc gca gcc act gat gaa acc gga ctt ggt gcc gtc   259
Gln Glu His Phe Ile Ala Ala Thr Asp Glu Thr Gly Leu Gly Ala Val
        40                  45                  50
```

```
gat gct gtt gct gat gac tct gca cca acc tcc atg tgg ggc gaa gcg   307
Asp Ala Val Ala Asp Asp Ser Ala Pro Thr Ser Met Trp Gly Glu Ala
     55                  60                  65

tgg cga gac ctt cgt cgt cga cca ctg ttc tgg gtc tct gcg gtg ttg   355
Trp Arg Asp Leu Arg Arg Arg Pro Leu Phe Trp Val Ser Ala Val Leu
 70                  75                  80                  85

att att ttg gcg ctt ctc ctg gcc gca gtt ccg cag ctg ttt acc tca   403
Ile Ile Leu Ala Leu Leu Leu Ala Ala Val Pro Gln Leu Phe Thr Ser
                 90                  95                 100

acg gat ccc cag ttc tgt gtg ctg gca aac tct ctt gat ggt cca cag   451
Thr Asp Pro Gln Phe Cys Val Leu Ala Asn Ser Leu Asp Gly Pro Gln
            105                 110                 115

tct gga cat ccc ttc gga ttc gac cgt caa ggt tgc gat att ttt gct   499
Ser Gly His Pro Phe Gly Phe Asp Arg Gln Gly Cys Asp Ile Phe Ala
        120                 125                 130

cgt acc gtc tac ggt gct cgt gcc tcg gtc gcc gtc ggt gtg ttg acc   547
Arg Thr Val Tyr Gly Ala Arg Ala Ser Val Ala Val Gly Val Leu Thr
    135                 140                 145

acg tta ctg gtc gcc ctc atc ggt act gta ttt ggt gct ttg gct ggc   595
Thr Leu Leu Val Ala Leu Ile Gly Thr Val Phe Gly Ala Leu Ala Gly
150                 155                 160                 165

ttc ttt ggt ggc atc atg gat acc atc ctc tcc cgc atc acc gac atg   643
Phe Phe Gly Gly Ile Met Asp Thr Ile Leu Ser Arg Ile Thr Asp Met
                170                 175                 180

ttc ttc gcc att cca ctg gtt ctg gca gcc atc gtt gtg atg cag atg   691
Phe Phe Ala Ile Pro Leu Val Leu Ala Ala Ile Val Val Met Gln Met
            185                 190                 195

ttc aag gaa cac cgc acc atc gtc acc gtg gtt ttg gtg ctt ggg ctt   739
Phe Lys Glu His Arg Thr Ile Val Thr Val Val Leu Val Leu Gly Leu
        200                 205                 210

ttc ggc tgg acc aac att gcg cgt att acc cgt gga gcg gtg atg acc   787
Phe Gly Trp Thr Asn Ile Ala Arg Ile Thr Arg Gly Ala Val Met Thr
    215                 220                 225

gca aag aat gaa gag tat gtc acc tcc gca cgt gcg ctt ggt gca tca   835
Ala Lys Asn Glu Glu Tyr Val Thr Ser Ala Arg Ala Leu Gly Ala Ser
230                 235                 240                 245

aaa gcc aag ata ctg ctg tct cac atc atg cca aac gcc gca gca ccc   883
Lys Ala Lys Ile Leu Leu Ser His Ile Met Pro Asn Ala Ala Ala Pro
                250                 255                 260

atc att gtg tat gca act gtg gca ctg gga aca ttc atc gtg gca gag   931
Ile Ile Val Tyr Ala Thr Val Ala Leu Gly Thr Phe Ile Val Ala Glu
            265                 270                 275

gcg acg ctc tcc ttc ctg ggc att ggc ctt cca cca tca att gtc tcc   979
Ala Thr Leu Ser Phe Leu Gly Ile Gly Leu Pro Pro Ser Ile Val Ser
        280                 285                 290

tgg ggt gct gat atc gcg aag gca caa acc tcc ctt cgt acc caa ccc   1027
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US 2006/0234350 A1 Oct. 19, 2006

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Trp Gly Ala Asp Ile Ala Lys Ala Gln Thr Ser Leu Arg Thr Gln Pro
    295                 300                 305

atg gtg ctg ttc tac ccc gca atg gca ctt gca cta acc gtt ttg agc   1075
Met Val Leu Phe Tyr Pro Ala Met Ala Leu Ala Leu Thr Val Leu Ser
310                 315                 320                 325

ttc atc atg atg ggc gat gtc gtc cgc gac gct ctg gat cct aag tcg   1123
Phe Ile Met Met Gly Asp Val Val Arg Asp Ala Leu Asp Pro Lys Ser
                330                 335                 340

agg aag cga tgaccaccaa catcccacaa acc                             1155
Arg Lys Arg
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<210> 288
<211> 344
<212> PRT
<213> Corynebacterium glutamicum

<400> 288

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Met Pro Asn Asn Glu Phe His Thr Asn His Ser Leu Gly Gln Asp Asp
  1               5                  10                  15

Gln Thr Pro Asp Gln Ala His Phe Phe Pro Gln Gly Arg Gly Glu Ala
            20                  25                  30

Leu Val Arg Pro Gly Gln Glu His Phe Ile Ala Ala Thr Asp Glu Thr
        35                  40                  45

Gly Leu Gly Ala Val Asp Ala Val Ala Asp Asp Ser Ala Pro Thr Ser
    50                  55                  60

Met Trp Gly Glu Ala Trp Arg Asp Leu Arg Arg Arg Pro Leu Phe Trp
65                  70                  75                  80

Val Ser Ala Val Leu Ile Ile Leu Ala Leu Leu Leu Ala Ala Val Pro
                85                  90                  95

Gln Leu Phe Thr Ser Thr Asp Pro Gln Phe Cys Val Leu Ala Asn Ser
            100                 105                 110

Leu Asp Gly Pro Gln Ser Gly His Pro Phe Gly Phe Asp Arg Gln Gly
        115                 120                 125

Cys Asp Ile Phe Ala Arg Thr Val Tyr Gly Ala Arg Ala Ser Val Ala
    130                 135                 140

Val Gly Val Leu Thr Thr Leu Leu Val Ala Leu Ile Gly Thr Val Phe
145                 150                 155                 160

Gly Ala Leu Ala Gly Phe Phe Gly Gly Ile Met Asp Thr Ile Leu Ser
                165                 170                 175

Arg Ile Thr Asp Met Phe Phe Ala Ile Pro Leu Val Leu Ala Ala Ile
            180                 185                 190

Val Val Met Gln Met Phe Lys Glu His Arg Thr Ile Val Thr Val Val
        195                 200                 205
```

Leu Val Leu Gly Leu Phe Gly Trp Thr Asn Ile Ala Arg Ile Thr Arg
210 215 220

Gly Ala Val Met Thr Ala Lys Asn Glu Glu Tyr Val Thr Ser Ala Arg
225 230 235 240

Ala Leu Gly Ala Ser Lys Ala Lys Ile Leu Leu Ser His Ile Met Pro
245 250 255

Asn Ala Ala Ala Pro Ile Ile Val Tyr Ala Thr Val Ala Leu Gly Thr
260 265 270

Phe Ile Val Ala Glu Ala Thr Leu Ser Phe Leu Gly Ile Gly Leu Pro
275 280 285

Pro Ser Ile Val Ser Trp Gly Ala Asp Ile Ala Lys Ala Gln Thr Ser
290 295 300

Leu Arg Thr Gln Pro Met Val Leu Phe Tyr Pro Ala Met Ala Leu Ala
305 310 315 320

Leu Thr Val Leu Ser Phe Ile Met Met Gly Asp Val Val Arg Asp Ala
325 330 335

Leu Asp Pro Lys Ser Arg Lys Arg
340

<210> 289
<211> 1632
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1609)
<223> RXA02035

<400> 289
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catttagttt cccggatcac accgactaat ctcagaagcc atg aag atc acg cgc 115
Met Lys Ile Thr Arg
1 5

gga ctc ctg cca tca ttg ctg ttg gca agc aca atc gtg gtg tcg tca 163
Gly Leu Leu Pro Ser Leu Leu Leu Ala Ser Thr Ile Val Val Ser Ser
10 15 20

tgc tct gct gga tcg act gcg tat cag cag ccc cct gct gtt gat caa 211
Cys Ser Ala Gly Ser Thr Ala Tyr Gln Gln Pro Pro Ala Val Asp Gln
25 30 35

tca tcc att gtc att gct acc acg gct gct gcg gcg tca ctt gat ttc 259
Ser Ser Ile Val Ile Ala Thr Thr Ala Ala Ala Ala Ser Leu Asp Phe
40 45 50

acc aat gct gcg ggc gct gct att ccg cag gcg atg atg tcc aat att 307
Thr Asn Ala Ala Gly Ala Ala Ile Pro Gln Ala Met Met Ser Asn Ile
55 60 65

```
tac gag ggg ctt gtg cgc atc gat gcg gag ggt gag att cag ccg ctg   355
Tyr Glu Gly Leu Val Arg Ile Asp Ala Glu Gly Glu Ile Gln Pro Leu
 70                  75                  80                  85

ctt gcc acg tcg tgg gat att tca gac gat cgc acc gag tac att ttc   403
Leu Ala Thr Ser Trp Asp Ile Ser Asp Asp Arg Thr Glu Tyr Ile Phe
                90                  95                 100

cat ttg cgg gag ggt gtg ctg ttt tcc aac ggc gat ccc ttc aat gct   451
His Leu Arg Glu Gly Val Leu Phe Ser Asn Gly Asp Pro Phe Asn Ala
            105                 110                 115

gat tct gcg aag ttt tcc att gat cgg gta aaa act gac tgg acc aat   499
Asp Ser Ala Lys Phe Ser Ile Asp Arg Val Lys Thr Asp Trp Thr Asn
        120                 125                 130

ggt ttg aaa agt ggc atg gat gtg gtg gag tcc acc gag gtg att gac   547
Gly Leu Lys Ser Gly Met Asp Val Val Glu Ser Thr Glu Val Ile Asp
    135                 140                 145

gat cac acg ctg aaa gtt tcg ctg gtc agg ccg tcc aac caa tgg ttg   595
Asp His Thr Leu Lys Val Ser Leu Val Arg Pro Ser Asn Gln Trp Leu
150                 155                 160                 165

tgg agc atg ggt acc gcg atc ggt gcc atg atg acg gag ggg ggc gtc   643
Trp Ser Met Gly Thr Ala Ile Gly Ala Met Met Thr Glu Gly Gly Val
                170                 175                 180

gat aag ctg gca act gat ccc gtt ggc acc ggc ccg tac acg gtg acg   691
Asp Lys Leu Ala Thr Asp Pro Val Gly Thr Gly Pro Tyr Thr Val Thr
            185                 190                 195

cac tgg gcg ccg ggc cgc gca att ggg ttc ggc gcg cgg gcc gat tat   739
His Trp Ala Pro Gly Arg Ala Ile Gly Phe Gly Ala Arg Ala Asp Tyr
        200                 205                 210

tgg ggg cag aag ccg ctt aac gac gcc gca acc atc cgc tac ttc agc   787
Trp Gly Gln Lys Pro Leu Asn Asp Ala Ala Thr Ile Arg Tyr Phe Ser
    215                 220                 225

gat gcg acg gcc tcg acc aat gcg ctg caa agc ggt gac gtg gac gtg   835
Asp Ala Thr Ala Ser Thr Asn Ala Leu Gln Ser Gly Asp Val Asp Val
230                 235                 240                 245

att tgg gcg atg caa gcg ccc gaa cag ctg gct acg ctg cag gaa tac   883
Ile Trp Ala Met Gln Ala Pro Glu Gln Leu Ala Thr Leu Gln Glu Tyr
                250                 255                 260

acc gtg gaa gtg ggc aca acc aat ggt gag atg ttg ctg tcg atg aat   931
Thr Val Glu Val Gly Thr Thr Asn Gly Glu Met Leu Leu Ser Met Asn
            265                 270                 275

aat cag cgt gca cct ttt gat gat gtg cgt gtg cgc cag gcg gtg atg   979
Asn Gln Arg Ala Pro Phe Asp Asp Val Arg Val Arg Gln Ala Val Met
        280                 285                 290

ttt gcg att gat cgc caa gcc gtc att gat acc gcg ttg gaa ggt tac  1027
Phe Ala Ile Asp Arg Gln Ala Val Ile Asp Thr Ala Leu Glu Gly Tyr
    295                 300                 305

ggc acc gac act ggt ggc gtg cct gtt ccg ccg act gat ccg tgg tac  1075
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```
Gly Thr Asp Thr Gly Gly Val Pro Val Pro Pro Thr Asp Pro Trp Tyr
310                 315                 320                 325

gag aaa tcc acg atg tac ccc tac gat ccg gac cgc gca cgg gca ttg   1123
Glu Lys Ser Thr Met Tyr Pro Tyr Asp Pro Asp Arg Ala Arg Ala Leu
                330                 335                 340

tta gag gag gcc ggc gcc gag gga acg cgg atc acc atg tcc att cct   1171
Leu Glu Glu Ala Gly Ala Glu Gly Thr Arg Ile Thr Met Ser Ile Pro
            345                 350                 355

tcg ttg ccg tac gct cag gca gcc tct gaa atc ctg tac tcg caa ctg   1219
Ser Leu Pro Tyr Ala Gln Ala Ala Ser Glu Ile Leu Tyr Ser Gln Leu
        360                 365                 370

cga gat gtt ggt ttt gat cct gtg att gaa tca acc gag ttc cca gcc   1267
Arg Asp Val Gly Phe Asp Pro Val Ile Glu Ser Thr Glu Phe Pro Ala
    375                 380                 385

gtc tgg ttg gca cag gtc atg ggg caa aaa gac tac gac atg tca cta   1315
Val Trp Leu Ala Gln Val Met Gly Gln Lys Asp Tyr Asp Met Ser Leu
390                 395                 400                 405

atc gcg cat gtg gaa ccc cgc gac atc ccc acg ctg ttt agc ccc aac   1363
Ile Ala His Val Glu Pro Arg Asp Ile Pro Thr Leu Phe Ser Pro Asn
                410                 415                 420

tac tat ttg ggc ttt gac gac acc gaa acc caa gcc ctc ctc gca gag   1411
Tyr Tyr Leu Gly Phe Asp Asp Thr Glu Thr Gln Ala Leu Leu Ala Glu
            425                 430                 435

gca gac agt tca gca aac gaa gtg gaa ttg atg caa caa gct gtc gat   1459
Ala Asp Ser Ser Ala Asn Glu Val Glu Leu Met Gln Gln Ala Val Asp
        440                 445                 450

cga atc atg gaa caa gcc gtc gcc gac aac ctc atg aac gtg gcc aac   1507
Arg Ile Met Glu Gln Ala Val Ala Asp Asn Leu Met Asn Val Ala Asn
    455                 460                 465

atc gtg gtg atg tca cca gag atc acc ggc att gat ccc aac gtg gtg   1555
Ile Val Val Met Ser Pro Glu Ile Thr Gly Ile Asp Pro Asn Val Val
470                 475                 480                 485

tcc ggg gcg ttg gaa ttg tcg ttg att ggt cgg aaa gaa tcc ggg gta   1603
Ser Gly Ala Leu Glu Leu Ser Leu Ile Gly Arg Lys Glu Ser Gly Val
                490                 495                 500

gcg cag tgagtaaaac aatcgcttgg act                                 1632
Ala Gln
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<210> 290
<211> 503
<212> PRT
<213> Corynebacterium glutamicum

<400> 290

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Met Lys Ile Thr Arg Gly Leu Leu Pro Ser Leu Leu Leu Ala Ser Thr
  1               5                  10                  15
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Ile Val Val Ser Ser Cys Ser Ala Gly Ser Thr Ala Tyr Gln Gln Pro
20 25 30

Pro Ala Val Asp Gln Ser Ser Ile Val Ile Ala Thr Thr Ala Ala Ala
35 40 45

Ala Ser Leu Asp Phe Thr Asn Ala Ala Gly Ala Ala Ile Pro Gln Ala
50 55 60

Met Met Ser Asn Ile Tyr Glu Gly Leu Val Arg Ile Asp Ala Glu Gly
65 70 75 80

Glu Ile Gln Pro Leu Leu Ala Thr Ser Trp Asp Ile Ser Asp Asp Arg
85 90 95

Thr Glu Tyr Ile Phe His Leu Arg Glu Gly Val Leu Phe Ser Asn Gly
100 105 110

Asp Pro Phe Asn Ala Asp Ser Ala Lys Phe Ser Ile Asp Arg Val Lys
115 120 125

Thr Asp Trp Thr Asn Gly Leu Lys Ser Gly Met Asp Val Val Glu Ser
130 135 140

Thr Glu Val Ile Asp Asp His Thr Leu Lys Val Ser Leu Val Arg Pro
145 150 155 160

Ser Asn Gln Trp Leu Trp Ser Met Gly Thr Ala Ile Gly Ala Met Met
165 170 175

Thr Glu Gly Gly Val Asp Lys Leu Ala Thr Asp Pro Val Gly Thr Gly
180 185 190

Pro Tyr Thr Val Thr His Trp Ala Pro Gly Arg Ala Ile Gly Phe Gly
195 200 205

Ala Arg Ala Asp Tyr Trp Gly Gln Lys Pro Leu Asn Asp Ala Ala Thr
210 215 220

Ile Arg Tyr Phe Ser Asp Ala Thr Ala Ser Thr Asn Ala Leu Gln Ser
225 230 235 240

Gly Asp Val Asp Val Ile Trp Ala Met Gln Ala Pro Glu Gln Leu Ala
245 250 255

Thr Leu Gln Glu Tyr Thr Val Glu Val Gly Thr Thr Asn Gly Glu Met
260 265 270

Leu Leu Ser Met Asn Asn Gln Arg Ala Pro Phe Asp Asp Val Arg Val
275 280 285

Arg Gln Ala Val Met Phe Ala Ile Asp Arg Gln Ala Val Ile Asp Thr
290 295 300

Ala Leu Glu Gly Tyr Gly Thr Asp Thr Gly Gly Val Pro Val Pro Pro
305 310 315 320

Thr Asp Pro Trp Tyr Glu Lys Ser Thr Met Tyr Pro Tyr Asp Pro Asp
325 330 335

Arg Ala Arg Ala Leu Leu Glu Glu Ala Gly Ala Glu Gly Thr Arg Ile

```
            340                 345                 350

Thr Met Ser Ile Pro Ser Leu Pro Tyr Ala Gln Ala Ala Ser Glu Ile
        355                 360                 365

Leu Tyr Ser Gln Leu Arg Asp Val Gly Phe Asp Pro Val Ile Glu Ser
    370                 375                 380

Thr Glu Phe Pro Ala Val Trp Leu Ala Gln Val Met Gly Gln Lys Asp
385                 390                 395                 400

Tyr Asp Met Ser Leu Ile Ala His Val Glu Pro Arg Asp Ile Pro Thr
                405                 410                 415

Leu Phe Ser Pro Asn Tyr Tyr Leu Gly Phe Asp Asp Thr Glu Thr Gln
            420                 425                 430

Ala Leu Leu Ala Glu Ala Asp Ser Ser Ala Asn Glu Val Glu Leu Met
        435                 440                 445

Gln Gln Ala Val Asp Arg Ile Met Glu Gln Ala Val Ala Asp Asn Leu
    450                 455                 460

Met Asn Val Ala Asn Ile Val Val Met Ser Pro Glu Ile Thr Gly Ile
465                 470                 475                 480

Asp Pro Asn Val Val Ser Gly Ala Leu Glu Leu Ser Leu Ile Gly Arg
                485                 490                 495

Lys Glu Ser Gly Val Ala Gln
            500
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US 2005/0196848 A1

<210> 291
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXN01002

<400> 291
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caactaattt ccctgtttcc aatactcaag gtgtgcgcat atg aat tct gat gct 115
                                        Met Asn Ser Asp Ala
                                          1               5

tcg gct acc acc aac tcc tgg gct atc aac ttc gac cat gtg tcg gtg 163
Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe Asp His Val Ser Val
                  10                  15                  20

acg tat ccc aat ggg acg aaa gcc ctc gat gat gtt tcc ctc acc atc 211
Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp Val Ser Leu Thr Ile
              25                  30                  35

aat ccc ggt gag atg gtt gcc atc gtg ggt ctg tca gga tcg ggt aaa 259
Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu Ser Gly Ser Gly Lys
          40                  45                  50
```
```

```
tcc acg ctg att cgc acg atc aac ggt ctt gtc cgc gct acg gaa ggc   307
Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val Arg Ala Thr Glu Gly
     55                  60                  65

acc gtg acg gtg ggg ccg cat cag atc aac acc ttg aag ggg aaa gca   355
Thr Val Thr Val Gly Pro His Gln Ile Asn Thr Leu Lys Gly Lys Ala
 70                  75                  80                  85

ctg cgt gat gcc cgt ggg cag atc ggc atg att ttc cag ggg ttc aac   403
Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile Phe Gln Gly Phe Asn
                 90                  95                 100

ctg tcg gaa cgc agc agt gtg ttc cag aat gtt ttg gtg ggc cgc ttc   451
Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val Leu Val Gly Arg Phe
            105                 110                 115

gcg cac aca gcg tgg tgg cgt aac ctc ctc ggg ttt ccc acg gag cac   499
Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly Phe Pro Thr Glu His
        120                 125                 130

gac aag cag att gct ttt cac gcg ttg gag tcc gtg ggc att ttg cac   547
Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val Gly Ile Leu His
    135                 140                 145

aaa gtg tgg acc cga gct ggt gct ttg tcg ggt gga cag aaa cag cgc   595
Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly Gln Lys Gln Arg
150                 155                 160                 165

gtt gct att gcg cgc gcc tta tcg caa gat ccg tct gtc atg ctg gca   643
Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser Val Met Leu Ala
                170                 175                 180

gat gag cct gtg gca agc ctt gat ccg cca acc gcg cat tcc gtg atg   691
Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala His Ser Val Met
            185                 190                 195

cgc gat cta gaa aac atc aac aac gtg gaa ggc ctc acc gtg ttg gtg   739
Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu Thr Val Leu Val
        200                 205                 210

aac ttg cac ttg att gat ttg gct cgt caa tac acc aca agg ctt gtg   787
Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr Thr Arg Leu Val
    215                 220                 225

ggt ttg cgt gcc ggc aag ctg gtc tat gac ggt cct atc tct gag gcc   835
Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro Ile Ser Glu Ala
230                 235                 240                 245

acc gat aaa gac ttt gaa gct atc tat ggt cgc ccc atc cag gct aaa   883
Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro Ile Gln Ala Lys
                250                 255                 260

gac ctg cta ggt gat cgc gca tgaccacgcc ttcttctaca ctt            927
Asp Leu Leu Gly Asp Arg Ala
            265
```

<210> 292
<211> 268
<212> PRT

<213> Corynebacterium glutamicum

<400> 292

```
Met Asn Ser Asp Ala Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe
  1               5                  10                  15

Asp His Val Ser Val Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp
             20                  25                  30

Val Ser Leu Thr Ile Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu
         35                  40                  45

Ser Gly Ser Gly Lys Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val
     50                  55                  60

Arg Ala Thr Glu Gly Thr Val Thr Val Gly Pro His Gln Ile Asn Thr
 65                  70                  75                  80

Leu Lys Gly Lys Ala Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile
                 85                  90                  95

Phe Gln Gly Phe Asn Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val
            100                 105                 110

Leu Val Gly Arg Phe Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly
        115                 120                 125

Phe Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser
    130                 135                 140

Val Gly Ile Leu His Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly
145                 150                 155                 160

Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro
                165                 170                 175

Ser Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr
            180                 185                 190

Ala His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly
        195                 200                 205

Leu Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr
    210                 215                 220

Thr Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly
225                 230                 235                 240

Pro Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg
                245                 250                 255

Pro Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
            260                 265
```

<210> 293
<211> 440
<212> DNA
<213> Corynebacterium glutamicum

<220>

US 20050136549A1

<221> CDS
<222> (1)..(417)
<223> FRXA01002

<400> 293

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ccc acg gag cac gac aag cag att gct ttt cac gcg ttg gag tcc gtg   48
Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val
  1               5                  10                  15

ggc att ttg gac aaa gtg tgg acc cga gct ggt gct ttg tcg ggt gga   96
Gly Ile Leu Asp Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly
             20                  25                  30

cag aaa cag cgc gtt gct att gcg cgc gcc tta tcg caa gat ccg tct   144
Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser
         35                  40                  45

gtc atg ctg gca gat gag cct gtg gca agc ctt gat ccg cca acc gcg   192
Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala
     50                  55                  60

cat tcc gtg atg cgc gat cta gaa aac atc aac aac gtg gaa ggc ctc   240
His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu
 65                  70                  75                  80

acc gtg ttg gtg aac ttg cac ttg att gat ttg gct cgt caa tac acc   288
Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr
                 85                  90                  95

aca agg ctt gtg ggt ttg cgt gcc ggc aag ctg gtc tat gac ggt cct   336
Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro
            100                 105                 110

atc tct gag gcc acc gat aaa gac ttt gaa gct atc tat ggt cgc ccc   384
Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro
        115                 120                 125

atc cag gct aaa gac ctg cta ggt gat cgc gca tgaccacgcc ttcttctaca 437
Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
    130                 135

ctt                                                               440
```

<210> 294
<211> 139
<212> PRT
<213> Corynebacterium glutamicum

<400> 294

```
Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val
  1               5                  10                  15

Gly Ile Leu Asp Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly
             20                  25                  30

Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser
         35                  40                  45

Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala
     50                  55                  60
```

```
His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu
 65                  70                  75                  80

Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr
                85                  90                  95

Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro
            100                 105                 110

Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro
        115                 120                 125

Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
    130                 135
```

<210> 295
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXN01000

<400> 295

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ctttctatgc ctacgcggat gtttccgtga tcattctgga aatcctcatc gtggtgattg 60

tcattgaagt aatctccaac gcacttcgaa agaggctggt atg agc acc tta acc   115
                                            Met Ser Thr Leu Thr
                                              1               5

tct cac cgc aca gta ccg gcc ccc agc tct ccc ccg gcg cgc ccc aac   163
Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro Pro Ala Arg Pro Asn
                  10                  15                  20

aaa ctg gcg cgc aat atc gtt gca att gtc gct gcg ctg att gtc ctt   211
Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala Ala Leu Ile Val Leu
              25                  30                  35

ata gct acc ggc acg ctc aag atc gag tgg aat gag ctt ccg cag atg   259
Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn Glu Leu Pro Gln Met
          40                  45                  50

ccc gcg cag gtg tgg cat tac tta gag ctg atg ttt agc gat ccc gat   307
Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met Phe Ser Asp Pro Asp
      55                  60                  65

tgg tcg aag ttt ggc cgc gcc gtc cag gaa atg tgg cgt tcc atc gcc   355
Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met Trp Arg Ser Ile Ala
 70                  75                  80                  85

atg gcg tgg ttg ggt gcc att tta tgc gtg gtg gtc tct gtc cct ctg   403
Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val Val Ser Val Pro Leu
                  90                  95                 100

gga atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt   451
Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val
            105                 110                 115
```

```
tta cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc   499
Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile
        120                 125                 130

gca att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg   547
Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala
    135                 140                 145

ctc gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat   595
Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr
150                 155                 160                 165

gaa gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca   643
Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala
                170                 175                 180

gcg ggt gga act acg ccg gag gtt ctg cgg tgg gcg ttg tgg cca cag   691
Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln
            185                 190                 195

gtt gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac   739
Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn
        200                 205                 210

atc cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt   787
Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly
    215                 220                 225

agt atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc   835
Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly
230                 235                 240                 245

atg ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc   883
Met Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile
                250                 255                 260

tcc ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc   931
Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val
            265                 270                 275

gtg gca cca agc aac tgacgctcca ccaagcatcc gca                    969
Val Ala Pro Ser Asn
        280
```

<210> 296
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 296

```
Met Ser Thr Leu Thr Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro
  1               5                  10                  15

Pro Ala Arg Pro Asn Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala
             20                  25                  30

Ala Leu Ile Val Leu Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn
         35                  40                  45
```

Glu Leu Pro Gln Met Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met
50 55 60

Phe Ser Asp Pro Asp Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met
65 70 75 80

Trp Arg Ser Ile Ala Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val
85 90 95

Val Ser Val Pro Leu Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr
100 105 110

Trp Leu Arg Thr Val Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe
115 120 125

Pro Glu Val Val Ile Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr
130 135 140

Pro Phe Thr Gly Ala Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln
145 150 155 160

Ala Lys Trp Thr Tyr Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser
165 170 175

Glu Ala Val Arg Ala Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp
180 185 190

Ala Leu Trp Pro Gln Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr
195 200 205

Arg Phe Glu Ile Asn Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly
210 215 220

Ala Gly Gly Ile Gly Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln
225 230 235 240

Trp Asp Thr Val Gly Met Leu Leu Ile Val Val Val Ala Thr Met
245 250 255

Ile Val Asp Leu Ile Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly
260 265 270

Ala Ser Asp Arg Val Val Ala Pro Ser Asn
275 280

<210> 297
<211> 563
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(540)
<223> FRXA01000

<400> 297
atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt tta 48
Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val Leu
1 5 10 15

```
cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc gca    96
Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile Ala
             20                  25                  30

att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg ctc   144
Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala Leu
         35                  40                  45

gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat gaa   192
Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr Glu
     50                  55                  60

gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca gcg   240
Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala Ala
 65                  70                  75                  80

ggt gga act acg ccg gag gtt ctg cgg tgg gcg ttg tgg cca cag gtt   288
Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln Val
                 85                  90                  95

gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac atc   336
Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn Ile
             100                 105                 110

cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt agt   384
Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Ser
         115                 120                 125

atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc atg   432
Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly Met
     130                 135                 140

ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc tcc   480
Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile Ser
145                 150                 155                 160

ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc gtg   528
Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val Val
                 165                 170                 175

gca cca agc aac tgacgctcca ccaagcatcc gca                        563
Ala Pro Ser Asn
             180
```

<210> 298
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 298

```
Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val Leu
  1               5                  10                  15

Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile Ala
             20                  25                  30

Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala Leu
         35                  40                  45

Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr Glu
```

```
     50                  55                  60

Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala Ala
 65                  70                  75                  80

Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln Val
                 85                  90                  95

Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn Ile
            100                 105                 110

Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Ser
        115                 120                 125

Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly Met
    130                 135                 140

Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile Ser
145                 150                 155                 160

Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val Val
                165                 170                 175

Ala Pro Ser Asn
            180
```

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<210> 299
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXA01003

<400> 299

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agctggtcta tgacggtcct atctctgagg ccaccgataa agactttgaa gctatctatg 60

gtcgccccat ccaggctaaa gacctgctag gtgatcgcgc atg acc acg cct tct   115
                                            Met Thr Thr Pro Ser
                                              1               5

tct aca ctt atc cca caa aag cct cgg gct ggg gta aag acc tat ctc   163
Ser Thr Leu Ile Pro Gln Lys Pro Arg Ala Gly Val Lys Thr Tyr Leu
                 10                  15                  20

atc atc ggc gcc atc gtt gtc ttc acc gtg gca aca gca acc cca gcg   211
Ile Ile Gly Ala Ile Val Val Phe Thr Val Ala Thr Ala Thr Pro Ala
             25                  30                  35

cta ggt ggc att gag ctt gat ttc gct tcc att gct gcg aat tgg cgc   259
Leu Gly Gly Ile Glu Leu Asp Phe Ala Ser Ile Ala Ala Asn Trp Arg
         40                  45                  50

aat ggt gcc aac aaa ctc ctg caa atg ctg cag ccc aac ttt gcg ttc   307
Asn Gly Ala Asn Lys Leu Leu Gln Met Leu Gln Pro Asn Phe Ala Phe
     55                  60                  65

ttg cct cgt acg tgg ctt ccc atg ttg gaa acc ctg cag atg gcg ctt   355
```

```
Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr Leu Gln Met Ala Leu
 70                  75                  80                  85

gtt gga gct gtc ttg tct gct gcc gta tcg gtg cct ttg acg ttg tgg   403
Val Gly Ala Val Leu Ser Ala Ala Val Ser Val Pro Leu Thr Leu Trp
                 90                  95                 100

gca gcg cag gca acc aac acc agt gcg att ggt cgt ggc att gtc cgc   451
Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly Arg Gly Ile Val Arg
            105                 110                 115

acc atc att aac gtg gtg cgc tct gtc ccc gac ttg gtg tat gcc acc   499
Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp Leu Val Tyr Ala Thr
        120                 125                 130

atc ttg gtc gcc atg gtt ggt gtc ggc gca tta cct ggc att ttg acg   547
Ile Leu Val Ala Met Val Gly Val Gly Ala Leu Pro Gly Ile Leu Thr
    135                 140                 145

ctg ttt ctg ttc aac ctg ggc atc gtg gtc aag ctt gtc tct gag gcc   595
Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys Leu Val Ser Glu Ala
150                 155                 160                 165

att gat tcc act gag cat ccc tat atg gaa gca gga cgc gca gca ggt   643
Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala Gly Arg Ala Ala Gly
                170                 175                 180

gga tca cag ttc caa atc aac cga gtc tcc gcg ctt cct gaa gtc atg   691
Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala Leu Pro Glu Val Met
            185                 190                 195

ccg ctc ttt gcc aac caa tgg ctc tac acc cta gag ctg aat gta cgc   739
Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu Glu Leu Asn Val Arg
        200                 205                 210

atc tcc gcc atc ctt ggc atc gtg ggc gca ggt ggc atc ggc agg ctg   787
Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Arg Leu
    215                 220                 225

ctt gat gaa cgc cga gct ttc tat gcc tac gcg gat gtt tcc gtg atc   835
Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala Asp Val Ser Val Ile
230                 235                 240                 245

att ctg gaa atc ctc atc gtg gtg att gtc att gaa gta atc tcc aac   883
Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile Glu Val Ile Ser Asn
                250                 255                 260

gca ctt cga aag agg ctg gta tgagcacctt aacctctcac cgc            927
Ala Leu Arg Lys Arg Leu Val
            265
```

<210> 300
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 300

```
Met Thr Thr Pro Ser Ser Thr Leu Ile Pro Gln Lys Pro Arg Ala Gly
  1               5                  10                  15
```

Val Lys Thr Tyr Leu Ile Ile Gly Ala Ile Val Val Phe Thr Val Ala
20 25 30

Thr Ala Thr Pro Ala Leu Gly Gly Ile Glu Leu Asp Phe Ala Ser Ile
35 40 45

Ala Ala Asn Trp Arg Asn Gly Ala Asn Lys Leu Leu Gln Met Leu Gln
50 55 60

Pro Asn Phe Ala Phe Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr
65 70 75 80

Leu Gln Met Ala Leu Val Gly Ala Val Leu Ser Ala Ala Val Ser Val
85 90 95

Pro Leu Thr Leu Trp Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly
100 105 110

Arg Gly Ile Val Arg Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp
115 120 125

Leu Val Tyr Ala Thr Ile Leu Val Ala Met Val Gly Val Gly Ala Leu
130 135 140

Pro Gly Ile Leu Thr Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys
145 150 155 160

Leu Val Ser Glu Ala Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala
165 170 175

Gly Arg Ala Ala Gly Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala
180 185 190

Leu Pro Glu Val Met Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu
195 200 205

Glu Leu Asn Val Arg Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly
210 215 220

Gly Ile Gly Arg Leu Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala
225 230 235 240

Asp Val Ser Val Ile Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile
245 250 255

Glu Val Ile Ser Asn Ala Leu Arg Lys Arg Leu Val
260 265

<210> 301
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(594)
<223> RXN00193

<400> 301
aaa gct ttc tnc caa cgc gaa ggt ttc atc tca gcc ttc ggt ttc acc 48

```
Lys Ala Phe Xaa Gln Arg Glu Gly Phe Ile Ser Ala Phe Gly Phe Thr
  1               5                  10                  15

gtc ctc gtg gtc atc gtc tcc gtg atc aca gtc aac atc ttc gcc ttc   96
Val Leu Val Val Ile Val Ser Val Ile Thr Val Asn Ile Phe Ala Phe
            20                  25                  30

ctc ttg gcg tgg ttg ctg acc cgc aaa ctc cgc ggt acc aac ttt ttc   144
Leu Leu Ala Trp Leu Leu Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe
        35                  40                  45

cgc aca gtc ttc ttt atg ccg aac ctt atc ggc ggc att gtg ctg ggt   192
Arg Thr Val Phe Phe Met Pro Asn Leu Ile Gly Gly Ile Val Leu Gly
    50                  55                  60

tat acc tgg cag acc atg atc aac gcc gtg ctt tcg cac tat gcc acg   240
Tyr Thr Trp Gln Thr Met Ile Asn Ala Val Leu Ser His Tyr Ala Thr
65                  70                  75                  80

act att agc gcg gac tgg aaa ttc ggc tac gcc ggc ctc atc atg cta   288
Thr Ile Ser Ala Asp Trp Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu
                85                  90                  95

ctt aac tgg cag ctc atc ggc tac atg atg atc att tac atc gcc ggc   336
Leu Asn Trp Gln Leu Ile Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly
            100                 105                 110

ctg caa aac gtc cca cca gag ctc att gag gct gcc gaa ctc gac ggc   384
Leu Gln Asn Val Pro Pro Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly
        115                 120                 125

gtc aac aag tgg gag atg ctg cgg cac gtc act att ccg atg gtc atg   432
Val Asn Lys Trp Glu Met Leu Arg His Val Thr Ile Pro Met Val Met
    130                 135                 140

cca tcc atc acc atc tgc ctc ttt ttg act ttg tcg aac tcc ttt aag   480
Pro Ser Ile Thr Ile Cys Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys
145                 150                 155                 160

ctc ttc gac cag aac ctg gcg ctg acc aac ggc gct cct ggc ggg caa   528
Leu Phe Asp Gln Asn Leu Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln
                165                 170                 175

act gag atg gtg gcg ctc aac atc atc aac acg ctg ttt aac cgt atg   576
Thr Glu Met Val Ala Leu Asn Ile Ile Asn Thr Leu Phe Asn Arg Met
            180                 185                 190

aat gtc gag ggc gtc ggt                                          594
Asn Val Glu Gly Val Gly
        195
```

<210> 302
<211> 198
<212> PRT
<213> Corynebacterium glutamicum

<400> 302

```
Lys Ala Phe Xaa Gln Arg Glu Gly Phe Ile Ser Ala Phe Gly Phe Thr
  1               5                  10                  15
```

Val Leu Val Val Ile Val Ser Val Ile Thr Val Asn Ile Phe Ala Phe
20 25 30

Leu Leu Ala Trp Leu Leu Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe
35 40 45

Arg Thr Val Phe Phe Met Pro Asn Leu Ile Gly Gly Ile Val Leu Gly
50 55 60

Tyr Thr Trp Gln Thr Met Ile Asn Ala Val Leu Ser His Tyr Ala Thr
65 70 75 80

Thr Ile Ser Ala Asp Trp Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu
85 90 95

Leu Asn Trp Gln Leu Ile Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly
100 105 110

Leu Gln Asn Val Pro Pro Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly
115 120 125

Val Asn Lys Trp Glu Met Leu Arg His Val Thr Ile Pro Met Val Met
130 135 140

Pro Ser Ile Thr Ile Cys Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys
145 150 155 160

Leu Phe Asp Gln Asn Leu Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln
165 170 175

Thr Glu Met Val Ala Leu Asn Ile Ile Asn Thr Leu Phe Asn Arg Met
180 185 190

Asn Val Glu Gly Val Gly
195

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<210> 303
<211> 940
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (75)..(917)
<223> FRXA00193

<400> 303
cctcagcctc ctctcctcac cgccttcccc gctgggaaac gtgtggcacc acctgaaatt 60

aaggtttcac caccatg caa gca acg ctg aag aag tac ttc cca gtc ttt 110
Met Gln Ala Thr Leu Lys Lys Tyr Phe Pro Val Phe
1 5 10

gtc ttg ccc acc ctt ctg gca ttc atg att gcc ttc ttg gtg ccg ttc 158
Val Leu Pro Thr Leu Leu Ala Phe Met Ile Ala Phe Leu Val Pro Phe
15 20 25

atc gtg ggt ttc ttc ctc tcc ttt acg aag ttc acc act atc acc aac 206
Ile Val Gly Phe Phe Leu Ser Phe Thr Lys Phe Thr Thr Ile Thr Asn
30 35 40

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gcc aag tgg gtt ggc ata gac aac tac gtc aaa gct ttc tcc caa cgc   254
Ala Lys Trp Val Gly Ile Asp Asn Tyr Val Lys Ala Phe Ser Gln Arg
 45                  50                  55                  60

gaa ggt ttc atc tca gcc ttc ggt ttc acc gtc ctc gtg gtc atc gtc   302
Glu Gly Phe Ile Ser Ala Phe Gly Phe Thr Val Leu Val Val Ile Val
                 65                  70                  75

tcc gtg atc aca gtc aac atc ttc gcc ttc ctc ttg gcg tgg ttg ctg   350
Ser Val Ile Thr Val Asn Ile Phe Ala Phe Leu Leu Ala Trp Leu Leu
             80                  85                  90

acc cgc aaa ctc cgc ggt acc aac ttt ttc cgc aca gtc ttc ttt atg   398
Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe Arg Thr Val Phe Phe Met
         95                 100                 105

ccg aac ctt atc ggc ggc att gtg ctg ggt tat acc tgg cag acc atg   446
Pro Asn Leu Ile Gly Gly Ile Val Leu Gly Tyr Thr Trp Gln Thr Met
    110                 115                 120

atc aac gcc gtg ctt tcg cac tat gcc acg act att agc gcg gac tgg   494
Ile Asn Ala Val Leu Ser His Tyr Ala Thr Thr Ile Ser Ala Asp Trp
125                 130                 135                 140

aaa ttc ggc tac gcc ggc ctc atc atg cta ctt aac tgg cag ctc atc   542
Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu Leu Asn Trp Gln Leu Ile
                145                 150                 155

ggc tac atg atg atc att tac atc gcc ggc ctg caa aac gtc cca cca   590
Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly Leu Gln Asn Val Pro Pro
            160                 165                 170

gag ctc att gag gct gcc gaa ctc gac ggc gtc aac aag tgg gag atg   638
Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly Val Asn Lys Trp Glu Met
        175                 180                 185

ctg cgg cac gtc act att ccg atg gtc atg cca tcc atc acc atc tgc   686
Leu Arg His Val Thr Ile Pro Met Val Met Pro Ser Ile Thr Ile Cys
    190                 195                 200

ctc ttt ttg act ttg tcg aac tcc ttt aag ctc ttc gac cag aac ctg   734
Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys Leu Phe Asp Gln Asn Leu
205                 210                 215                 220

gcg ctg acc aac ggc gct cct ggc ggg caa act gag atg gtg gcg ctc   782
Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln Thr Glu Met Val Ala Leu
                225                 230                 235

aac atc atc aac acg ctg ttt aac cgt atg aat gtc gag ggc gtc ggt   830
Asn Ile Ile Asn Thr Leu Phe Asn Arg Met Asn Val Glu Gly Val Gly
            240                 245                 250

cag gcc aag gcc gtt atc ttc gtc gtc gtt gtg gtc gtc atc gcg tac   878
Gln Ala Lys Ala Val Ile Phe Val Val Val Val Val Val Ile Ala Tyr
        255                 260                 265

ttc cag ctg cgc gcg acc cgc tcc aag gaa atc gag gct taagttatga    927
Phe Gln Leu Arg Ala Thr Arg Ser Lys Glu Ile Glu Ala
    270                 275                 280
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ctaccagcac ttc 940

<210> 304
<211> 281
<212> PRT
<213> Corynebacterium glutamicum

<400> 304

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Met Gln Ala Thr Leu Lys Lys Tyr Phe Pro Val Phe Val Leu Pro Thr
  1               5                  10                  15

Leu Leu Ala Phe Met Ile Ala Phe Leu Val Pro Phe Ile Val Gly Phe
             20                  25                  30

Phe Leu Ser Phe Thr Lys Phe Thr Thr Ile Thr Asn Ala Lys Trp Val
         35                  40                  45

Gly Ile Asp Asn Tyr Val Lys Ala Phe Ser Gln Arg Glu Gly Phe Ile
     50                  55                  60

Ser Ala Phe Gly Phe Thr Val Leu Val Val Ile Val Ser Val Ile Thr
 65                  70                  75                  80

Val Asn Ile Phe Ala Phe Leu Leu Ala Trp Leu Leu Thr Arg Lys Leu
                 85                  90                  95

Arg Gly Thr Asn Phe Phe Arg Thr Val Phe Phe Met Pro Asn Leu Ile
            100                 105                 110

Gly Gly Ile Val Leu Gly Tyr Thr Trp Gln Thr Met Ile Asn Ala Val
        115                 120                 125

Leu Ser His Tyr Ala Thr Thr Ile Ser Ala Asp Trp Lys Phe Gly Tyr
    130                 135                 140

Ala Gly Leu Ile Met Leu Leu Asn Trp Gln Leu Ile Gly Tyr Met Met
145                 150                 155                 160

Ile Ile Tyr Ile Ala Gly Leu Gln Asn Val Pro Pro Glu Leu Ile Glu
                165                 170                 175

Ala Ala Glu Leu Asp Gly Val Asn Lys Trp Glu Met Leu Arg His Val
            180                 185                 190

Thr Ile Pro Met Val Met Pro Ser Ile Thr Ile Cys Leu Phe Leu Thr
        195                 200                 205

Leu Ser Asn Ser Phe Lys Leu Phe Asp Gln Asn Leu Ala Leu Thr Asn
    210                 215                 220

Gly Ala Pro Gly Gly Gln Thr Glu Met Val Ala Leu Asn Ile Ile Asn
225                 230                 235                 240

Thr Leu Phe Asn Arg Met Asn Val Glu Gly Val Gly Gln Ala Lys Ala
                245                 250                 255

Val Ile Phe Val Val Val Val Val Val Ile Ala Tyr Phe Gln Leu Arg
            260                 265                 270

Ala Thr Arg Ser Lys Glu Ile Glu Ala
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275 280

<210> 305
<211> 1053
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1030)
<223> RXN01298

<400> 305
cttaaacgtc accttattta tgcattatgt tggtttcaga ctcgaacaat tcaattagaa 60

aacactaatc ggacatttag gtcacataac atttccgctc gtg tcc aca tta att 115
Val Ser Thr Leu Ile
1 5

tct gaa ccc gag gtg gat aag cta cgt aaa cgt gcc aag aga tca agg 163
Ser Glu Pro Glu Val Asp Lys Leu Arg Lys Arg Ala Lys Arg Ser Arg
10 15 20

cgg aca gaa tgg tgg ctt gcc gcc gca ctt ctt gcc cca aac ttg ctt 211
Arg Thr Glu Trp Trp Leu Ala Ala Ala Leu Leu Ala Pro Asn Leu Leu
25 30 35

ctc ttg gcc atc ttt acg tat cgg cca ctg tta gat aac ttc cgg ttg 259
Leu Leu Ala Ile Phe Thr Tyr Arg Pro Leu Leu Asp Asn Phe Arg Leu
40 45 50

tcc ttt ttc aac tgg aac att tcc tcg ccc aca tca acc ttc att ggg 307
Ser Phe Phe Asn Trp Asn Ile Ser Ser Pro Thr Ser Thr Phe Ile Gly
55 60 65

ttt gat aac tac gtt gag ttc ttc act cgt agt gac act ctc caa gtt 355
Phe Asp Asn Tyr Val Glu Phe Phe Thr Arg Ser Asp Thr Leu Gln Val
70 75 80 85

gtt tta aac acc gtc atc ttc acg gca tgt gct gtg atc gga tcg atg 403
Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala Val Ile Gly Ser Met
90 95 100

gtg ctc ggt ttg ctc ctg gcc atg ttg ttg gat cag aag ctt ttc ggc 451
Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp Gln Lys Leu Phe Gly
105 110 115

cgt aac ttt gtg cgt tcc atg gtg ttt gcc ccg ttt gtg att tcc ggt 499
Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro Phe Val Ile Ser Gly
120 125 130

gct gcc att ggt gtt gct ttc cag ttc gtt ttt gac cct aat ttt ggt 547
Ala Ala Ile Gly Val Ala Phe Gln Phe Val Phe Asp Pro Asn Phe Gly
135 140 145

ttg gtt cag gac ttg ctg gga cgc atc ggc gtt gat tcg cca cag ttc 595
Leu Val Gln Asp Leu Leu Gly Arg Ile Gly Val Asp Ser Pro Gln Phe
150 155 160 165

tac caa aac cct aac tgg gca ttg ttc atg gtg acg ttc act ttc gtg 643

```
Tyr Gln Asn Pro Asn Trp Ala Leu Phe Met Val Thr Phe Thr Phe Val
                170                 175                 180

tgg aag aac ttg ggc tac tcc ttt gtt atc tac ctg gct gca ttg cag   691
Trp Lys Asn Leu Gly Tyr Ser Phe Val Ile Tyr Leu Ala Ala Leu Gln
            185                 190                 195

ggg cta aac aag gat ttg tct gag gcc gca ccg gtg gat ggc gcg agc   739
Gly Leu Asn Lys Asp Leu Ser Glu Ala Ala Pro Val Asp Gly Ala Ser
        200                 205                 210

gcg tgg aca cgt ttt tgg aag gtt act ctt ccg cag ctt cgc cca acc   787
Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro Gln Leu Arg Pro Thr
    215                 220                 225

acg ttc ttc ctt tct att act gtc acg ctg aac tcg gtt cag gtc ttc   835
Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn Ser Val Gln Val Phe
230                 235                 240                 245

gac atc att cac acc atg act cgt ggt ggc ccc ttg ggt aac ggt acg   883
Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro Leu Gly Asn Gly Thr
                250                 255                 260

acc acc ttg gtt tac cag gtg tac acc gag act ttc acc aac tat cgc   931
Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr Phe Thr Asn Tyr Arg
            265                 270                 275

gcg gga tat ggt gca aca atc gca acg att ttg ttc ctg ttg ctg ctg   979
Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu Phe Leu Leu Leu Leu
        280                 285                 290

att atc act gtt atc cag gtt cga tac atg gat aag gag aac aag cag   1027
Ile Ile Thr Val Ile Gln Val Arg Tyr Met Asp Lys Glu Asn Lys Gln
    295                 300                 305

aaa tgatctcgac tgatagaaac gtt                                     1053
Lys
310
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<210> 306
<211> 310
<212> PRT
<213> Corynebacterium glutamicum

<400> 306

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Val Ser Thr Leu Ile Ser Glu Pro Glu Val Asp Lys Leu Arg Lys Arg
  1               5                  10                  15

Ala Lys Arg Ser Arg Arg Thr Glu Trp Trp Leu Ala Ala Ala Leu Leu
            20                  25                  30

Ala Pro Asn Leu Leu Leu Leu Ala Ile Phe Thr Tyr Arg Pro Leu Leu
        35                  40                  45

Asp Asn Phe Arg Leu Ser Phe Phe Asn Trp Asn Ile Ser Ser Pro Thr
    50                  55                  60

Ser Thr Phe Ile Gly Phe Asp Asn Tyr Val Glu Phe Phe Thr Arg Ser
65                  70                  75                  80
```

Asp Thr Leu Gln Val Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala
85 90 95

Val Ile Gly Ser Met Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp
100 105 110

Gln Lys Leu Phe Gly Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro
115 120 125

Phe Val Ile Ser Gly Ala Ala Ile Gly Val Ala Phe Gln Phe Val Phe
130 135 140

Asp Pro Asn Phe Gly Leu Val Gln Asp Leu Leu Gly Arg Ile Gly Val
145 150 155 160

Asp Ser Pro Gln Phe Tyr Gln Asn Pro Asn Trp Ala Leu Phe Met Val
165 170 175

Thr Phe Thr Phe Val Trp Lys Asn Leu Gly Tyr Ser Phe Val Ile Tyr
180 185 190

Leu Ala Ala Leu Gln Gly Leu Asn Lys Asp Leu Ser Glu Ala Ala Pro
195 200 205

Val Asp Gly Ala Ser Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro
210 215 220

Gln Leu Arg Pro Thr Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn
225 230 235 240

Ser Val Gln Val Phe Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro
245 250 255

Leu Gly Asn Gly Thr Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr
260 265 270

Phe Thr Asn Tyr Arg Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu
275 280 285

Phe Leu Leu Leu Leu Ile Ile Thr Val Ile Gln Val Arg Tyr Met Asp
290 295 300

Lys Glu Asn Lys Gln Lys
305 310

<210> 307
<211> 416
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(393)
<223> FRXA01298

<400> 307
ttc gtg tgg aag aac ttg ggc tac tcc ttt gtt atc tac ctg gct gca 48
Phe Val Trp Lys Asn Leu Gly Tyr Ser Phe Val Ile Tyr Leu Ala Ala
1 5 10 15

```
ttg cag ggg cta aac aag gat ttg tct gag gcc gca ccg gtg gat ggc   96
Leu Gln Gly Leu Asn Lys Asp Leu Ser Glu Ala Ala Pro Val Asp Gly
            20                  25                  30

gcg agc gcg tgg aca cgt ttt tgg aag gtt act ctt ccg cag ctt cgc  144
Ala Ser Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro Gln Leu Arg
        35                  40                  45

cca acc acg ttc ttc ctt tct att act gtc acg ctg aac tcg gtt cag  192
Pro Thr Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn Ser Val Gln
    50                  55                  60

gtc ttc gac atc att cac acc atg act cgt ggt ggc ccc ttg ggt aac  240
Val Phe Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro Leu Gly Asn
65                  70                  75                  80

ggt acg acc acc ttg gtt tac cag gtg tac acc gag act ttc acc aac  288
Gly Thr Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr Phe Thr Asn
                85                  90                  95

tat cgc gcg gga tat ggt gca aca atc gca acg att ttg ttc ctg ttg  336
Tyr Arg Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu Phe Leu Leu
            100                 105                 110

ctg ctg att atc act gtt atc cag gtt cga tac atg gat aag gag aac  384
Leu Leu Ile Ile Thr Val Ile Gln Val Arg Tyr Met Asp Lys Glu Asn
        115                 120                 125

aag cag aaa tgatctcgac tgatagaaac gtt                            416
Lys Gln Lys
    130
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<210> 308
<211> 131
<212> PRT
<213> Corynebacterium glutamicum

<400> 308

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Phe Val Trp Lys Asn Leu Gly Tyr Ser Phe Val Ile Tyr Leu Ala Ala
  1               5                  10                  15

Leu Gln Gly Leu Asn Lys Asp Leu Ser Glu Ala Ala Pro Val Asp Gly
            20                  25                  30

Ala Ser Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro Gln Leu Arg
        35                  40                  45

Pro Thr Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn Ser Val Gln
    50                  55                  60

Val Phe Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro Leu Gly Asn
65                  70                  75                  80

Gly Thr Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr Phe Thr Asn
                85                  90                  95

Tyr Arg Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu Phe Leu Leu
            100                 105                 110

Leu Leu Ile Ile Thr Val Ile Gln Val Arg Tyr Met Asp Lys Glu Asn
```

```
        115                 120                 125

Lys Gln Lys
    130


<210> 309
<211> 535
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> FRXA02422

<400> 309
cttaaacgtc accttattta tgcattatgt tggtttcaga ctcgaacaat tcaattagaa 60

aacactaatc ggacatttag gtcacataac atttccgctc gtg tcc aca tta att   115
                                        Val Ser Thr Leu Ile
                                          1               5

tct gaa ccc gag gtg gat aag cta cgt aaa cgt gcc aag aga tca agg   163
Ser Glu Pro Glu Val Asp Lys Leu Arg Lys Arg Ala Lys Arg Ser Arg
                 10                  15                  20

cgg aca gaa tgg tgg ctt gcc gcc gca ctt ctt gcc cca aac ttg ctt   211
Arg Thr Glu Trp Trp Leu Ala Ala Ala Leu Leu Ala Pro Asn Leu Leu
             25                  30                  35

ctc ttg gcc atc ttt acg tat cgg cca ctg tta gat aac ttc cgg ttg   259
Leu Leu Ala Ile Phe Thr Tyr Arg Pro Leu Leu Asp Asn Phe Arg Leu
         40                  45                  50

tcc ttt ttc aac tgg aac att tcc tcg ccc aca tca acc ttc att ggg   307
Ser Phe Phe Asn Trp Asn Ile Ser Ser Pro Thr Ser Thr Phe Ile Gly
     55                  60                  65

ttt gat aac tac gtt gag ttc ttc act cgt agt gac act ctc caa gtt   355
Phe Asp Asn Tyr Val Glu Phe Phe Thr Arg Ser Asp Thr Leu Gln Val
 70                  75                  80                  85

gtt tta aac acc gtc atc ttc acg gca tgt gct gtg atc gga tcg atg   403
Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala Val Ile Gly Ser Met
                 90                  95                 100

gtg ctc ggt ttg ctc ctg gcc atg ttg ttg gat cag aag ctt ttc ggc   451
Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp Gln Lys Leu Phe Gly
            105                 110                 115

cgt aac ttt gtg cgt tcc atg gtg ttt gcc ccg ttt gtg att tcc ggt   499
Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro Phe Val Ile Ser Gly
        120                 125                 130

gct gcc att ggt ggt gct ttc cag ttc gtt ttt gac                   535
Ala Ala Ile Gly Gly Ala Phe Gln Phe Val Phe Asp
    135                 140                 145


<210> 310
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<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 310
Val Ser Thr Leu Ile Ser Glu Pro Glu Val Asp Lys Leu Arg Lys Arg
1 5 10 15

Ala Lys Arg Ser Arg Arg Thr Glu Trp Trp Leu Ala Ala Ala Leu Leu
20 25 30

Ala Pro Asn Leu Leu Leu Leu Ala Ile Phe Thr Tyr Arg Pro Leu Leu
35 40 45

Asp Asn Phe Arg Leu Ser Phe Phe Asn Trp Asn Ile Ser Ser Pro Thr
50 55 60

Ser Thr Phe Ile Gly Phe Asp Asn Tyr Val Glu Phe Phe Thr Arg Ser
65 70 75 80

Asp Thr Leu Gln Val Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala
85 90 95

Val Ile Gly Ser Met Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp
100 105 110

Gln Lys Leu Phe Gly Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro
115 120 125

Phe Val Ile Ser Gly Ala Ala Ile Gly Gly Ala Phe Gln Phe Val Phe
130 135 140

Asp
145

US-10-765-330-pg-404.txt

<210> 311
<211> 879
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(856)
<223> RXN02515

<400> 311
gtggctaagc acagttactt ggccaagctg ggcggcagaa aaaccggccc agctaatact 60

tcagtttaaa attcgcttca accctgaaag attgtgacag atg agc act ctt gaa 115
Met Ser Thr Leu Glu
1 5

atc cgt aac ctg cac gca cag gtc ctg ccg tcc gat gag tcc gct gag 163
Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser Asp Glu Ser Ala Glu
10 15 20

cct aag gaa atc ctc aag ggc gtc aac ctc acc atc aac tct ggt gag 211
Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr Ile Asn Ser Gly Glu
25 30 35

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atc cac gcc atc atg ggc cct aac ggt tcc ggc aag tcc act ctt gct   259
Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ala
         40                  45                  50

tac acc ctt ggt gga cac cca cgc tac gag gta acc gca ggc gag gtc   307
Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val Thr Ala Gly Glu Val
     55                  60                  65

ctc ctc gac ggc gag aac atc ctg gag atg gaa gtt gat gag cgt gca   355
Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu Val Asp Glu Arg Ala
 70                  75                  80                  85

cgc gct ggt ctc ttc ctg gcc atg cag tat cca act gaa atc cct ggc   403
Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro Thr Glu Ile Pro Gly
                 90                  95                 100

gtt tcc gtt gct aac ttc ctg cgt tcc gca gcg acc gca atc cgc ggc   451
Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala Thr Ala Ile Arg Gly
            105                 110                 115

gag gct cct aag ctt cgc gag tgg gtt aag gaa gtc cgc acc gct cag   499
Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu Val Arg Thr Ala Gln
        120                 125                 130

gaa gct ctg gca att gac cct gag ttc tcc aac cgc tca gtc aac gaa   547
Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn Arg Ser Val Asn Glu
    135                 140                 145

ggt ttc tcc ggt ggc gag aag aag cgc cac gag gtt ctg cag ctt gat   595
Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu Val Leu Gln Leu Asp
150                 155                 160                 165

ctg ctg aag cca aag ttc gcg atc atg gat gag acc gac tcc ggc ctt   643
Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu Thr Asp Ser Gly Leu
                170                 175                 180

gac gtg gat gca ctg cgc att gtt tcc gag ggc atc aac tcc tac aag   691
Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly Ile Asn Ser Tyr Lys
            185                 190                 195

cag gag acc gaa ggt ggc atc ttg atg atc acc cac tac aag cgc atc   739
Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr His Tyr Lys Arg Ile
        200                 205                 210

ctc aac tac gtt aag cct gac ttc att cac gtt ttc gcg aat ggc cag   787
Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val Phe Ala Asn Gly Gln
    215                 220                 225

att gtg acc acc ggt ggc gct gag ctt gct gac aag ctc gag gct gac   835
Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp Lys Leu Glu Ala Asp
230                 235                 240                 245

ggc tac gac cag ttc atc aag taacatgtcc gatttcctca atg             879
Gly Tyr Asp Gln Phe Ile Lys
                250
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<210> 312
<211> 252
<212> PRT
<213> Corynebacterium glutamicum

<400> 312

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Met Ser Thr Leu Glu Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser
  1               5                  10                  15

Asp Glu Ser Ala Glu Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr
             20                  25                  30

Ile Asn Ser Gly Glu Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly
         35                  40                  45

Lys Ser Thr Leu Ala Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val
     50                  55                  60

Thr Ala Gly Glu Val Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu
 65                  70                  75                  80

Val Asp Glu Arg Ala Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro
                 85                  90                  95

Thr Glu Ile Pro Gly Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala
            100                 105                 110

Thr Ala Ile Arg Gly Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu
        115                 120                 125

Val Arg Thr Ala Gln Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn
    130                 135                 140

Arg Ser Val Asn Glu Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu
145                 150                 155                 160

Val Leu Gln Leu Asp Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu
                165                 170                 175

Thr Asp Ser Gly Leu Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly
            180                 185                 190

Ile Asn Ser Tyr Lys Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr
        195                 200                 205

His Tyr Lys Arg Ile Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val
    210                 215                 220

Phe Ala Asn Gly Gln Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp
225                 230                 235                 240

Lys Leu Glu Ala Asp Gly Tyr Asp Gln Phe Ile Lys
                245                 250
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<210> 313
<211> 879
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(856)
<223> FRXA02515

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Phe Phe Pro Glu Met Phe Ala Ser Ser Val Arg Tyr Thr Gly Met Ala
    210                 215                 220

Met Gly Asn Gln Leu Gly Leu Ile Ile Val Gly Phe Ala Pro Thr Ile
225                 230                 235                 240

Ala Thr Ala Leu Tyr Ala Trp Asn Gly Trp Glu Ala Val Ala Gly Phe
                245                 250                 255

Ile Ile Gly Ala Ile Ala Leu Ser Ala Ala Val Ile Leu Thr Thr Lys
            260                 265                 270

Glu Thr Ala Phe Thr Lys Leu Glu Asp Leu Gly Lys Lys
        275                 280                 285
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<210> 325
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXA00312

<400> 325
ccattgaatg ggaagaactt ggttgtgtgt ttgtgacacc tattctaaag aacattaaac 60

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gtgattaagt tcatgattct taatgagaaa gggtgatcac atg gaa acc gtg agg   115
                                            Met Glu Thr Val Arg
                                              1               5

acc gca acc gcc gct cct gaa act gca tct ttg aag ctg cgt gag gca   163
Thr Ala Thr Ala Ala Pro Glu Thr Ala Ser Leu Lys Leu Arg Glu Ala
                  10                  15                  20

gaa agc cca gca aag tcc cca aag aaa gcc gcc ttg gcg tca ctt ttg   211
Glu Ser Pro Ala Lys Ser Pro Lys Lys Ala Ala Leu Ala Ser Leu Leu
              25                  30                  35

ggt tcg act ctg gag tac tac gac ttt gtc att tac ggc acc gcc tcc   259
Gly Ser Thr Leu Glu Tyr Tyr Asp Phe Val Ile Tyr Gly Thr Ala Ser
          40                  45                  50

gcg ctg ctg ttc aat cac ctc ttc ttc cca cag ggc gac cca gtc gtc   307
Ala Leu Leu Phe Asn His Leu Phe Phe Pro Gln Gly Asp Pro Val Val
      55                  60                  65

gcg acg atc ggc tct ctc gcc tca ttc ggt gtt gcg tac att gcg cgc   355
Ala Thr Ile Gly Ser Leu Ala Ser Phe Gly Val Ala Tyr Ile Ala Arg
  70                  75                  80                  85

ccc atc ggt ggt ctg gtg atg gga cat gtt ggc gat aag atc agt cgc   403
Pro Ile Gly Gly Leu Val Met Gly His Val Gly Asp Lys Ile Ser Arg
                  90                  95                 100

aaa acc gcc ctc atg gtg acg ttg atg atc atg ggt atc gcc tcc att   451
Lys Thr Ala Leu Met Val Thr Leu Met Ile Met Gly Ile Ala Ser Ile
              105                 110                 115
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<400> 313
gtggctaagc acagttactt ggccaagctg ggcggcagaa aaaccggccc agctaatact 60

tcagtttaaa attcgcttca accctgaaag attgtgacag atg agc act ctt gaa 115
Met Ser Thr Leu Glu
1 5

atc cgt aac ctg cac gca cag gtc ctg ccg tcc gat gag tcc gct gag 163
Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser Asp Glu Ser Ala Glu
10 15 20

cct aag gaa atc ctc aag ggc gtc aac ctc acc atc aac tct ggt gag 211
Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr Ile Asn Ser Gly Glu
25 30 35

atc cac gcc atc atg ggc cct aac ggt tcc ggc aag tcc act ctt gct 259
Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ala
40 45 50

tac acc ctt ggt gga cac cca cgc tac gag gta acc gca ggc gag gtc 307
Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val Thr Ala Gly Glu Val
55 60 65

ctc ctc gac ggc gag aac atc ctg gag atg gaa gtt gat gag cgt gca 355
Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu Val Asp Glu Arg Ala
70 75 80 85

cgc gct ggt ctc ttc ctg gcc atg cag tat cca act gaa atc cct ggc 403
Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro Thr Glu Ile Pro Gly
90 95 100

gtt tcc gtt gct aac ttc ctg cgt tcc gca gcg acc gca atc cgc ggc 451
Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala Thr Ala Ile Arg Gly
105 110 115

gag gct cct aag ctt cgc gag tgg gtt aag gaa gtc cgc acc gct cag 499
Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu Val Arg Thr Ala Gln
120 125 130

gaa gct ctg gca att gac cct gag ttc tcc aac cgc tca gtc aac gaa 547
Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn Arg Ser Val Asn Glu
135 140 145

ggt ttc tcc ggt ggc gag aag aag cgc cac gag gtt ctg cag ctt gat 595
Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu Val Leu Gln Leu Asp
150 155 160 165

ctg ctg aag cca aag ttc gcg atc atg gat gag acc gac tcc ggc ctt 643
Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu Thr Asp Ser Gly Leu
170 175 180

gac gtg gat gca ctg cgc att gtt tcc gag ggc atc aac tcc tac aag 691
Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly Ile Asn Ser Tyr Lys
185 190 195

cag gag acc gaa ggt ggc atc ttg atg atc acc cac tac aag cgc atc 739
Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr His Tyr Lys Arg Ile
200 205 210

ctc aac tac gtt aag cct gac ttc att cac gtt ttc gcg aat ggc cag 787
Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val Phe Ala Asn Gly Gln

```
    215                 220                 225

att gtg acc acc ggt ggc gct gag ctt gct gac aag ctc gag gct gac   835
Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp Lys Leu Glu Ala Asp
230                 235                 240                 245

ggc tac gac cag ttc atc aag taacatgtcc gatttcctca atg             879
Gly Tyr Asp Gln Phe Ile Lys
                250
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<210> 314
<211> 252
<212> PRT
<213> Corynebacterium glutamicum

<400> 314

```
Met Ser Thr Leu Glu Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser
  1               5                  10                  15

Asp Glu Ser Ala Glu Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr
             20                  25                  30

Ile Asn Ser Gly Glu Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly
         35                  40                  45

Lys Ser Thr Leu Ala Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val
     50                  55                  60

Thr Ala Gly Glu Val Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu
 65                  70                  75                  80

Val Asp Glu Arg Ala Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro
                85                  90                  95

Thr Glu Ile Pro Gly Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala
            100                 105                 110

Thr Ala Ile Arg Gly Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu
        115                 120                 125

Val Arg Thr Ala Gln Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn
    130                 135                 140

Arg Ser Val Asn Glu Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu
145                 150                 155                 160

Val Leu Gln Leu Asp Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu
                165                 170                 175

Thr Asp Ser Gly Leu Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly
            180                 185                 190

Ile Asn Ser Tyr Lys Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr
        195                 200                 205

His Tyr Lys Arg Ile Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val
    210                 215                 220

Phe Ala Asn Gly Gln Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp
225                 230                 235                 240
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Lys Leu Glu Ala Asp Gly Tyr Asp Gln Phe Ile Lys
245 250

<210> 315
<211> 1461
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1438)
<223> RXN01995

<400> 315
ccgacgcaaa ggcatgcgcc tgcgtgtctc gagtagtctc ctccccttcc tcgtccccaa 60

cctcgaccat tacggtcgcc ctctcctaaa ggagcctggc atg gat atc cgc caa 115
Met Asp Ile Arg Gln
1 5

aca att aac gac aca gca atg tcg aga tat cag tgg ttc att gta ttt 163
Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln Trp Phe Ile Val Phe
10 15 20

atc gca gtg ctg ctc aac gca ctg gac ggc ttt gat gtc ctc gcc atg 211
Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe Asp Val Leu Ala Met
25 30 35

tct ttt act gcg aat gca gtg acc gaa gaa ttt gga ctg agt ggc agc 259
Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe Gly Leu Ser Gly Ser
40 45 50

cag ctt ggt gtg ctg ctg agt tcc gcg ctg ttc ggc atg acc gct gga 307
Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe Gly Met Thr Ala Gly
55 60 65

tct ttg ctg ttc ggt ccg atc ggt gac cgt ttc ggc cgt aag aat gcc 355
Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe Gly Arg Lys Asn Ala
70 75 80 85

ctg atg atc gcg ctg ctg ttc aac gtg gtg gga ttg gta ttg tcc gcc 403
Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly Leu Val Leu Ser Ala
90 95 100

acc gcg cag tcc gca ggc cag ttg ggc gtg tgg cgt ttg atc act ggt 451
Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp Arg Leu Ile Thr Gly
105 110 115

atc ggc atc ggc gga atc ctc gcc tgc atc aca gtg gtg atc agt gag 499
Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr Val Val Ile Ser Glu
120 125 130

ttc tcc aac aac aaa aac cgc ggc atg gcc atg tcc atc tac gct gct 547
Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met Ser Ile Tyr Ala Ala
135 140 145

ggt tac ggc atc ggc gcg tcc ttg ggc ggt ttc ggc gca gcg cag ctc 595
Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe Gly Ala Ala Gln Leu
150 155 160 165

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```
atc cca aca ttt gga tgg cgc tcc gtg ttc gca gcc ggt gcg atc gca   643
Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala Ala Gly Ala Ile Ala
                170                 175                 180

act ggt atc gcc acc atc gct act ttc ttc ttc ctg cca gaa tcc gtt   691
Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe Leu Pro Glu Ser Val
            185                 190                 195

gat tgg ctg agc act cgc cgc cct gcg ggc gct cgc gac aag atc aat   739
Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala Arg Asp Lys Ile Asn
        200                 205                 210

tac att gcg cgc cgc ctg ggc aaa gtc ggt acc ttt gag ctt cca ggc   787
Tyr Ile Ala Arg Arg Leu Gly Lys Val Gly Thr Phe Glu Leu Pro Gly
    215                 220                 225

gaa caa agc ttg tcg acg aaa aaa gcc ggt ctc caa tcg tat gca gtg   835
Glu Gln Ser Leu Ser Thr Lys Lys Ala Gly Leu Gln Ser Tyr Ala Val
230                 235                 240                 245

ctc gtt aac aaa gag aac cgt gga acc agc atc aag ctg tgg gtt gcg   883
Leu Val Asn Lys Glu Asn Arg Gly Thr Ser Ile Lys Leu Trp Val Ala
                250                 255                 260

ttc ggc atc gtg atg ttc ggc ttc tac ttc gcc aac act tgg acc ccg   931
Phe Gly Ile Val Met Phe Gly Phe Tyr Phe Ala Asn Thr Trp Thr Pro
            265                 270                 275

aag ctg ctc gtg gaa acc gga atg tca gaa cag cag ggc atc atc ggt   979
Lys Leu Leu Val Glu Thr Gly Met Ser Glu Gln Gln Gly Ile Ile Gly
        280                 285                 290

ggt ttg atg ttg tcc atg ggt gga gca ttc ggc tcc ctg ctc tac ggt  1027
Gly Leu Met Leu Ser Met Gly Gly Ala Phe Gly Ser Leu Leu Tyr Gly
    295                 300                 305

ttc ctc acc acc aag ttc agc tcc cga aac aca ctg atg acc ttc atg  1075
Phe Leu Thr Thr Lys Phe Ser Ser Arg Asn Thr Leu Met Thr Phe Met
310                 315                 320                 325

gtg ctg tcc ggc ctg acg ctg atc ctg ttc att tcc tcc acc tct gtt  1123
Val Leu Ser Gly Leu Thr Leu Ile Leu Phe Ile Ser Ser Thr Ser Val
                330                 335                 340

cca tcc atc gcg ttt gcc agc ggc gtt gtc gtg ggc atg ctg atc aat  1171
Pro Ser Ile Ala Phe Ala Ser Gly Val Val Val Gly Met Leu Ile Asn
            345                 350                 355

ggt tgt gtg gct ggt ctg tac acc ctg tcc cca cag ctg tac tcc gct  1219
Gly Cys Val Ala Gly Leu Tyr Thr Leu Ser Pro Gln Leu Tyr Ser Ala
        360                 365                 370

gaa gta cgc acc act ggt gtg ggc gct gcg att ggt atg ggt cgt gtc  1267
Glu Val Arg Thr Thr Gly Val Gly Ala Ala Ile Gly Met Gly Arg Val
    375                 380                 385

ggt gcg att tcc gcg cca ctg ctg gtg ggt ggc ctg ctg gat tct ggc  1315
Gly Ala Ile Ser Ala Pro Leu Leu Val Gly Gly Leu Leu Asp Ser Gly
390                 395                 400                 405
```

```
tgg tcc cca acg cag ctg tat gtt ggt gtg gca gtg att gtt att gcc   1363
Trp Ser Pro Thr Gln Leu Tyr Val Gly Val Ala Val Ile Val Ile Ala
                410                 415                 420

ggt gca acc gca ttg att ggg atg cgc act cag gcg gta gcc gtc gaa   1411
Gly Ala Thr Ala Leu Ile Gly Met Arg Thr Gln Ala Val Ala Val Glu
            425                 430                 435

aag cag cct gaa gcc cta gcg acc aaa tagggccgcg attcctagca        1458
Lys Gln Pro Glu Ala Leu Ala Thr Lys
        440                 445

tgc                                                              1461
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<210> 316
<211> 446
<212> PRT
<213> Corynebacterium glutamicum

<400> 316

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Met Asp Ile Arg Gln Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln
  1               5                  10                  15

Trp Phe Ile Val Phe Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe
             20                  25                  30

Asp Val Leu Ala Met Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe
         35                  40                  45

Gly Leu Ser Gly Ser Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe
     50                  55                  60

Gly Met Thr Ala Gly Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe
 65                  70                  75                  80

Gly Arg Lys Asn Ala Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly
                85                  90                  95

Leu Val Leu Ser Ala Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp
            100                 105                 110

Arg Leu Ile Thr Gly Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr
        115                 120                 125

Val Val Ile Ser Glu Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met
    130                 135                 140

Ser Ile Tyr Ala Ala Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe
145                 150                 155                 160

Gly Ala Ala Gln Leu Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala
                165                 170                 175

Ala Gly Ala Ile Ala Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe
            180                 185                 190

Leu Pro Glu Ser Val Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala
        195                 200                 205

Arg Asp Lys Ile Asn Tyr Ile Ala Arg Arg Leu Gly Lys Val Gly Thr
```

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```
    210                 215                 220

Phe Glu Leu Pro Gly Glu Gln Ser Leu Ser Thr Lys Lys Ala Gly Leu
225                 230                 235                 240

Gln Ser Tyr Ala Val Leu Val Asn Lys Glu Asn Arg Gly Thr Ser Ile
                245                 250                 255

Lys Leu Trp Val Ala Phe Gly Ile Val Met Phe Gly Phe Tyr Phe Ala
            260                 265                 270

Asn Thr Trp Thr Pro Lys Leu Leu Val Glu Thr Gly Met Ser Glu Gln
        275                 280                 285

Gln Gly Ile Ile Gly Gly Leu Met Leu Ser Met Gly Gly Ala Phe Gly
    290                 295                 300

Ser Leu Leu Tyr Gly Phe Leu Thr Thr Lys Phe Ser Ser Arg Asn Thr
305                 310                 315                 320

Leu Met Thr Phe Met Val Leu Ser Gly Leu Thr Leu Ile Leu Phe Ile
                325                 330                 335

Ser Ser Thr Ser Val Pro Ser Ile Ala Phe Ala Ser Gly Val Val Val
            340                 345                 350

Gly Met Leu Ile Asn Gly Cys Val Ala Gly Leu Tyr Thr Leu Ser Pro
        355                 360                 365

Gln Leu Tyr Ser Ala Glu Val Arg Thr Thr Gly Val Gly Ala Ala Ile
    370                 375                 380

Gly Met Gly Arg Val Gly Ala Ile Ser Ala Pro Leu Leu Val Gly Gly
385                 390                 395                 400

Leu Leu Asp Ser Gly Trp Ser Pro Thr Gln Leu Tyr Val Gly Val Ala
                405                 410                 415

Val Ile Val Ile Ala Gly Ala Thr Ala Leu Ile Gly Met Arg Thr Gln
            420                 425                 430

Ala Val Ala Val Glu Lys Gln Pro Glu Ala Leu Ala Thr Lys
        435                 440                 445
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<210> 317
<211> 754
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(754)
<223> FRXA01995

<400> 317
ccgacgcaaa ggcatgcgcc tgcgtgtctc gagtagtctc ctccccttcc tcgtccccaa 60

cctcgaccat tacggtcgcc ctctcctaaa ggagcctggc atg gat atc cgc caa 115
                                    Met Asp Ile Arg Gln
                                      1               5

```
aca att aac gac aca gca atg tcg aga tat cag tgg ttc att gta ttt   163
Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln Trp Phe Ile Val Phe
                 10                  15                  20

atc gca gtg ctg ctc aac gca ctg gac ggc ttt gat gtc ctc gcc atg   211
Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe Asp Val Leu Ala Met
             25                  30                  35

tct ttt act gcg aat gca gtg acc gaa gaa ttt gga ctg agt ggc agc   259
Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe Gly Leu Ser Gly Ser
         40                  45                  50

cag ctt ggt gtg ctg ctg agt tcc gcg ctg ttc ggc atg acc gct gga   307
Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe Gly Met Thr Ala Gly
     55                  60                  65

tct ttg ctg ttc ggt ccg atc ggt gac cgt ttc ggc cgt aag aat gcc   355
Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe Gly Arg Lys Asn Ala
 70                  75                  80                  85

ctg atg atc gcg ctg ctg ttc aac gtg gtg gga ttg gta ttg tcc gcc   403
Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly Leu Val Leu Ser Ala
                 90                  95                 100

acc gcg cag tcc gca ggc cag ttg ggc gtg tgg cgt ttg atc act ggt   451
Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp Arg Leu Ile Thr Gly
             105                 110                 115

atc ggc atc ggc gga atc ctc gcc tgc atc aca gtg gtg atc agt gag   499
Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr Val Val Ile Ser Glu
         120                 125                 130

ttc tcc aac aac aaa aac cgc ggc atg gcc atg tcc atc tac gct gct   547
Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met Ser Ile Tyr Ala Ala
     135                 140                 145

ggt tac ggc atc ggc gcg tcc ttg ggc ggt ttc ggc gca gcg cag ctc   595
Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe Gly Ala Ala Gln Leu
150                 155                 160                 165

atc cca aca ttt gga tgg cgc tcc gtg ttc gca gcc ggt gcg atc gca   643
Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala Ala Gly Ala Ile Ala
                170                 175                 180

act ggt atc gcc acc atc gct act ttc ttc ttc ctg cca gaa tcc gtt   691
Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe Leu Pro Glu Ser Val
            185                 190                 195

gat tgg ctg agc act cgc cgc cct gcg ggc gct cgc gac aag atc aat   739
Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala Arg Asp Lys Ile Asn
        200                 205                 210

tac att gcg cgc cgc                                             754
Tyr Ile Ala Arg Arg
    215
```

<210> 318
<211> 218
<212> PRT

<213> Corynebacterium glutamicum

<400> 318

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Met Asp Ile Arg Gln Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln
  1               5                  10                  15

Trp Phe Ile Val Phe Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe
             20                  25                  30

Asp Val Leu Ala Met Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe
         35                  40                  45

Gly Leu Ser Gly Ser Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe
     50                  55                  60

Gly Met Thr Ala Gly Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe
 65                  70                  75                  80

Gly Arg Lys Asn Ala Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly
                 85                  90                  95

Leu Val Leu Ser Ala Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp
            100                 105                 110

Arg Leu Ile Thr Gly Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr
        115                 120                 125

Val Val Ile Ser Glu Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met
    130                 135                 140

Ser Ile Tyr Ala Ala Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe
145                 150                 155                 160

Gly Ala Ala Gln Leu Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala
                165                 170                 175

Ala Gly Ala Ile Ala Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe
            180                 185                 190

Leu Pro Glu Ser Val Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala
        195                 200                 205

Arg Asp Lys Ile Asn Tyr Ile Ala Arg Arg
    210                 215
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<210> 319
<211> 1227
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1204)
<223> RXA01188

<400> 319

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aaacagttag aagcacctaa acagtttttc cgataactgt tgtcattttg tgaccgcctg 60

gctttgtagt tttccctccg gtgtccaaga tgaatatgac atg atg aat ggc gtg   115
                                            Met Met Asn Gly Val
```

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```
                                                    1               5

gta cag cct cag gaa cat ctc gat gca acg ttg att gct gca gac ttc   163
Val Gln Pro Gln Glu His Leu Asp Ala Thr Leu Ile Ala Ala Asp Phe
                10                  15                  20

cac ggc aac ccc gaa aac tct ggt gac cgc aaa gag cgc ctg aat ttt   211
His Gly Asn Pro Glu Asn Ser Gly Asp Arg Lys Glu Arg Leu Asn Phe
            25                  30                  35

caa ggt tgg aag tat gcc ctt aat cgc acg gtc agg gat gtt ttt cca   259
Gln Gly Trp Lys Tyr Ala Leu Asn Arg Thr Val Arg Asp Val Phe Pro
        40                  45                  50

gat ggc ctg ctc gat ttg gcg gcc ttg ttg acg ttc ttt tcc att ctg   307
Asp Gly Leu Leu Asp Leu Ala Ala Leu Leu Thr Phe Phe Ser Ile Leu
    55                  60                  65

tcg atc gcc cct gca gtg ctg ctg ggc tat tcg gtg atc acg att ttt   355
Ser Ile Ala Pro Ala Val Leu Leu Gly Tyr Ser Val Ile Thr Ile Phe
70                  75                  80                  85

ctg gcc agt gac tcc acc gaa atc ctc aac ctt gtc cgc gat gag gta   403
Leu Ala Ser Asp Ser Thr Glu Ile Leu Asn Leu Val Arg Asp Glu Val
                90                  95                  100

aat cag tac gtt ccg gaa gat caa tcc cat gtt gtc aac ggc gtg att   451
Asn Gln Tyr Val Pro Glu Asp Gln Ser His Val Val Asn Gly Val Ile
            105                 110                 115

gat tcg atc gca ggc tcg gca gct gca ggt cag gtc ggt gtc gcg gtc   499
Asp Ser Ile Ala Gly Ser Ala Ala Ala Gly Gln Val Gly Val Ala Val
        120                 125                 130

ggt gtg atc acg gca ttg tgg aca tct tcg gca tat gtg cgc gct ttt   547
Gly Val Ile Thr Ala Leu Trp Thr Ser Ser Ala Tyr Val Arg Ala Phe
    135                 140                 145

tcc aga tgt gcc aac gct gtt tat ggc cga agc gaa ggc cgc aca ttg   595
Ser Arg Cys Ala Asn Ala Val Tyr Gly Arg Ser Glu Gly Arg Thr Leu
150                 155                 160                 165

atc aaa cgc tgg gca atg ctg ctt ttc ctc aac ctt gct ttg ctg ctt   643
Ile Lys Arg Trp Ala Met Leu Leu Phe Leu Asn Leu Ala Leu Leu Leu
                170                 175                 180

gga atc atc atc att ttg gtc tcc tgg gtg ctc aac gag acc ttg gtg   691
Gly Ile Ile Ile Ile Leu Val Ser Trp Val Leu Asn Glu Thr Leu Val
            185                 190                 195

atg gga att ttc gcc ccc atc gcg gaa cca ctt cat ctc acg aat gtg   739
Met Gly Ile Phe Ala Pro Ile Ala Glu Pro Leu His Leu Thr Asn Val
        200                 205                 210

ctc agc ttc ctc acg gac cgg ttc atg ccg atc tgg atc tgg gtg cgg   787
Leu Ser Phe Leu Thr Asp Arg Phe Met Pro Ile Trp Ile Trp Val Arg
    215                 220                 225

ttc cca gtg att gtg ggg gtg ctc atc atg ttc gtg gcc acg ctg tat   835
Phe Pro Val Ile Val Gly Val Leu Ile Met Phe Val Ala Thr Leu Tyr
230                 235                 240                 245
```

```
tac tgg gcc ccg aac gcc cgc ccg tgg aag ttt cgc tgg ctc agc ctc   883
Tyr Trp Ala Pro Asn Ala Arg Pro Trp Lys Phe Arg Trp Leu Ser Leu
                250                 255                 260

gga tca ttc ttg gcg atc gtt ggc atc ctg ctc gca ggc gtg ggc ttg   931
Gly Ser Phe Leu Ala Ile Val Gly Ile Leu Leu Ala Gly Val Gly Leu
            265                 270                 275

aat ttc tac ttc acg ctg ttc gcc gct ttt agt tcc tac ggc gcg gtg   979
Asn Phe Tyr Phe Thr Leu Phe Ala Ala Phe Ser Ser Tyr Gly Ala Val
        280                 285                 290

ggt tcg ctg ctc gcg gtt ttt att gcg ctg tgg gtg ttc aac att tgc   1027
Gly Ser Leu Leu Ala Val Phe Ile Ala Leu Trp Val Phe Asn Ile Cys
    295                 300                 305

tta atc atc ggc ctg aaa atc gac gtg gag atc agc cgc gcc aag caa   1075
Leu Ile Ile Gly Leu Lys Ile Asp Val Glu Ile Ser Arg Ala Lys Gln
310                 315                 320                 325

ctg cag gca gga atg ccg gcg gag gat tac agt tta gtg cca cca cgc   1123
Leu Gln Ala Gly Met Pro Ala Glu Asp Tyr Ser Leu Val Pro Pro Arg
                330                 335                 340

tct atc gag aag gtg gcg aaa atg aag cag cgc cag cag cgc ttg atg   1171
Ser Ile Glu Lys Val Ala Lys Met Lys Gln Arg Gln Gln Arg Leu Met
            345                 350                 355

gat cag gct gcg gcg atc cgg gag gaa agc aat taaaaaattg cttatcgacg 1224
Asp Gln Ala Ala Ala Ile Arg Glu Glu Ser Asn
        360                 365

tcc                                                               1227
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<210> 320
<211> 368
<212> PRT
<213> Corynebacterium glutamicum

<400> 320

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Met Met Asn Gly Val Val Gln Pro Gln Glu His Leu Asp Ala Thr Leu
  1               5                  10                  15

Ile Ala Ala Asp Phe His Gly Asn Pro Glu Asn Ser Gly Asp Arg Lys
             20                  25                  30

Glu Arg Leu Asn Phe Gln Gly Trp Lys Tyr Ala Leu Asn Arg Thr Val
         35                  40                  45

Arg Asp Val Phe Pro Asp Gly Leu Leu Asp Leu Ala Ala Leu Leu Thr
     50                  55                  60

Phe Phe Ser Ile Leu Ser Ile Ala Pro Ala Val Leu Leu Gly Tyr Ser
 65                  70                  75                  80

Val Ile Thr Ile Phe Leu Ala Ser Asp Ser Thr Glu Ile Leu Asn Leu
                 85                  90                  95

Val Arg Asp Glu Val Asn Gln Tyr Val Pro Glu Asp Gln Ser His Val
```

```
                100                 105                 110

Val Asn Gly Val Ile Asp Ser Ile Ala Gly Ser Ala Ala Ala Gly Gln
        115                 120                 125

Val Gly Val Ala Val Gly Val Ile Thr Ala Leu Trp Thr Ser Ser Ala
    130                 135                 140

Tyr Val Arg Ala Phe Ser Arg Cys Ala Asn Ala Val Tyr Gly Arg Ser
145                 150                 155                 160

Glu Gly Arg Thr Leu Ile Lys Arg Trp Ala Met Leu Leu Phe Leu Asn
                165                 170                 175

Leu Ala Leu Leu Leu Gly Ile Ile Ile Ile Leu Val Ser Trp Val Leu
            180                 185                 190

Asn Glu Thr Leu Val Met Gly Ile Phe Ala Pro Ile Ala Glu Pro Leu
        195                 200                 205

His Leu Thr Asn Val Leu Ser Phe Leu Thr Asp Arg Phe Met Pro Ile
    210                 215                 220

Trp Ile Trp Val Arg Phe Pro Val Ile Val Gly Val Leu Ile Met Phe
225                 230                 235                 240

Val Ala Thr Leu Tyr Tyr Trp Ala Pro Asn Ala Arg Pro Trp Lys Phe
                245                 250                 255

Arg Trp Leu Ser Leu Gly Ser Phe Leu Ala Ile Val Gly Ile Leu Leu
            260                 265                 270

Ala Gly Val Gly Leu Asn Phe Tyr Phe Thr Leu Phe Ala Ala Phe Ser
        275                 280                 285

Ser Tyr Gly Ala Val Gly Ser Leu Leu Ala Val Phe Ile Ala Leu Trp
    290                 295                 300

Val Phe Asn Ile Cys Leu Ile Ile Gly Leu Lys Ile Asp Val Glu Ile
305                 310                 315                 320

Ser Arg Ala Lys Gln Leu Gln Ala Gly Met Pro Ala Glu Asp Tyr Ser
                325                 330                 335

Leu Val Pro Pro Arg Ser Ile Glu Lys Val Ala Lys Met Lys Gln Arg
            340                 345                 350

Gln Gln Arg Leu Met Asp Gln Ala Ala Ala Ile Arg Glu Glu Ser Asn
        355                 360                 365
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<210> 321
<211> 717
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(694)
<223> RXA01972

<400> 321
acgcgttgct ggatatcacc ctggccgtcg atgacaacgc cgaatgcatc gacgccggat 60

gcgccgtacc tgggtgtgtc actggacagg agagtgcgta gtg gca acc ggt cta 115
Val Ala Thr Gly Leu
1 5

ctg tcg gcg att ggt ctg ttt atc gcc acc aat atc gac gac atc atc 163
Leu Ser Ala Ile Gly Leu Phe Ile Ala Thr Asn Ile Asp Asp Ile Ile
10 15 20

gtg ctc tcg ctg ttt ttt gcc cgc ggg gcg ggg caa aaa ggg acc acg 211
Val Leu Ser Leu Phe Phe Ala Arg Gly Ala Gly Gln Lys Gly Thr Thr
25 30 35

ctt cgg att ctg gct ggt cag tac ctc ggc ttc atg ggc atc ctc gcg 259
Leu Arg Ile Leu Ala Gly Gln Tyr Leu Gly Phe Met Gly Ile Leu Ala
40 45 50

gcc gca gtc ctg gtc acg ctg ggg gca gga gca ttc cta cct gct gag 307
Ala Ala Val Leu Val Thr Leu Gly Ala Gly Ala Phe Leu Pro Ala Glu
55 60 65

gcg atc ccg tac ttc gga cta att ccc ctg gcc ctg gga cta tgg gcg 355
Ala Ile Pro Tyr Phe Gly Leu Ile Pro Leu Ala Leu Gly Leu Trp Ala
70 75 80 85

gcc tgg cag gcc tgg cga agc gat gat gac gac gat gat gat gcg gag 403
Ala Trp Gln Ala Trp Arg Ser Asp Asp Asp Asp Asp Asp Asp Ala Glu
90 95 100

atc gcc ggg aaa aag gtg ggt gtg ctg acc gtc gcc ggt gtg acg ttt 451
Ile Ala Gly Lys Lys Val Gly Val Leu Thr Val Ala Gly Val Thr Phe
105 110 115

gcc aac ggt ggc gac aat atc ggc gtc tac gtc ccg gtc ttc ctc aac 499
Ala Asn Gly Gly Asp Asn Ile Gly Val Tyr Val Pro Val Phe Leu Asn
120 125 130

gtg gac act gcc gcc gtc atc atc tac tgc atc gtt ttc ctc gtc ctg 547
Val Asp Thr Ala Ala Val Ile Ile Tyr Cys Ile Val Phe Leu Val Leu
135 140 145

gtg gca ggc ctg gtc ctg ctg gca aag ttc gtg gcc acc cgc ccg ccc 595
Val Ala Gly Leu Val Leu Leu Ala Lys Phe Val Ala Thr Arg Pro Pro
150 155 160 165

atc gca gaa gtc ctt gag cgc tgg gag cac gtg ctg ttc ccg atc gtc 643
Ile Ala Glu Val Leu Glu Arg Trp Glu His Val Leu Phe Pro Ile Val
170 175 180

ctg atc ggc ctg ggc atc ttc atc ctc gtc agc ggc ggc gcc ttc ggc 691
Leu Ile Gly Leu Gly Ile Phe Ile Leu Val Ser Gly Gly Ala Phe Gly
185 190 195

ctc taataagccc atcccgagcg ccc 717
Leu

<210> 322
<211> 198
<212> PRT
<213> Corynebacterium glutamicum

<400> 322
Val Ala Thr Gly Leu Leu Ser Ala Ile Gly Leu Phe Ile Ala Thr Asn
1 5 10 15

Ile Asp Asp Ile Ile Val Leu Ser Leu Phe Phe Ala Arg Gly Ala Gly
20 25 30

Gln Lys Gly Thr Thr Leu Arg Ile Leu Ala Gly Gln Tyr Leu Gly Phe
35 40 45

Met Gly Ile Leu Ala Ala Ala Val Leu Val Thr Leu Gly Ala Gly Ala
50 55 60

Phe Leu Pro Ala Glu Ala Ile Pro Tyr Phe Gly Leu Ile Pro Leu Ala
65 70 75 80

Leu Gly Leu Trp Ala Ala Trp Gln Ala Trp Arg Ser Asp Asp Asp Asp
85 90 95

Asp Asp Asp Ala Glu Ile Ala Gly Lys Lys Val Gly Val Leu Thr Val
100 105 110

Ala Gly Val Thr Phe Ala Asn Gly Gly Asp Asn Ile Gly Val Tyr Val
115 120 125

Pro Val Phe Leu Asn Val Asp Thr Ala Ala Val Ile Ile Tyr Cys Ile
130 135 140

Val Phe Leu Val Leu Val Ala Gly Leu Val Leu Leu Ala Lys Phe Val
145 150 155 160

Ala Thr Arg Pro Pro Ile Ala Glu Val Leu Glu Arg Trp Glu His Val
165 170 175

Leu Phe Pro Ile Val Leu Ile Gly Leu Gly Ile Phe Ile Leu Val Ser
180 185 190

Gly Gly Ala Phe Gly Leu
195

<210> 323
<211> 978
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(955)
<223> RXA00311

<400> 323
cggacagatc ggcatttggg cgaccgtgct gttgatgatc gcccgcatcg catagggatt 60

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ctctgcagtc gcagaagctg caggtgcatc cacactgacc atg gaa cat tct cct   115
                                            Met Glu His Ser Pro
                                              1               5

gaa ggc aag cgt gga ttc ttc acc tca tcg gtg atg gcg ggt tgc tca   163
Glu Gly Lys Arg Gly Phe Phe Thr Ser Ser Val Met Ala Gly Cys Ser
                  10                  15                  20

gtt gga aac gtc ctg gct ggc ttg gta ttt atc ccg ttc ttg atg ctg   211
Val Gly Asn Val Leu Ala Gly Leu Val Phe Ile Pro Phe Leu Met Leu
              25                  30                  35

ccg gaa gaa cac ctc atg tca tgg ggc tgg cgc gta cct ttc ctg ctt   259
Pro Glu Glu His Leu Met Ser Trp Gly Trp Arg Val Pro Phe Leu Leu
          40                  45                  50

tcc gca ctg gtt tta gtt gtc gca tac ttc gtg cgc acc cga ctg gag   307
Ser Ala Leu Val Leu Val Val Ala Tyr Phe Val Arg Thr Arg Leu Glu
      55                  60                  65

gaa gca tca act gag aag gcc gaa gag gac gca ggc gct ccg gct ttg   355
Glu Ala Ser Thr Glu Lys Ala Glu Glu Asp Ala Gly Ala Pro Ala Leu
 70                  75                  80                  85

gct gtg ctg cgc acc cag ggc att gat gtc gca cga gtt ttc ctg atc   403
Ala Val Leu Arg Thr Gln Gly Ile Asp Val Ala Arg Val Phe Leu Ile
                  90                  95                 100

acc ttc ttc gcc gtt gtt cag acc act ttc aac gtt tac gca ctg gca   451
Thr Phe Phe Ala Val Val Gln Thr Thr Phe Asn Val Tyr Ala Leu Ala
              105                 110                 115

tac gcc gcc aac gaa atc ggc atc gat cgt tcc ttc atg gtg atg gtg   499
Tyr Ala Ala Asn Glu Ile Gly Ile Asp Arg Ser Phe Met Val Met Val
          120                 125                 130

aac acc atc gcg ctg ggg ctt tcc atc gga acg att cct ttg gcc gcg   547
Asn Thr Ile Ala Leu Gly Leu Ser Ile Gly Thr Ile Pro Leu Ala Ala
      135                 140                 145

tgg gtc tct gac cgc att ggc cgc aag cca gtc ttg ctg ttc ggg gcc   595
Trp Val Ser Asp Arg Ile Gly Arg Lys Pro Val Leu Leu Phe Gly Ala
150                 155                 160                 165

atc acc tgt gca atc acc acc tac ttc tac ttc cag gca atc tct gaa   643
Ile Thr Cys Ala Ile Thr Thr Tyr Phe Tyr Phe Gln Ala Ile Ser Glu
                  170                 175                 180

gct gac ctt gtg ctg atc ttc gca ctg tgc ttg gtc aac caa ggt ttg   691
Ala Asp Leu Val Leu Ile Phe Ala Leu Cys Leu Val Asn Gln Gly Leu
              185                 190                 195

ttc tac tcc tgc tgg aac ggc gtg tgg acc att ttc ttc cca gaa atg   739
Phe Tyr Ser Cys Trp Asn Gly Val Trp Thr Ile Phe Phe Pro Glu Met
          200                 205                 210

ttc gca tct tcc gtg cgc tac acc ggc atg gct atg ggc aac cag ctc   787
Phe Ala Ser Ser Val Arg Tyr Thr Gly Met Ala Met Gly Asn Gln Leu
      215                 220                 225

ggt ctg atc atc gtt ggt ttc gca cca acc atc gcc acc gcc ctg tac   835
```

```
Gly Leu Ile Ile Val Gly Phe Ala Pro Thr Ile Ala Thr Ala Leu Tyr
230                 235                 240                 245

gca tgg aac ggt tgg gaa gct gtt gcg gga ttc atc atc ggc gca atc   883
Ala Trp Asn Gly Trp Glu Ala Val Ala Gly Phe Ile Ile Gly Ala Ile
                250                 255                 260

gca ctg tct gcc gca gtt att ttg acc acc aag gaa acc gcc ttc acc   931
Ala Leu Ser Ala Ala Val Ile Leu Thr Thr Lys Glu Thr Ala Phe Thr
            265                 270                 275

aag ctt gaa gat cta ggg aag aaa taatgtctga caagatctgg aaa         978
Lys Leu Glu Asp Leu Gly Lys Lys
        280                 285
```

<210> 324
<211> 285
<212> PRT
<213> Corynebacterium glutamicum

<400> 324

```
Met Glu His Ser Pro Glu Gly Lys Arg Gly Phe Phe Thr Ser Ser Val
  1               5                  10                  15

Met Ala Gly Cys Ser Val Gly Asn Val Leu Ala Gly Leu Val Phe Ile
            20                  25                  30

Pro Phe Leu Met Leu Pro Glu Glu His Leu Met Ser Trp Gly Trp Arg
        35                  40                  45

Val Pro Phe Leu Leu Ser Ala Leu Val Leu Val Val Ala Tyr Phe Val
    50                  55                  60

Arg Thr Arg Leu Glu Glu Ala Ser Thr Glu Lys Ala Glu Glu Asp Ala
65                  70                  75                  80

Gly Ala Pro Ala Leu Ala Val Leu Arg Thr Gln Gly Ile Asp Val Ala
                85                  90                  95

Arg Val Phe Leu Ile Thr Phe Phe Ala Val Val Gln Thr Thr Phe Asn
            100                 105                 110

Val Tyr Ala Leu Ala Tyr Ala Ala Asn Glu Ile Gly Ile Asp Arg Ser
        115                 120                 125

Phe Met Val Met Val Asn Thr Ile Ala Leu Gly Leu Ser Ile Gly Thr
    130                 135                 140

Ile Pro Leu Ala Ala Trp Val Ser Asp Arg Ile Gly Arg Lys Pro Val
145                 150                 155                 160

Leu Leu Phe Gly Ala Ile Thr Cys Ala Ile Thr Thr Tyr Phe Tyr Phe
                165                 170                 175

Gln Ala Ile Ser Glu Ala Asp Leu Val Leu Ile Phe Ala Leu Cys Leu
            180                 185                 190

Val Asn Gln Gly Leu Phe Tyr Ser Cys Trp Asn Gly Val Trp Thr Ile
        195                 200                 205
```

```
tcc atc gga ctt ctg ccc acc tac gga cag atc ggc att tgg gcg acc   499
Ser Ile Gly Leu Leu Pro Thr Tyr Gly Gln Ile Gly Ile Trp Ala Thr
        120                 125                 130

gtg ctg ttg atg atc gcc cgc atc gca tagggattct ctgcagtcgc         546
Val Leu Leu Met Ile Ala Arg Ile Ala
    135                 140

aga                                                               549
```

<210> 326
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 326

```
Met Glu Thr Val Arg Thr Ala Thr Ala Ala Pro Glu Thr Ala Ser Leu
  1               5                  10                  15

Lys Leu Arg Glu Ala Glu Ser Pro Ala Lys Ser Pro Lys Lys Ala Ala
             20                  25                  30

Leu Ala Ser Leu Leu Gly Ser Thr Leu Glu Tyr Tyr Asp Phe Val Ile
         35                  40                  45

Tyr Gly Thr Ala Ser Ala Leu Leu Phe Asn His Leu Phe Phe Pro Gln
     50                  55                  60

Gly Asp Pro Val Val Ala Thr Ile Gly Ser Leu Ala Ser Phe Gly Val
 65                  70                  75                  80

Ala Tyr Ile Ala Arg Pro Ile Gly Gly Leu Val Met Gly His Val Gly
                85                  90                  95

Asp Lys Ile Ser Arg Lys Thr Ala Leu Met Val Thr Leu Met Ile Met
            100                 105                 110

Gly Ile Ala Ser Ile Ser Ile Gly Leu Leu Pro Thr Tyr Gly Gln Ile
        115                 120                 125

Gly Ile Trp Ala Thr Val Leu Leu Met Ile Ala Arg Ile Ala
    130                 135                 140
```

<210> 327
<211> 888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> RXN01411

<400> 327

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cttatcgacg tccccatccc cctcgccaat gcttcggcga ggggttctat ttattgtgtg 60

tgctagcctt ttcgcaatcg ttcagcccgc cccgacgtca atg ttg gga gtg ggc   115
                                              Met Leu Gly Val Gly
                                                1               5
```

```
tgg cgc att cca ttc ctg atg gcc gtg cca cta ggg ctt atc ggc tgg   163
Trp Arg Ile Pro Phe Leu Met Ala Val Pro Leu Gly Leu Ile Gly Trp
                10                  15                  20

tgg atc cgc acc ggt gcc cag gaa aat gta cgc ccc gca tcc gaa cgc   211
Trp Ile Arg Thr Gly Ala Gln Glu Asn Val Arg Pro Ala Ser Glu Arg
            25                  30                  35

ccc gaa gct cct att aag cag gca ttg cgt act gag tgg aag atg atg   259
Pro Glu Ala Pro Ile Lys Gln Ala Leu Arg Thr Glu Trp Lys Met Met
        40                  45                  50

ttg cgg gta ggt ggc ttt atc tct tgc acc ggt ctg agc ttc tac att   307
Leu Arg Val Gly Gly Phe Ile Ser Cys Thr Gly Leu Ser Phe Tyr Ile
    55                  60                  65

ttc acc acg tac atg acc act ttc ctg cgc agc acc gtc gga ctg gag   355
Phe Thr Thr Tyr Met Thr Thr Phe Leu Arg Ser Thr Val Gly Leu Glu
70                  75                  80                  85

ggc acg tta gtg ctg gct gga aac atc atc gct ctc agc atg gca gca   403
Gly Thr Leu Val Leu Ala Gly Asn Ile Ile Ala Leu Ser Met Ala Ala
                90                  95                  100

att gtg gcc cca ttt gtt ggc cgc gca att gat aaa ttc ccc cgc cgg   451
Ile Val Ala Pro Phe Val Gly Arg Ala Ile Asp Lys Phe Pro Arg Arg
            105                 110                 115

aac atc atg gct ttc gct acc tta agc aca gta att atg gcg atc ccg   499
Asn Ile Met Ala Phe Ala Thr Leu Ser Thr Val Ile Met Ala Ile Pro
        120                 125                 130

gcc tac atc att gca ggt caa ggt act ttg act gct tct ttg att gcg   547
Ala Tyr Ile Ile Ala Gly Gln Gly Thr Leu Thr Ala Ser Leu Ile Ala
    135                 140                 145

cag gta atg ctt gga atc ggc gcg gtt acc gct aac tgc gtt acc tca   595
Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala Asn Cys Val Thr Ser
150                 155                 160                 165

gta atg atg gcc gag gtc ttc caa gag gtc acc cgc ggt act tcc gcc   643
Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly Thr Ser Ala
                170                 175                 180

ggc att acc tac aac gtc act tac gca atc ttc ggc ggc tcg gct cca   691
Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly Ser Ala Pro
            185                 190                 195

ttt atc tcc acc gca ttg gtc tcc tgg acc ggc agc ccg ctg gcc cct   739
Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro Leu Ala Pro
        200                 205                 210

gcg gta tac atg atc atc att gcg ctc ttc gcc ttc acc gcg tcc cgc   787
Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr Ala Ser Arg
    215                 220                 225

ttc att cct gaa acc tcc cca gtt ttt gtc acc gca acc ccg gcc att   835
Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr Pro Ala Ile
230                 235                 240                 245
```

aag gca cca aag gtg ctg gtc aac ccg ggt taaaccacgc ttttcgacga 885
Lys Ala Pro Lys Val Leu Val Asn Pro Gly
250 255

aaa 888

<210> 328
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 328

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Met | Leu | Gly | Val | Gly | Trp | Arg | Ile | Pro | Phe | Leu | Met | Ala | Val | Pro | Leu |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Gly | Leu | Ile | Gly | Trp | Trp | Ile | Arg | Thr | Gly | Ala | Gln | Glu | Asn | Val | Arg |
| | | 20 | | | | | 25 | | | | | 30 | | | |
| Pro | Ala | Ser | Glu | Arg | Pro | Glu | Ala | Pro | Ile | Lys | Gln | Ala | Leu | Arg | Thr |
| | 35 | | | | | 40 | | | | | 45 | | | | |
| Glu | Trp | Lys | Met | Met | Leu | Arg | Val | Gly | Gly | Phe | Ile | Ser | Cys | Thr | Gly |
| 50 | | | | | 55 | | | | | 60 | | | | | |
| Leu | Ser | Phe | Tyr | Ile | Phe | Thr | Thr | Tyr | Met | Thr | Thr | Phe | Leu | Arg | Ser |
| 65 | | | | 70 | | | | | 75 | | | | | | 80 |
| Thr | Val | Gly | Leu | Glu | Gly | Thr | Leu | Val | Leu | Ala | Gly | Asn | Ile | Ile | Ala |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Leu | Ser | Met | Ala | Ala | Ile | Val | Ala | Pro | Phe | Val | Gly | Arg | Ala | Ile | Asp |
| | | 100 | | | | | 105 | | | | | 110 | | | |
| Lys | Phe | Pro | Arg | Arg | Asn | Ile | Met | Ala | Phe | Ala | Thr | Leu | Ser | Thr | Val |
| | 115 | | | | | 120 | | | | | 125 | | | | |
| Ile | Met | Ala | Ile | Pro | Ala | Tyr | Ile | Ile | Ala | Gly | Gln | Gly | Thr | Leu | Thr |
| 130 | | | | | 135 | | | | | 140 | | | | | |
| Ala | Ser | Leu | Ile | Ala | Gln | Val | Met | Leu | Gly | Ile | Gly | Ala | Val | Thr | Ala |
| 145 | | | | 150 | | | | | 155 | | | | | | 160 |
| Asn | Cys | Val | Thr | Ser | Val | Met | Met | Ala | Glu | Val | Phe | Gln | Glu | Val | Thr |
| | | | 165 | | | | | 170 | | | | | 175 | | |
| Arg | Gly | Thr | Ser | Ala | Gly | Ile | Thr | Tyr | Asn | Val | Thr | Tyr | Ala | Ile | Phe |
| | | 180 | | | | | 185 | | | | | 190 | | | |
| Gly | Gly | Ser | Ala | Pro | Phe | Ile | Ser | Thr | Ala | Leu | Val | Ser | Trp | Thr | Gly |
| | 195 | | | | | 200 | | | | | 205 | | | | |
| Ser | Pro | Leu | Ala | Pro | Ala | Val | Tyr | Met | Ile | Ile | Ile | Ala | Leu | Phe | Ala |
| 210 | | | | | 215 | | | | | 220 | | | | | |
| Phe | Thr | Ala | Ser | Arg | Phe | Ile | Pro | Glu | Thr | Ser | Pro | Val | Phe | Val | Thr |
| 225 | | | | 230 | | | | | 235 | | | | | | 240 |
| Ala | Thr | Pro | Ala | Ile | Lys | Ala | Pro | Lys | Val | Leu | Val | Asn | Pro | Gly | |
| | | | 245 | | | | | 250 | | | | | 255 | | |

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<210> 329
<211> 350
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(327)
<223> FRXA01411

<400> 329
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ttc att gcg cag gta atg ctt gga atc ggc gcg gtt acc gct aac tgc   48
Phe Ile Ala Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala Asn Cys
  1               5                  10                  15

gtt acc tca gta atg atg gcc gag gtc ttc caa gag gtc acc cgc ggt   96
Val Thr Ser Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly
             20                  25                  30

act tcc gcc ggc att acc tac aac gtc act tac gca atc ttc ggc ggc   144
Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly
         35                  40                  45

tcg gct cca ttt atc tcc acc gca ttg gtc tcc tgg acc ggc agc ccg   192
Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro
     50                  55                  60

ctg gcc cct gcg gta tac atg atc atc att gcg ctc ttc gcc ttc acc   240
Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr
 65                  70                  75                  80

gcg tcc cgc ttc att cct gaa acc tcc cca gtt ttt gtc acc gca acc   288
Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr
                 85                  90                  95

ccg gcc att aag gca cca aag gtg ctg gtc aac ccg ggt taaaccacgc   337
Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly
            100                 105

ttttcgacga aaa                                                  350
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<210> 330
<211> 109
<212> PRT
<213> Corynebacterium glutamicum

<400> 330
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Phe Ile Ala Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala Asn Cys
  1               5                  10                  15

Val Thr Ser Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly
             20                  25                  30

Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly
         35                  40                  45

Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro
     50                  55                  60
```

```
Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr
 65                  70                  75                  80

Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr
                 85                  90                  95

Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly
            100                 105
```

<210> 331
<211> 1422
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1399)
<223> RXA01900

<400> 331

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aaaggtgaca cgccttacat tcttgtggtc tgaccatgag gttgggccaa tcggtttcag 60

cccgtttact cccgccgtcc gtttcagaga agaggtcacc atg aca acc gca gta   115
                                            Met Thr Thr Ala Val
                                              1               5

gat caa aac tca ccg ccc aag cag caa ctc aac aag cgc gtc ctg ctg   163
Asp Gln Asn Ser Pro Pro Lys Gln Gln Leu Asn Lys Arg Val Leu Leu
                 10                  15                  20

ggc agc ttg agt ggc agc gtt atc gaa tgg ttc gac ttc ctg gtt tac   211
Gly Ser Leu Ser Gly Ser Val Ile Glu Trp Phe Asp Phe Leu Val Tyr
            25                  30                  35

gga acc gtc gcc gcg ctg gtc ttc aac aag atg tac ttc ccc agc ggc   259
Gly Thr Val Ala Ala Leu Val Phe Asn Lys Met Tyr Phe Pro Ser Gly
        40                  45                  50

aac gag ttc ctc tcc aca atc ctg gcg tac gca tcc ttc tcc ctg acc   307
Asn Glu Phe Leu Ser Thr Ile Leu Ala Tyr Ala Ser Phe Ser Leu Thr
    55                  60                  65

ttc ttc ttc cgc ccc att ggt ggc gtc atc ttc gcc cac atc ggc gac   355
Phe Phe Phe Arg Pro Ile Gly Gly Val Ile Phe Ala His Ile Gly Asp
70                  75                  80                  85

cgc att ggg cgt aag aag acc ctg ttc atc acc ttg atg ctc atg ggt   403
Arg Ile Gly Arg Lys Lys Thr Leu Phe Ile Thr Leu Met Leu Met Gly
                90                  95                 100

ggc ggc acc gtc gcc att ggt ttg ctg ccc gac tac aac gcc atc ggc   451
Gly Gly Thr Val Ala Ile Gly Leu Leu Pro Asp Tyr Asn Ala Ile Gly
            105                 110                 115

att tgg gca cca atc ctt ctg atg ttc ctc cgc att ttg cag ggc atc   499
Ile Trp Ala Pro Ile Leu Leu Met Phe Leu Arg Ile Leu Gln Gly Ile
        120                 125                 130

gga att ggc ggc gaa tgg ggt ggc gca ctg ctc ctg gca tac gaa tac   547
Gly Ile Gly Gly Glu Trp Gly Gly Ala Leu Leu Leu Ala Tyr Glu Tyr
```

```
    135                 140                 145

gct cca aag aag cag cgt ggg ctc tac ggc gca gtt cct caa atg ggc   595
Ala Pro Lys Lys Gln Arg Gly Leu Tyr Gly Ala Val Pro Gln Met Gly
150                 155                 160                 165

att tcc ctg ggc atg ctg ctt gca gct ggc gtg atc tct ctg ctc acc   643
Ile Ser Leu Gly Met Leu Leu Ala Ala Gly Val Ile Ser Leu Leu Thr
                170                 175                 180

ctc atg ccg gaa gat cag ttc ctc acc tgg ggc tgg cgc atc cca ttc   691
Leu Met Pro Glu Asp Gln Phe Leu Thr Trp Gly Trp Arg Ile Pro Phe
            185                 190                 195

gtc gga tcc atc ctc cta gtg ttc atc ggc ctg ttc atc cga aac ggc   739
Val Gly Ser Ile Leu Leu Val Phe Ile Gly Leu Phe Ile Arg Asn Gly
        200                 205                 210

ctt gat gaa acc ccc gag ttc aag cgt atc cgc gat tcc ggc cag cag   787
Leu Asp Glu Thr Pro Glu Phe Lys Arg Ile Arg Asp Ser Gly Gln Gln
    215                 220                 225

gta aag atg cct ctg aag gaa gtt ctg acc aag tac tgg cca gcc gtt   835
Val Lys Met Pro Leu Lys Glu Val Leu Thr Lys Tyr Trp Pro Ala Val
230                 235                 240                 245

ctg gtc tcc atc ggc gca aaa gct gcc gag acc ggc ccc ttc tac atc   883
Leu Val Ser Ile Gly Ala Lys Ala Ala Glu Thr Gly Pro Phe Tyr Ile
                250                 255                 260

ttc ggc acc tac atc gtt gct tac gca acc aac ttc ctg aac atc cgc   931
Phe Gly Thr Tyr Ile Val Ala Tyr Ala Thr Asn Phe Leu Asn Ile Arg
            265                 270                 275

gac aac att gtc ctt ctg gca gtt gct tgc gcc gcc ctc gtt gcc acc   979
Asp Asn Ile Val Leu Leu Ala Val Ala Cys Ala Ala Leu Val Ala Thr
        280                 285                 290

atc tgg atg cca ctg ttc gga tcc ttc tcc gac cgc gtc aac cgt gca  1027
Ile Trp Met Pro Leu Phe Gly Ser Phe Ser Asp Arg Val Asn Arg Ala
    295                 300                 305

gtg ctc tac agg atc tgt gca tcc gca acc atc gtg ctg att gtc cct  1075
Val Leu Tyr Arg Ile Cys Ala Ser Ala Thr Ile Val Leu Ile Val Pro
310                 315                 320                 325

tac tac ttg gtc ctc aac acc ggc gaa att tgg gca ctg ttt atc act  1123
Tyr Tyr Leu Val Leu Asn Thr Gly Glu Ile Trp Ala Leu Phe Ile Thr
                330                 335                 340

acc gtg att ggc ttc ggc atc ctc tgg ggt agc gtc aac gca atc ctc  1171
Thr Val Ile Gly Phe Gly Ile Leu Trp Gly Ser Val Asn Ala Ile Leu
            345                 350                 355

gga acc gtc atc gca gaa aac ttc gca cct gag gtc cgc tac acc ggc  1219
Gly Thr Val Ile Ala Glu Asn Phe Ala Pro Glu Val Arg Tyr Thr Gly
        360                 365                 370

gct acc ctg ggt tac caa gtc gga gca gca ctc ttc ggc ggt acc gca  1267
Ala Thr Leu Gly Tyr Gln Val Gly Ala Ala Leu Phe Gly Gly Thr Ala
    375                 380                 385
```

```
ccc att atc gca gca tgg ctg ttc gaa atc tcc ggc gga caa tgg tgg   1315
Pro Ile Ile Ala Ala Trp Leu Phe Glu Ile Ser Gly Gly Gln Trp Trp
390                 395                 400                 405

cca atc gcc gtc tac gtc gct gca tgt tgc ctt ctc tct gtg atc gcc   1363
Pro Ile Ala Val Tyr Val Ala Ala Cys Cys Leu Leu Ser Val Ile Ala
                410                 415                 420

tcg ttc ttc atc caa cgc gtc gcg cac caa gag aac taaaatctaa        1409
Ser Phe Phe Ile Gln Arg Val Ala His Gln Glu Asn
            425                 430

gtaaaacccc tcc                                                   1422


<210> 332
<211> 433
<212> PRT
<213> Corynebacterium glutamicum

<400> 332
Met Thr Thr Ala Val Asp Gln Asn Ser Pro Pro Lys Gln Gln Leu Asn
  1               5                  10                  15

Lys Arg Val Leu Leu Gly Ser Leu Ser Gly Ser Val Ile Glu Trp Phe
             20                  25                  30

Asp Phe Leu Val Tyr Gly Thr Val Ala Ala Leu Val Phe Asn Lys Met
         35                  40                  45

Tyr Phe Pro Ser Gly Asn Glu Phe Leu Ser Thr Ile Leu Ala Tyr Ala
     50                  55                  60

Ser Phe Ser Leu Thr Phe Phe Phe Arg Pro Ile Gly Gly Val Ile Phe
 65                  70                  75                  80

Ala His Ile Gly Asp Arg Ile Gly Arg Lys Lys Thr Leu Phe Ile Thr
                 85                  90                  95

Leu Met Leu Met Gly Gly Gly Thr Val Ala Ile Gly Leu Leu Pro Asp
            100                 105                 110

Tyr Asn Ala Ile Gly Ile Trp Ala Pro Ile Leu Leu Met Phe Leu Arg
        115                 120                 125

Ile Leu Gln Gly Ile Gly Ile Gly Gly Glu Trp Gly Gly Ala Leu Leu
    130                 135                 140

Leu Ala Tyr Glu Tyr Ala Pro Lys Lys Gln Arg Gly Leu Tyr Gly Ala
145                 150                 155                 160

Val Pro Gln Met Gly Ile Ser Leu Gly Met Leu Leu Ala Ala Gly Val
                165                 170                 175

Ile Ser Leu Leu Thr Leu Met Pro Glu Asp Gln Phe Leu Thr Trp Gly
            180                 185                 190

Trp Arg Ile Pro Phe Val Gly Ser Ile Leu Leu Val Phe Ile Gly Leu
        195                 200                 205
```

```
Phe Ile Arg Asn Gly Leu Asp Glu Thr Pro Glu Phe Lys Arg Ile Arg
    210                 215                 220

Asp Ser Gly Gln Gln Val Lys Met Pro Leu Lys Glu Val Leu Thr Lys
225                 230                 235                 240

Tyr Trp Pro Ala Val Leu Val Ser Ile Gly Ala Lys Ala Ala Glu Thr
                245                 250                 255

Gly Pro Phe Tyr Ile Phe Gly Thr Tyr Ile Val Ala Tyr Ala Thr Asn
            260                 265                 270

Phe Leu Asn Ile Arg Asp Asn Ile Val Leu Leu Ala Val Ala Cys Ala
        275                 280                 285

Ala Leu Val Ala Thr Ile Trp Met Pro Leu Phe Gly Ser Phe Ser Asp
    290                 295                 300

Arg Val Asn Arg Ala Val Leu Tyr Arg Ile Cys Ala Ser Ala Thr Ile
305                 310                 315                 320

Val Leu Ile Val Pro Tyr Tyr Leu Val Leu Asn Thr Gly Glu Ile Trp
                325                 330                 335

Ala Leu Phe Ile Thr Thr Val Ile Gly Phe Gly Ile Leu Trp Gly Ser
            340                 345                 350

Val Asn Ala Ile Leu Gly Thr Val Ile Ala Glu Asn Phe Ala Pro Glu
        355                 360                 365

Val Arg Tyr Thr Gly Ala Thr Leu Gly Tyr Gln Val Gly Ala Ala Leu
    370                 375                 380

Phe Gly Gly Thr Ala Pro Ile Ile Ala Ala Trp Leu Phe Glu Ile Ser
385                 390                 395                 400

Gly Gly Gln Trp Trp Pro Ile Ala Val Tyr Val Ala Ala Cys Cys Leu
                405                 410                 415

Leu Ser Val Ile Ala Ser Phe Phe Ile Gln Arg Val Ala His Gln Glu
            420                 425                 430

Asn
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Document ID: 20040224.0001

<210> 333
<211> 1524
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1501)
<223> RXA02507

<400> 333
attacccaca atttcaatcg gtttatacaa ccagcctcta actggcaaca ggactgcaga 60

cagaaactgt tgctggaacc ttcgatgaac aggatcgaca atg agc gaa caa ctt 115
                                    Met Ser Glu Gln Leu

```
                                                    1               5

cag ggt gta act cac tcc gaa tca act ccg ggc aag acg ccc aag cga   163
Gln Gly Val Thr His Ser Glu Ser Thr Pro Gly Lys Thr Pro Lys Arg
                10                  15                  20

gca gca cta tcc agc tgg atc ggc tca gct ctc gaa tac tac gac ttc   211
Ala Ala Leu Ser Ser Trp Ile Gly Ser Ala Leu Glu Tyr Tyr Asp Phe
            25                  30                  35

gct gtt tac gga acc gct gca gcg ctg gtt ctt aac cac ctc ttc ttc   259
Ala Val Tyr Gly Thr Ala Ala Ala Leu Val Leu Asn His Leu Phe Phe
        40                  45                  50

cca gct gat act tca cca ggc atc gca att ttg gct gcg atg ggt acc   307
Pro Ala Asp Thr Ser Pro Gly Ile Ala Ile Leu Ala Ala Met Gly Thr
    55                  60                  65

gtg ggt gtt gct tat gtg gtt cgc cct ctt ggt gcg ctg atc atg ggt   355
Val Gly Val Ala Tyr Val Val Arg Pro Leu Gly Ala Leu Ile Met Gly
70                  75                  80                  85

cca tta ggt gac cgt tac gga cgt aaa ttt gtc ctc atg ctg tgc ctc   403
Pro Leu Gly Asp Arg Tyr Gly Arg Lys Phe Val Leu Met Leu Cys Leu
                90                  95                  100

ttc ctg att gga gca tcc act ttc gca gtt ggc tgc ttg cca aca ttt   451
Phe Leu Ile Gly Ala Ser Thr Phe Ala Val Gly Cys Leu Pro Thr Phe
            105                 110                 115

gat cag gtc ggt tac ttg gct ccg gca ctg ttg gtg ctg tgc cgt gtg   499
Asp Gln Val Gly Tyr Leu Ala Pro Ala Leu Leu Val Leu Cys Arg Val
        120                 125                 130

atc cag gga ctg tct gca tcc ggt gag cag tcc agt gcg att tcc gtt   547
Ile Gln Gly Leu Ser Ala Ser Gly Glu Gln Ser Ser Ala Ile Ser Val
    135                 140                 145

tct ttg gag cac gcc gat gag cgt cac cgc gca ttt act gct agc tgg   595
Ser Leu Glu His Ala Asp Glu Arg His Arg Ala Phe Thr Ala Ser Trp
150                 155                 160                 165

act ctt cac gga acc cag ttc ggt acc ttg ctg gca acc gga gta ttt   643
Thr Leu His Gly Thr Gln Phe Gly Thr Leu Leu Ala Thr Gly Val Phe
                170                 175                 180

atc cca ttc acc ttg ttc ctg agt gaa gat gct cta atg tca tgg ggt   691
Ile Pro Phe Thr Leu Phe Leu Ser Glu Asp Ala Leu Met Ser Trp Gly
            185                 190                 195

tgg cgc gtt ccg ttc tgg ctg tcc gct gct gtt gtt ttg gtt gct ttc   739
Trp Arg Val Pro Phe Trp Leu Ser Ala Ala Val Val Leu Val Ala Phe
        200                 205                 210

ctc atc cgt cgt gga ctg gaa gag cca cca gca ttc cgt gaa aac aag   787
Leu Ile Arg Arg Gly Leu Glu Glu Pro Pro Ala Phe Arg Glu Asn Lys
    215                 220                 225

gaa gca gtt gca ggc gca gca tct cca ctg gcg atg acc ttg cgt tac   835
Glu Ala Val Ala Gly Ala Ala Ser Pro Leu Ala Met Thr Leu Arg Tyr
230                 235                 240                 245
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```
cac aag gcg gcg gtt gct cgc gtt gct att gct gcg atg atc aac tcc   883
His Lys Ala Ala Val Ala Arg Val Ala Ile Ala Ala Met Ile Asn Ser
                250                 255                 260

gtg aac att gtg ttt act gtg tgg gca ctg tcg ttc gcc acc aac att   931
Val Asn Ile Val Phe Thr Val Trp Ala Leu Ser Phe Ala Thr Asn Ile
            265                 270                 275

gtt ggc ctg gat cgt tca act gtt ttg ctg gtt cca gtt gtt gcg aac   979
Val Gly Leu Asp Arg Ser Thr Val Leu Leu Val Pro Val Val Ala Asn
        280                 285                 290

ttg gtt gca ctg att gcg att cct ttg tcc ggc atg ctg gct gac cgc   1027
Leu Val Ala Leu Ile Ala Ile Pro Leu Ser Gly Met Leu Ala Asp Arg
    295                 300                 305

att ggt cgc cga cca gtg ttc atc atg ggt gcc att ggt ggt ggc ctg   1075
Ile Gly Arg Arg Pro Val Phe Ile Met Gly Ala Ile Gly Gly Gly Leu
310                 315                 320                 325

gcc atg aac ggt tac ctg gga gct atc tac tcc ggc aat tgg acc atg   1123
Ala Met Asn Gly Tyr Leu Gly Ala Ile Tyr Ser Gly Asn Trp Thr Met
                330                 335                 340

atc ttc ttc atg ggc gtg ttg atg tct ggt ctg ctg tac tcc atg ggt   1171
Ile Phe Phe Met Gly Val Leu Met Ser Gly Leu Leu Tyr Ser Met Gly
            345                 350                 355

aat gcc gtg tgg cca gcg ttc tac gca gaa atg ttc cca acc tct gtg   1219
Asn Ala Val Trp Pro Ala Phe Tyr Ala Glu Met Phe Pro Thr Ser Val
        360                 365                 370

cgt gtc acc ggc ttg gct ctt gga act cag att ggt ttc gca gtc tct   1267
Arg Val Thr Gly Leu Ala Leu Gly Thr Gln Ile Gly Phe Ala Val Ser
    375                 380                 385

ggt ggt ttc gtc cca gtt atc gca tcc gcg ctt gct ggt gat cag ggt   1315
Gly Gly Phe Val Pro Val Ile Ala Ser Ala Leu Ala Gly Asp Gln Gly
390                 395                 400                 405

gac cag tgg atg aag gtg tcc atc ttc gtt ggt gtt gtt tgt gtg att   1363
Asp Gln Trp Met Lys Val Ser Ile Phe Val Gly Val Val Cys Val Ile
                410                 415                 420

tct gca ctg gtt gcc atg acc gct aag gaa acc aag gct ctg act ctg   1411
Ser Ala Leu Val Ala Met Thr Ala Lys Glu Thr Lys Ala Leu Thr Leu
            425                 430                 435

gat gag atc gat gct ctg cac act gct ggt ggt gag gcc gca gac ctg   1459
Asp Glu Ile Asp Ala Leu His Thr Ala Gly Gly Glu Ala Ala Asp Leu
        440                 445                 450

gca gcc gca agc aaa gcc tcc gag gcc caa ctc gcg gct cag           1501
Ala Ala Ala Ser Lys Ala Ser Glu Ala Gln Leu Ala Ala Gln
    455                 460                 465

taaaaccaaa aggaatcttt gac                                        1524
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<210> 334

<211> 467
<212> PRT
<213> Corynebacterium glutamicum

<400> 334

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Met Ser Glu Gln Leu Gln Gly Val Thr His Ser Glu Ser Thr Pro Gly
  1               5                  10                  15

Lys Thr Pro Lys Arg Ala Ala Leu Ser Ser Trp Ile Gly Ser Ala Leu
             20                  25                  30

Glu Tyr Tyr Asp Phe Ala Val Tyr Gly Thr Ala Ala Ala Leu Val Leu
         35                  40                  45

Asn His Leu Phe Phe Pro Ala Asp Thr Ser Pro Gly Ile Ala Ile Leu
     50                  55                  60

Ala Ala Met Gly Thr Val Gly Val Ala Tyr Val Val Arg Pro Leu Gly
 65                  70                  75                  80

Ala Leu Ile Met Gly Pro Leu Gly Asp Arg Tyr Gly Arg Lys Phe Val
                 85                  90                  95

Leu Met Leu Cys Leu Phe Leu Ile Gly Ala Ser Thr Phe Ala Val Gly
            100                 105                 110

Cys Leu Pro Thr Phe Asp Gln Val Gly Tyr Leu Ala Pro Ala Leu Leu
        115                 120                 125

Val Leu Cys Arg Val Ile Gln Gly Leu Ser Ala Ser Gly Glu Gln Ser
    130                 135                 140

Ser Ala Ile Ser Val Ser Leu Glu His Ala Asp Glu Arg His Arg Ala
145                 150                 155                 160

Phe Thr Ala Ser Trp Thr Leu His Gly Thr Gln Phe Gly Thr Leu Leu
                165                 170                 175

Ala Thr Gly Val Phe Ile Pro Phe Thr Leu Phe Leu Ser Glu Asp Ala
            180                 185                 190

Leu Met Ser Trp Gly Trp Arg Val Pro Phe Trp Leu Ser Ala Ala Val
        195                 200                 205

Val Leu Val Ala Phe Leu Ile Arg Arg Gly Leu Glu Glu Pro Pro Ala
    210                 215                 220

Phe Arg Glu Asn Lys Glu Ala Val Ala Gly Ala Ala Ser Pro Leu Ala
225                 230                 235                 240

Met Thr Leu Arg Tyr His Lys Ala Ala Val Ala Arg Val Ala Ile Ala
                245                 250                 255

Ala Met Ile Asn Ser Val Asn Ile Val Phe Thr Val Trp Ala Leu Ser
            260                 265                 270

Phe Ala Thr Asn Ile Val Gly Leu Asp Arg Ser Thr Val Leu Leu Val
        275                 280                 285

Pro Val Val Ala Asn Leu Val Ala Leu Ile Ala Ile Pro Leu Ser Gly
    290                 295                 300
```

Met Leu Ala Asp Arg Ile Gly Arg Arg Pro Val Phe Ile Met Gly Ala
305 310 315 320

Ile Gly Gly Gly Leu Ala Met Asn Gly Tyr Leu Gly Ala Ile Tyr Ser
325 330 335

Gly Asn Trp Thr Met Ile Phe Phe Met Gly Val Leu Met Ser Gly Leu
340 345 350

Leu Tyr Ser Met Gly Asn Ala Val Trp Pro Ala Phe Tyr Ala Glu Met
355 360 365

Phe Pro Thr Ser Val Arg Val Thr Gly Leu Ala Leu Gly Thr Gln Ile
370 375 380

Gly Phe Ala Val Ser Gly Gly Phe Val Pro Val Ile Ala Ser Ala Leu
385 390 395 400

Ala Gly Asp Gln Gly Asp Gln Trp Met Lys Val Ser Ile Phe Val Gly
405 410 415

Val Val Cys Val Ile Ser Ala Leu Val Ala Met Thr Ala Lys Glu Thr
420 425 430

Lys Ala Leu Thr Leu Asp Glu Ile Asp Ala Leu His Thr Ala Gly Gly
435 440 445

Glu Ala Ala Asp Leu Ala Ala Ala Ser Lys Ala Ser Glu Ala Gln Leu
450 455 460

Ala Ala Gln
465

<210> 335
<211> 955
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (21)..(932)
<223> RXA00445

<400> 335
ggtgcaaaaa aggactaacc atg gcg gat ctg agc att gaa cac gta tca agg 53
Met Ala Asp Leu Ser Ile Glu His Val Ser Arg
1 5 10

ttt ttc ggc gat gcc atc gcc ttg aac gat gtg tca ttg acc gtc ccc 101
Phe Phe Gly Asp Ala Ile Ala Leu Asn Asp Val Ser Leu Thr Val Pro
15 20 25

tca ggc tcc atc acc gcc atc atc ggg ccg tcc ggg agc ggt aaa acc 149
Ser Gly Ser Ile Thr Ala Ile Ile Gly Pro Ser Gly Ser Gly Lys Thr
30 35 40

acg tta ctg cgt ttg ctg gca ggc ctt gat tca ccc gat gaa ggc acc 197
Thr Leu Leu Arg Leu Leu Ala Gly Leu Asp Ser Pro Asp Glu Gly Thr
45 50 55

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gtg agc att ggg aat aag atc gcc aag ctg ggt gac act gcg ctg tgt   245
Val Ser Ile Gly Asn Lys Ile Ala Lys Leu Gly Asp Thr Ala Leu Cys
 60                  65                  70                  75

ttc cag gat tcg cct ttg tat ccg cac ctt aat gtg tgg gaa aac gtg   293
Phe Gln Asp Ser Pro Leu Tyr Pro His Leu Asn Val Trp Glu Asn Val
                 80                  85                  90

gca ttt ccg ctc aag ctc aaa gcc acc aat act gca gat gag gtg gtg   341
Ala Phe Pro Leu Lys Leu Lys Ala Thr Asn Thr Ala Asp Glu Val Val
             95                 100                 105

aaa aag cgg gtg agt gat gtt ttg gaa atg ctc gaa att gct ccc ctc   389
Lys Lys Arg Val Ser Asp Val Leu Glu Met Leu Glu Ile Ala Pro Leu
        110                 115                 120

gcc cgc cgg aaa att acc gaa ctc tcc ggc ggg caa aaa cag cgc gtc   437
Ala Arg Arg Lys Ile Thr Glu Leu Ser Gly Gly Gln Lys Gln Arg Val
    125                 130                 135

ggc att gct cga gca ctg gtc aga gac gta gag gtt tac ctt ttc gac   485
Gly Ile Ala Arg Ala Leu Val Arg Asp Val Glu Val Tyr Leu Phe Asp
140                 145                 150                 155

gaa ccg atg gcc cac ctc gac caa gcc tta gcc cgc gat att gtg gcc   533
Glu Pro Met Ala His Leu Asp Gln Ala Leu Ala Arg Asp Ile Val Ala
                160                 165                 170

gat ctg cgc aaa att caa caa tcg ttg gga ctg acg ttt gta tac gtc   581
Asp Leu Arg Lys Ile Gln Gln Ser Leu Gly Leu Thr Phe Val Tyr Val
            175                 180                 185

acc cac agc aaa tcc gag gca ttc gcg ctc gcc gac caa att gtc gtg   629
Thr His Ser Lys Ser Glu Ala Phe Ala Leu Ala Asp Gln Ile Val Val
        190                 195                 200

ctg gta gat ggc caa gtc gcg cag gtt ggt gag gcg gag gag ctc gtc   677
Leu Val Asp Gly Gln Val Ala Gln Val Gly Glu Ala Glu Glu Leu Val
    205                 210                 215

gaa aag cca aaa acc cta gaa ata gcc gag ttc ctc tcc ccc acc gag   725
Glu Lys Pro Lys Thr Leu Glu Ile Ala Glu Phe Leu Ser Pro Thr Glu
220                 225                 230                 235

ctc aat gtg cgc cgg cgt ggg gac gcc gtg gag gca tgg cga ccc gaa   773
Leu Asn Val Arg Arg Arg Gly Asp Ala Val Glu Ala Trp Arg Pro Glu
                240                 245                 250

gac acc cag ctc gcc cgc ggt ggc act gcg acc gtg gaa gcc gtg acg   821
Asp Thr Gln Leu Ala Arg Gly Gly Thr Ala Thr Val Glu Ala Val Thr
            255                 260                 265

tat ttg ggc cgc gag tgg ctt gta caa acc acc gag ggg cac gcc gtg   869
Tyr Leu Gly Arg Glu Trp Leu Val Gln Thr Thr Glu Gly His Ala Val
        270                 275                 280

tcg gag gaa aaa ttc gac gtc ggc gaa agc gtc acg cta acc cag aag   917
Ser Glu Glu Lys Phe Asp Val Gly Glu Ser Val Thr Leu Thr Gln Lys
    285                 290                 295
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aag gtg ttt agt ttc tagccgcctg caaaaggagg gag 955
Lys Val Phe Ser Phe
300

<210> 336
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 336
Met Ala Asp Leu Ser Ile Glu His Val Ser Arg Phe Phe Gly Asp Ala
1 5 10 15

Ile Ala Leu Asn Asp Val Ser Leu Thr Val Pro Ser Gly Ser Ile Thr
20 25 30

Ala Ile Ile Gly Pro Ser Gly Ser Gly Lys Thr Thr Leu Leu Arg Leu
35 40 45

Leu Ala Gly Leu Asp Ser Pro Asp Glu Gly Thr Val Ser Ile Gly Asn
50 55 60

Lys Ile Ala Lys Leu Gly Asp Thr Ala Leu Cys Phe Gln Asp Ser Pro
65 70 75 80

Leu Tyr Pro His Leu Asn Val Trp Glu Asn Val Ala Phe Pro Leu Lys
85 90 95

Leu Lys Ala Thr Asn Thr Ala Asp Glu Val Val Lys Lys Arg Val Ser
100 105 110

Asp Val Leu Glu Met Leu Glu Ile Ala Pro Leu Ala Arg Arg Lys Ile
115 120 125

Thr Glu Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala
130 135 140

Leu Val Arg Asp Val Glu Val Tyr Leu Phe Asp Glu Pro Met Ala His
145 150 155 160

Leu Asp Gln Ala Leu Ala Arg Asp Ile Val Ala Asp Leu Arg Lys Ile
165 170 175

Gln Gln Ser Leu Gly Leu Thr Phe Val Tyr Val Thr His Ser Lys Ser
180 185 190

Glu Ala Phe Ala Leu Ala Asp Gln Ile Val Val Leu Val Asp Gly Gln
195 200 205

Val Ala Gln Val Gly Glu Ala Glu Glu Leu Val Glu Lys Pro Lys Thr
210 215 220

Leu Glu Ile Ala Glu Phe Leu Ser Pro Thr Glu Leu Asn Val Arg Arg
225 230 235 240

Arg Gly Asp Ala Val Glu Ala Trp Arg Pro Glu Asp Thr Gln Leu Ala
245 250 255

Arg Gly Gly Thr Ala Thr Val Glu Ala Val Thr Tyr Leu Gly Arg Glu
260 265 270

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Trp Leu Val Gln Thr Thr Glu Gly His Ala Val Ser Glu Glu Lys Phe
        275                 280                 285

Asp Val Gly Glu Ser Val Thr Leu Thr Gln Lys Lys Val Phe Ser Phe
    290                 295                 300
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<210> 337
<211> 491
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(468)
<223> RXA02353

<400> 337

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atg gca ctg ctg atc ctc gcc ggt ctg caa atg atc ccg aag gaa acc   48
Met Ala Leu Leu Ile Leu Ala Gly Leu Gln Met Ile Pro Lys Glu Thr
  1               5                  10                  15

tac gaa gca gcc cgc gtc gat ggc gca acc gcg tgg cag caa ttc acc   96
Tyr Glu Ala Ala Arg Val Asp Gly Ala Thr Ala Trp Gln Gln Phe Thr
             20                  25                  30

aag atc acc ctc ccg ctg gtg cgc cca gct ttg atg gtg gca gta ctc  144
Lys Ile Thr Leu Pro Leu Val Arg Pro Ala Leu Met Val Ala Val Leu
         35                  40                  45

ttc cgc acc ctc gat gcg cta cgc atg tat gac ctc ccc gtc atc atg  192
Phe Arg Thr Leu Asp Ala Leu Arg Met Tyr Asp Leu Pro Val Ile Met
     50                  55                  60

atc tcc agc tcc tcc aac tcc ccc acc gct gtt atc tcc cag ctg gtt  240
Ile Ser Ser Ser Ser Asn Ser Pro Thr Ala Val Ile Ser Gln Leu Val
 65                  70                  75                  80

gtg gaa gac atg cgc caa aac aac ttc aac tcc gct tcc gcc ctt tcc  288
Val Glu Asp Met Arg Gln Asn Asn Phe Asn Ser Ala Ser Ala Leu Ser
                 85                  90                  95

aca ctg atc ttc ctg ctg atc ttc ttc gtg gcg ttc atc atg atc cga  336
Thr Leu Ile Phe Leu Leu Ile Phe Phe Val Ala Phe Ile Met Ile Arg
            100                 105                 110

ttc ctc ggc gca gat gtt tcg ggc caa cgc gga ata aag aaa aag aaa  384
Phe Leu Gly Ala Asp Val Ser Gly Gln Arg Gly Ile Lys Lys Lys Lys
        115                 120                 125

ctg ggc gga acc aag gat gag aaa ccc acc gct aag gat gct gtt gta  432
Leu Gly Gly Thr Lys Asp Glu Lys Pro Thr Ala Lys Asp Ala Val Val
    130                 135                 140

aag gcc gat tct gct gtg aag gaa gcc gct aag cca tgactaaacg       478
Lys Ala Asp Ser Ala Val Lys Glu Ala Ala Lys Pro
145                 150                 155
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aacaaaagga ctc 491

<210> 338
<211> 156
<212> PRT
<213> Corynebacterium glutamicum

<400> 338

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Met | Ala | Leu | Leu | Ile | Leu | Ala | Gly | Leu | Gln | Met | Ile | Pro | Lys | Glu | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Tyr | Glu | Ala | Ala | Arg | Val | Asp | Gly | Ala | Thr | Ala | Trp | Gln | Gln | Phe | Thr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Ile | Thr | Leu | Pro | Leu | Val | Arg | Pro | Ala | Leu | Met | Val | Ala | Val | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Phe | Arg | Thr | Leu | Asp | Ala | Leu | Arg | Met | Tyr | Asp | Leu | Pro | Val | Ile | Met |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ile | Ser | Ser | Ser | Ser | Asn | Ser | Pro | Thr | Ala | Val | Ile | Ser | Gln | Leu | Val |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Val | Glu | Asp | Met | Arg | Gln | Asn | Asn | Phe | Asn | Ser | Ala | Ser | Ala | Leu | Ser |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Thr | Leu | Ile | Phe | Leu | Leu | Ile | Phe | Phe | Val | Ala | Phe | Ile | Met | Ile | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Phe | Leu | Gly | Ala | Asp | Val | Ser | Gly | Gln | Arg | Gly | Ile | Lys | Lys | Lys | Lys |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Gly | Gly | Thr | Lys | Asp | Glu | Lys | Pro | Thr | Ala | Lys | Asp | Ala | Val | Val |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Lys | Ala | Asp | Ser | Ala | Val | Lys | Glu | Ala | Ala | Lys | Pro | | | | |
| 145 | | | | | 150 | | | | | 155 | | | | | |

<210> 339
<211> 921
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(898)
<223> RXA01297

<400> 339
tcctgttgct gctgattatc actgttatcc aggttcgata catggataag gagaacaagc 60

agaaatgatc tcgactgata gaaacgtttt ggtcaaaatc atg ggc tat gtc ggc 115
Met Gly Tyr Val Gly
1 5

atg gtt ctt gcc atc ttg ttc att ggc ctt ccg ctg gta ttt att gtg 163
Met Val Leu Ala Ile Leu Phe Ile Gly Leu Pro Leu Val Phe Ile Val
10 15 20

```
ctg act agc ttc aag cag cag tca gag att tac acc cag ccg gtc acg   211
Leu Thr Ser Phe Lys Gln Gln Ser Glu Ile Tyr Thr Gln Pro Val Thr
            25                  30                  35

tgg ttc cct tcg gaa ttt aat ttc gat aac tat gca aat gtt ttc gag   259
Trp Phe Pro Ser Glu Phe Asn Phe Asp Asn Tyr Ala Asn Val Phe Glu
        40                  45                  50

cgg gtt ccg ttc ctg aac tac ttc cgc aac tcg atc atc atc acg gtt   307
Arg Val Pro Phe Leu Asn Tyr Phe Arg Asn Ser Ile Ile Ile Thr Val
    55                  60                  65

att ttg tgt ctg gtg aag att atc ttg ggt gtg atc tct gca tat gcg   355
Ile Leu Cys Leu Val Lys Ile Ile Leu Gly Val Ile Ser Ala Tyr Ala
70                  75                  80                  85

ttg tcg att ttg cgc ttc ccg ggt cga aac ctt gtg ttc ttg ctg gtt   403
Leu Ser Ile Leu Arg Phe Pro Gly Arg Asn Leu Val Phe Leu Leu Val
                90                  95                  100

atc tcc gcg ctg atg gtg cct tcc gaa gtg act gtt att tcc aac tat   451
Ile Ser Ala Leu Met Val Pro Ser Glu Val Thr Val Ile Ser Asn Tyr
            105                 110                 115

gcg ttg gtc agt cag ctt ggt tgg cgc gat acc tac cag ggc atc atc   499
Ala Leu Val Ser Gln Leu Gly Trp Arg Asp Thr Tyr Gln Gly Ile Ile
        120                 125                 130

gtt ccg cta gcg ggt att gct ttc gga acg ttc ctc atg cgt aac cac   547
Val Pro Leu Ala Gly Ile Ala Phe Gly Thr Phe Leu Met Arg Asn His
    135                 140                 145

ttc atg tct att cct tct gag ctc att gaa gct gcg cga atg gat cac   595
Phe Met Ser Ile Pro Ser Glu Leu Ile Glu Ala Ala Arg Met Asp His
150                 155                 160                 165

tgt gga cac ttc agg ttg ctc tgg aag gtt ttg ctt cca atc tct atg   643
Cys Gly His Phe Arg Leu Leu Trp Lys Val Leu Leu Pro Ile Ser Met
                170                 175                 180

cct acg ttg gtg gcg ttc tcc atg atc acc gtg gtg aat gaa tgg aac   691
Pro Thr Leu Val Ala Phe Ser Met Ile Thr Val Val Asn Glu Trp Asn
            185                 190                 195

caa tac ctg tgg cct ttc ctg atg gca gaa acc gat aat tca gca act   739
Gln Tyr Leu Trp Pro Phe Leu Met Ala Glu Thr Asp Asn Ser Ala Thr
        200                 205                 210

ctg ccc att ggt ttg acc atg ctt caa aac aat gag ggt gtc tcc aac   787
Leu Pro Ile Gly Leu Thr Met Leu Gln Asn Asn Glu Gly Val Ser Asn
    215                 220                 225

tgg gga cct gtc atg gcc gca acg atc atg acc atg ttg cct gtg ctt   835
Trp Gly Pro Val Met Ala Ala Thr Ile Met Thr Met Leu Pro Val Leu
230                 235                 240                 245

gtg atg ttc ttg gca ctg cag gag tac atg atc aag gga ctt atc tcc   883
Val Met Phe Leu Ala Leu Gln Glu Tyr Met Ile Lys Gly Leu Ile Ser
                250                 255                 260
```

ggc gcc gtc aag ggc taaaaacttc tcgctaaaaa ctt 921
Gly Ala Val Lys Gly
265

<210> 340
<211> 266
<212> PRT
<213> Corynebacterium glutamicum

<400> 340
Met Gly Tyr Val Gly Met Val Leu Ala Ile Leu Phe Ile Gly Leu Pro
1 5 10 15

Leu Val Phe Ile Val Leu Thr Ser Phe Lys Gln Gln Ser Glu Ile Tyr
20 25 30

Thr Gln Pro Val Thr Trp Phe Pro Ser Glu Phe Asn Phe Asp Asn Tyr
35 40 45

Ala Asn Val Phe Glu Arg Val Pro Phe Leu Asn Tyr Phe Arg Asn Ser
50 55 60

Ile Ile Ile Thr Val Ile Leu Cys Leu Val Lys Ile Ile Leu Gly Val
65 70 75 80

Ile Ser Ala Tyr Ala Leu Ser Ile Leu Arg Phe Pro Gly Arg Asn Leu
85 90 95

Val Phe Leu Leu Val Ile Ser Ala Leu Met Val Pro Ser Glu Val Thr
100 105 110

Val Ile Ser Asn Tyr Ala Leu Val Ser Gln Leu Gly Trp Arg Asp Thr
115 120 125

Tyr Gln Gly Ile Ile Val Pro Leu Ala Gly Ile Ala Phe Gly Thr Phe
130 135 140

Leu Met Arg Asn His Phe Met Ser Ile Pro Ser Glu Leu Ile Glu Ala
145 150 155 160

Ala Arg Met Asp His Cys Gly His Phe Arg Leu Leu Trp Lys Val Leu
165 170 175

Leu Pro Ile Ser Met Pro Thr Leu Val Ala Phe Ser Met Ile Thr Val
180 185 190

Val Asn Glu Trp Asn Gln Tyr Leu Trp Pro Phe Leu Met Ala Glu Thr
195 200 205

Asp Asn Ser Ala Thr Leu Pro Ile Gly Leu Thr Met Leu Gln Asn Asn
210 215 220

Glu Gly Val Ser Asn Trp Gly Pro Val Met Ala Ala Thr Ile Met Thr
225 230 235 240

Met Leu Pro Val Leu Val Met Phe Leu Ala Leu Gln Glu Tyr Met Ile
245 250 255

Lys Gly Leu Ile Ser Gly Ala Val Lys Gly
260 265

<210> 341
<211> 899
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(876)
<223> RXS00088

<400> 341

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atc gaa gac aac cac ggc acc gaa ggg atc tcc ctg cca atc gag ggc   48
Ile Glu Asp Asn His Gly Thr Glu Gly Ile Ser Leu Pro Ile Glu Gly
  1               5                  10                  15

gtc gct gcg acc gac aac cgc gca ttc gaa ctg ctt gat cgc tgg ggt   96
Val Ala Ala Thr Asp Asn Arg Ala Phe Glu Leu Leu Asp Arg Trp Gly
             20                  25                  30

gta gag ctc gtt gca gct cca ctt cag ctg gtt cca ttt acc gtt acg   144
Val Glu Leu Val Ala Ala Pro Leu Gln Leu Val Pro Phe Thr Val Thr
         35                  40                  45

ggc tac acc gaa gag ggc ggc gtc gct aac ctt ggc tcc cac cgc gag   192
Gly Tyr Thr Glu Glu Gly Gly Val Ala Asn Leu Gly Ser His Arg Glu
     50                  55                  60

cca gac ctg gaa gca ctt gct gct gca cag cct tcc ctg atc atc aac   240
Pro Asp Leu Glu Ala Leu Ala Ala Ala Gln Pro Ser Leu Ile Ile Asn
 65                  70                  75                  80

ggc cag cgc ttc gct cag tac tac gat gac atc att gcc ctg aac cct   288
Gly Gln Arg Phe Ala Gln Tyr Tyr Asp Asp Ile Ile Ala Leu Asn Pro
                 85                  90                  95

gac gca acc gtt gtt gag cta gac cca cgc gat ggc gag cca ctt gac   336
Asp Ala Thr Val Val Glu Leu Asp Pro Arg Asp Gly Glu Pro Leu Asp
            100                 105                 110

cag gag ctt atc cgc cag gct gaa acc ctc ggt gag atc ttc ggc gaa   384
Gln Glu Leu Ile Arg Gln Ala Glu Thr Leu Gly Glu Ile Phe Gly Glu
        115                 120                 125

gaa gaa gat gct gca aag atc gtt gct gat ttc gag tcc gca ctt gag   432
Glu Glu Asp Ala Ala Lys Ile Val Ala Asp Phe Glu Ser Ala Leu Glu
    130                 135                 140

cgc gct aag acc gca tac gca gca atc tcc gac cag acc gtc atg gca   480
Arg Ala Lys Thr Ala Tyr Ala Ala Ile Ser Asp Gln Thr Val Met Ala
145                 150                 155                 160

gtt aac gtt tcc ggc gga aac att ggc tac atc gct cct tcc gtt gga   528
Val Asn Val Ser Gly Gly Asn Ile Gly Tyr Ile Ala Pro Ser Val Gly
                165                 170                 175

cgc acc tac ggt cca atc ttc gac ctg gtt gga ctc acc cca gca ctc   576
Arg Thr Tyr Gly Pro Ile Phe Asp Leu Val Gly Leu Thr Pro Ala Leu
            180                 185                 190
```

```
gag gtt ggc aac gcg tcc tcc gac cac gag ggc gac gac att aac gtc   624
Glu Val Gly Asn Ala Ser Ser Asp His Glu Gly Asp Asp Ile Asn Val
        195                 200                 205

gaa gca atc gca gct gca aac cca gac ctg atc ctg gtc atg gac cgc   672
Glu Ala Ile Ala Ala Ala Asn Pro Asp Leu Ile Leu Val Met Asp Arg
    210                 215                 220

gat ggt ggc acc agc acc cgc aac gaa gct gat tac gtt cca gca gag   720
Asp Gly Gly Thr Ser Thr Arg Asn Glu Ala Asp Tyr Val Pro Ala Glu
225                 230                 235                 240

cag atc gtc tcc gac aat gaa gca ctg gca aac gtc aag gct gtc acc   768
Gln Ile Val Ser Asp Asn Glu Ala Leu Ala Asn Val Lys Ala Val Thr
                245                 250                 255

gac gga tac gtt tac tac gca cct gca gat acc tac acc aac gaa aac   816
Asp Gly Tyr Val Tyr Tyr Ala Pro Ala Asp Thr Tyr Thr Asn Glu Asn
            260                 265                 270

atc atc acc tac acc gag atc ctc aac ggc atg gca gat atg ttc gag   864
Ile Ile Thr Tyr Thr Glu Ile Leu Asn Gly Met Ala Asp Met Phe Glu
        275                 280                 285

aag gca gct cag taggggatcg atcccacact gac                        899
Lys Ala Ala Gln
    290
```

<210> 342
<211> 292
<212> PRT
<213> Corynebacterium glutamicum

<400> 342

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Ile Glu Asp Asn His Gly Thr Glu Gly Ile Ser Leu Pro Ile Glu Gly
  1               5                  10                  15

Val Ala Ala Thr Asp Asn Arg Ala Phe Glu Leu Leu Asp Arg Trp Gly
             20                  25                  30

Val Glu Leu Val Ala Ala Pro Leu Gln Leu Val Pro Phe Thr Val Thr
         35                  40                  45

Gly Tyr Thr Glu Glu Gly Gly Val Ala Asn Leu Gly Ser His Arg Glu
     50                  55                  60

Pro Asp Leu Glu Ala Leu Ala Ala Ala Gln Pro Ser Leu Ile Ile Asn
 65                  70                  75                  80

Gly Gln Arg Phe Ala Gln Tyr Tyr Asp Asp Ile Ile Ala Leu Asn Pro
                 85                  90                  95

Asp Ala Thr Val Val Glu Leu Asp Pro Arg Asp Gly Glu Pro Leu Asp
            100                 105                 110

Gln Glu Leu Ile Arg Gln Ala Glu Thr Leu Gly Glu Ile Phe Gly Glu
        115                 120                 125

Glu Glu Asp Ala Ala Lys Ile Val Ala Asp Phe Glu Ser Ala Leu Glu
    130                 135                 140
```

```
Arg Ala Lys Thr Ala Tyr Ala Ala Ile Ser Asp Gln Thr Val Met Ala
145                 150                 155                 160

Val Asn Val Ser Gly Gly Asn Ile Gly Tyr Ile Ala Pro Ser Val Gly
                165                 170                 175

Arg Thr Tyr Gly Pro Ile Phe Asp Leu Val Gly Leu Thr Pro Ala Leu
            180                 185                 190

Glu Val Gly Asn Ala Ser Ser Asp His Glu Gly Asp Asp Ile Asn Val
        195                 200                 205

Glu Ala Ile Ala Ala Ala Asn Pro Asp Leu Ile Leu Val Met Asp Arg
    210                 215                 220

Asp Gly Gly Thr Ser Thr Arg Asn Glu Ala Asp Tyr Val Pro Ala Glu
225                 230                 235                 240

Gln Ile Val Ser Asp Asn Glu Ala Leu Ala Asn Val Lys Ala Val Thr
                245                 250                 255

Asp Gly Tyr Val Tyr Tyr Ala Pro Ala Asp Thr Tyr Thr Asn Glu Asn
            260                 265                 270

Ile Ile Thr Tyr Thr Glu Ile Leu Asn Gly Met Ala Asp Met Phe Glu
        275                 280                 285

Lys Ala Ala Gln
    290
```

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<210> 343
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1177)
<223> RXS00372

<400> 343

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gcagacattt ccataagtcc tgcgaaatgc gcccattcat gtaaagatgt tatttcctcc 60

cccaaacact ccttaaaatt tcaagaaggg ccttattttc atg tct tcg aag cac   115
                                              Met Ser Ser Lys His
                                                1               5

cct ttg aag cgc act gcc gtt act gtt ttt gca ctc ggc gct tcc gct   163
Pro Leu Lys Arg Thr Ala Val Thr Val Phe Ala Leu Gly Ala Ser Ala
                  10                  15                  20

gct ctc ctc gtg gct tgc tct gaa cct tct gag gac gtt tcc acc gca   211
Ala Leu Leu Val Ala Cys Ser Glu Pro Ser Glu Asp Val Ser Thr Ala
              25                  30                  35

gag acc acc act gca agc tct tcc gct aac gca tcc gat gca gcc ggt   259
Glu Thr Thr Thr Ala Ser Ser Ser Ala Asn Ala Ser Asp Ala Ala Gly
          40                  45                  50
```

```
gaa aaa gta acc atc acc gtc tac acc tct gag cct gag gaa aag gtc   307
Glu Lys Val Thr Ile Thr Val Tyr Thr Ser Glu Pro Glu Glu Lys Val
     55                  60                  65

gat gag atc aac aag gcg ttc atg gaa gcc aac cca gat att gag gtt   355
Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn Pro Asp Ile Glu Val
 70                  75                  80                  85

gag gtg tac cgc gct ggt act ggc gat ctg act gct cgc att gaa gct   403
Glu Val Tyr Arg Ala Gly Thr Gly Asp Leu Thr Ala Arg Ile Glu Ala
                 90                  95                 100

gaa aag gca tcc ggt tct atc gag gct gat gtg ttg tgg gct gcg gat   451
Glu Lys Ala Ser Gly Ser Ile Glu Ala Asp Val Leu Trp Ala Ala Asp
            105                 110                 115

gct gca acc ttt gaa act tat gca gca cag ggc gac ctt gca gag ctg   499
Ala Ala Thr Phe Glu Thr Tyr Ala Ala Gln Gly Asp Leu Ala Glu Leu
        120                 125                 130

gaa gat gtt gag act tcc gac atc att gaa gag gct ctg gat gct gag   547
Glu Asp Val Glu Thr Ser Asp Ile Ile Glu Glu Ala Leu Asp Ala Glu
    135                 140                 145

aac ttt tat gta ggc acc cgc atc atc cca acc gtg att gca tac aac   595
Asn Phe Tyr Val Gly Thr Arg Ile Ile Pro Thr Val Ile Ala Tyr Asn
150                 155                 160                 165

act gaa gtt gtt gat cag gct gag ctt cct acg tct tgg gct gat ctg   643
Thr Glu Val Val Asp Gln Ala Glu Leu Pro Thr Ser Trp Ala Asp Leu
                170                 175                 180

act gat cct aag tat gca ggc caa ctg gtc atg ccg gat cca gct gtg   691
Thr Asp Pro Lys Tyr Ala Gly Gln Leu Val Met Pro Asp Pro Ala Val
            185                 190                 195

tct ggt gct gca gcc ttc aat gct tct gtg tgg aag aac gac cct gcg   739
Ser Gly Ala Ala Ala Phe Asn Ala Ser Val Trp Lys Asn Asp Pro Ala
        200                 205                 210

ctt ggc gaa gcc tgg atc acc gcc ttg ggt gaa aac caa cca atg atc   787
Leu Gly Glu Ala Trp Ile Thr Ala Leu Gly Glu Asn Gln Pro Met Ile
    215                 220                 225

gct cag tcc aac ggc cca acc tcc cag gag atc gct ggc ggt ggc cac   835
Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile Ala Gly Gly Gly His
230                 235                 240                 245

cca gtg ggc atc gtg gtg gac tac ttg gtg cgc gac ttg gct gct gct   883
Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg Asp Leu Ala Ala Ala
                250                 255                 260

gga tct cca atc gac acc atc tac gca tcg gag ggt tct cct tac atc   931
Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu Gly Ser Pro Tyr Ile
            265                 270                 275

act gag cct gca ggt gtg ttc gct gat tct gaa aag aag gaa gca gcc   979
Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu Lys Lys Glu Ala Ala
        280                 285                 290

gag cgc tac atc aac ttc ctg ctg tct gtt gaa ggc cag gaa atc gca  1027
```

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```
Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu Gly Gln Glu Ile Ala
    295                 300                 305

gtt gag cag gca tac ctg cca gtg cgt gaa gat gtc gga act cca gag   1075
Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp Val Gly Thr Pro Glu
310                 315                 320                 325

ggc acc ccc gag ttg gct gac atc gag ctc atg acc cct gac ctg gag   1123
Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met Thr Pro Asp Leu Glu
                330                 335                 340

gtt gta acc gct gat aag gcg gct gct gtt gag ttc ttc caa aac gca   1171
Val Val Thr Ala Asp Lys Ala Ala Ala Val Glu Phe Phe Gln Asn Ala
            345                 350                 355

atg aac tagttttcct atgcagttat ctc                                1200
Met Asn
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<210> 344
<211> 359
<212> PRT
<213> Corynebacterium glutamicum

<400> 344

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Met Ser Ser Lys His Pro Leu Lys Arg Thr Ala Val Thr Val Phe Ala
  1               5                  10                  15

Leu Gly Ala Ser Ala Ala Leu Leu Val Ala Cys Ser Glu Pro Ser Glu
            20                  25                  30

Asp Val Ser Thr Ala Glu Thr Thr Thr Ala Ser Ser Ser Ala Asn Ala
        35                  40                  45

Ser Asp Ala Ala Gly Glu Lys Val Thr Ile Thr Val Tyr Thr Ser Glu
    50                  55                  60

Pro Glu Glu Lys Val Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn
65                  70                  75                  80

Pro Asp Ile Glu Val Glu Val Tyr Arg Ala Gly Thr Gly Asp Leu Thr
                85                  90                  95

Ala Arg Ile Glu Ala Glu Lys Ala Ser Gly Ser Ile Glu Ala Asp Val
            100                 105                 110

Leu Trp Ala Ala Asp Ala Ala Thr Phe Glu Thr Tyr Ala Ala Gln Gly
        115                 120                 125

Asp Leu Ala Glu Leu Glu Asp Val Glu Thr Ser Asp Ile Ile Glu Glu
    130                 135                 140

Ala Leu Asp Ala Glu Asn Phe Tyr Val Gly Thr Arg Ile Ile Pro Thr
145                 150                 155                 160

Val Ile Ala Tyr Asn Thr Glu Val Val Asp Gln Ala Glu Leu Pro Thr
                165                 170                 175

Ser Trp Ala Asp Leu Thr Asp Pro Lys Tyr Ala Gly Gln Leu Val Met
            180                 185                 190
```

Pro Asp Pro Ala Val Ser Gly Ala Ala Ala Phe Asn Ala Ser Val Trp
195 200 205

Lys Asn Asp Pro Ala Leu Gly Glu Ala Trp Ile Thr Ala Leu Gly Glu
210 215 220

Asn Gln Pro Met Ile Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile
225 230 235 240

Ala Gly Gly Gly His Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg
245 250 255

Asp Leu Ala Ala Ala Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu
260 265 270

Gly Ser Pro Tyr Ile Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu
275 280 285

Lys Lys Glu Ala Ala Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu
290 295 300

Gly Gln Glu Ile Ala Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp
305 310 315 320

Val Gly Thr Pro Glu Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met
325 330 335

Thr Pro Asp Leu Glu Val Val Thr Ala Asp Lys Ala Ala Ala Val Glu
340 345 350

Phe Phe Gln Asn Ala Met Asn
355

<210> 345
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXS02590

<400> 345
gccccaaagg cttaaagtaa tgggcatgcc cactccttct tcgaccaaaa gctacgctgc 60

ggtcttacct ccacctggcc cctcgtgggc tggttccctc atg ggc atc tca ttg 115
Met Gly Ile Ser Leu
1 5

ttg tca tca ctg ttg aaa atc cat ggt ttt cca gtc gtc gca gat ttc 163
Leu Ser Ser Leu Leu Lys Ile His Gly Phe Pro Val Val Ala Asp Phe
10 15 20

ttc ttc gcg tta gct gtt gtg gtg gca att gtc att att ggc ggt tgg 211
Phe Phe Ala Leu Ala Val Val Val Ala Ile Val Ile Ile Gly Gly Trp
25 30 35

cta atc tac cgc tct cct tca ttc aaa act gaa gtc atg ccg gca tgg 259

```
Leu Ile Tyr Arg Ser Pro Ser Phe Lys Thr Glu Val Met Pro Ala Trp
          40                  45                  50

gca atg ctg tcc atg ggt ttg atc gca ttg gga act gca agc ccc gta   307
Ala Met Leu Ser Met Gly Leu Ile Ala Leu Gly Thr Ala Ser Pro Val
     55                  60                  65

gtt ttg ggt gat gat ctg tgg gga ttt atg ttt gtg tgc tgg tct att   355
Val Leu Gly Asp Asp Leu Trp Gly Phe Met Phe Val Cys Trp Ser Ile
 70                  75                  80                  85

ggc aca gcc gtg gga ctt gtt gcc tat tcc tta tat ata acg gcc att   403
Gly Thr Ala Val Gly Leu Val Ala Tyr Ser Leu Tyr Ile Thr Ala Ile
                 90                  95                 100

ttg cga tct aag gcg ggc aca cca act ttt gcg tgg ggt ctt cct ctt   451
Leu Arg Ser Lys Ala Gly Thr Pro Thr Phe Ala Trp Gly Leu Pro Leu
            105                 110                 115

gtc acg ccg atg gtt gct tcc acc tcg gca gca caa ctc cat gag cac   499
Val Thr Pro Met Val Ala Ser Thr Ser Ala Ala Gln Leu His Glu His
        120                 125                 130

ttt gaa ctt ccg gcg atg ctg tgg gtt tct ttc ggg ctc ttc ctt tta   547
Phe Glu Leu Pro Ala Met Leu Trp Val Ser Phe Gly Leu Phe Leu Leu
    135                 140                 145

act ttg gcg tct gca cca gca gtt ttt acc cga gtg tat ttc tac tat   595
Thr Leu Ala Ser Ala Pro Ala Val Phe Thr Arg Val Tyr Phe Tyr Tyr
150                 155                 160                 165

ttc ggc ccc aag gcg cag ggc atc cca ctg atg gca aca cca aca tca   643
Phe Gly Pro Lys Ala Gln Gly Ile Pro Leu Met Ala Thr Pro Thr Ser
                170                 175                 180

tgg att cct ttg ggt atg gtg ggc caa tcc act gca gca gct cag ctc   691
Trp Ile Pro Leu Gly Met Val Gly Gln Ser Thr Ala Ala Ala Gln Leu
            185                 190                 195

atc ggt gcg tcc ttt gga tcc aag aca gca atc aca atg ggc att att   739
Ile Gly Ala Ser Phe Gly Ser Lys Thr Ala Ile Thr Met Gly Ile Ile
        200                 205                 210

tac ggc atc atc atg gga att ttt acg att cct ctg gga gcc atc gct   787
Tyr Gly Ile Ile Met Gly Ile Phe Thr Ile Pro Leu Gly Ala Ile Ala
    215                 220                 225

cac ttt gtg ttc tac aga gct gtt ttc aaa ggg gcg aca tac agc ccc   835
His Phe Val Phe Tyr Arg Ala Val Phe Lys Gly Ala Thr Tyr Ser Pro
230                 235                 240                 245

aca tgg tgg gcc agt acc ttc cca gtt ggc act ttg agt ttg ggt gcg   883
Thr Trp Trp Ala Ser Thr Phe Pro Val Gly Thr Leu Ser Leu Gly Ala
                250                 255                 260

cat ttt tta tca cag agc acc gga gtg gag tgg ttt aac tac ttc agc   931
His Phe Leu Ser Gln Ser Thr Gly Val Glu Trp Phe Asn Tyr Phe Ser
            265                 270                 275

ctg tac ttg att gct tta atg ctc ttt cat gtc atc gtg tcc acc atc   979
Leu Tyr Leu Ile Ala Leu Met Leu Phe His Val Ile Val Ser Thr Ile
```

```
        280                 285                 290

gcc ggt acg att gca gta atg aga aga atc gtc gga aag ctt aaa tct   1027
Ala Gly Thr Ile Ala Val Met Arg Arg Ile Val Gly Lys Leu Lys Ser
    295                 300                 305

caa ctg gcc taaattgcag cgagaggtct aaa                            1059
Gln Leu Ala
310
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<210> 346
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 346

```
Met Gly Ile Ser Leu Leu Ser Ser Leu Leu Lys Ile His Gly Phe Pro
  1               5                  10                  15

Val Val Ala Asp Phe Phe Phe Ala Leu Ala Val Val Val Ala Ile Val
             20                  25                  30

Ile Ile Gly Gly Trp Leu Ile Tyr Arg Ser Pro Ser Phe Lys Thr Glu
         35                  40                  45

Val Met Pro Ala Trp Ala Met Leu Ser Met Gly Leu Ile Ala Leu Gly
     50                  55                  60

Thr Ala Ser Pro Val Val Leu Gly Asp Asp Leu Trp Gly Phe Met Phe
 65                  70                  75                  80

Val Cys Trp Ser Ile Gly Thr Ala Val Gly Leu Val Ala Tyr Ser Leu
                 85                  90                  95

Tyr Ile Thr Ala Ile Leu Arg Ser Lys Ala Gly Thr Pro Thr Phe Ala
            100                 105                 110

Trp Gly Leu Pro Leu Val Thr Pro Met Val Ala Ser Thr Ser Ala Ala
        115                 120                 125

Gln Leu His Glu His Phe Glu Leu Pro Ala Met Leu Trp Val Ser Phe
    130                 135                 140

Gly Leu Phe Leu Leu Thr Leu Ala Ser Ala Pro Ala Val Phe Thr Arg
145                 150                 155                 160

Val Tyr Phe Tyr Tyr Phe Gly Pro Lys Ala Gln Gly Ile Pro Leu Met
                165                 170                 175

Ala Thr Pro Thr Ser Trp Ile Pro Leu Gly Met Val Gly Gln Ser Thr
            180                 185                 190

Ala Ala Ala Gln Leu Ile Gly Ala Ser Phe Gly Ser Lys Thr Ala Ile
        195                 200                 205

Thr Met Gly Ile Ile Tyr Gly Ile Ile Met Gly Ile Phe Thr Ile Pro
    210                 215                 220

Leu Gly Ala Ile Ala His Phe Val Phe Tyr Arg Ala Val Phe Lys Gly
225                 230                 235                 240
```

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```
Ala Thr Tyr Ser Pro Thr Trp Trp Ala Ser Thr Phe Pro Val Gly Thr
                245                 250                 255

Leu Ser Leu Gly Ala His Phe Leu Ser Gln Ser Thr Gly Val Glu Trp
            260                 265                 270

Phe Asn Tyr Phe Ser Leu Tyr Leu Ile Ala Leu Met Leu Phe His Val
        275                 280                 285

Ile Val Ser Thr Ile Ala Gly Thr Ile Ala Val Met Arg Arg Ile Val
    290                 295                 300

Gly Lys Leu Lys Ser Gln Leu Ala
305                 310
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<210> 347
<211> 1725
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1702)
<223> RXS00758

<400> 347

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ttcaagtttg gctgtgactc atgtcgcaca tagtatttca atcaccggat ccgcacgatt 60

gcaaaatcct ggggaatatt cataacaacg gaggtcactc atg act ttg aag aag   115
                                              Met Thr Leu Lys Lys
                                                1               5

tct ctc gct gta acc acg gcg gct gca ctt gct ttg agc ctt gcc gct   163
Ser Leu Ala Val Thr Thr Ala Ala Ala Leu Ala Leu Ser Leu Ala Ala
                10                  15                  20

tgc tcg tcc gac tcc tcg tcc gac agc tcc tca tcc tca tca ggc agc   211
Cys Ser Ser Asp Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Gly Ser
            25                  30                  35

gaa ggc ggc gac aac tac gtc ctc gtc aac ggc act gag cca cag aac   259
Glu Gly Gly Asp Asn Tyr Val Leu Val Asn Gly Thr Glu Pro Gln Asn
        40                  45                  50

ccg ctc gtc cca ggc aac acc aac gaa gta ggt ggc ggt cgc atc gtc   307
Pro Leu Val Pro Gly Asn Thr Asn Glu Val Gly Gly Gly Arg Ile Val
    55                  60                  65

gac agc atc ttc tcc ggc ctg gtc tac tac gac gtc gac ggc tcc cct   355
Asp Ser Ile Phe Ser Gly Leu Val Tyr Tyr Asp Val Asp Gly Ser Pro
70                  75                  80                  85

gtc aac gat gtt gca gag tcc atc gaa ctc gaa ggt gac aag acc tac   403
Val Asn Asp Val Ala Glu Ser Ile Glu Leu Glu Gly Asp Lys Thr Tyr
                90                  95                  100

cgc atc acc atc aaa gac ggc cag acc ttc acc gat ggc acc cca gtt   451
Arg Ile Thr Ile Lys Asp Gly Gln Thr Phe Thr Asp Gly Thr Pro Val
            105                 110                 115
```

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acc gct gag agc ttt gtc aac gca tgg aac tac aac gta gct aac agc   499
Thr Ala Glu Ser Phe Val Asn Ala Trp Asn Tyr Asn Val Ala Asn Ser
        120                 125                 130

acg ctg tcc tcc tac ttc ttt gag tcc atc ctc ggc tac gaa gaa ggc   547
Thr Leu Ser Ser Tyr Phe Phe Glu Ser Ile Leu Gly Tyr Glu Glu Gly
    135                 140                 145

gtc gag tcc atg gaa ggc ctc cag gtc gtc gac gac acc acc ttc acc   595
Val Glu Ser Met Glu Gly Leu Gln Val Val Asp Asp Thr Thr Phe Thr
150                 155                 160                 165

gtc gag ctc acc cag cct gag tcc gac ttc cca ctg cgc ctg gga tac   643
Val Glu Leu Thr Gln Pro Glu Ser Asp Phe Pro Leu Arg Leu Gly Tyr
                170                 175                 180

tcc gca ttc ttc ccg ctt cct gaa tcc gca ttt gac gac atg gac gca   691
Ser Ala Phe Phe Pro Leu Pro Glu Ser Ala Phe Asp Asp Met Asp Ala
            185                 190                 195

ttc ggt gag aac cca atc ggc aac ggt cca tac aag ctc caa gag tgg   739
Phe Gly Glu Asn Pro Ile Gly Asn Gly Pro Tyr Lys Leu Gln Glu Trp
        200                 205                 210

aac cac aac cag gac gcc acc atc gtt cct aac gcg gac tac acc ggt   787
Asn His Asn Gln Asp Ala Thr Ile Val Pro Asn Ala Asp Tyr Thr Gly
    215                 220                 225

gga cgc cag gct cag aac gac ggc gtg aag ttc atc ttc tac cca acc   835
Gly Arg Gln Ala Gln Asn Asp Gly Val Lys Phe Ile Phe Tyr Pro Thr
230                 235                 240                 245

ttc gac tcc gct tac gcg gac ctg ctc tcc gac aac ttg gat gtg ctg   883
Phe Asp Ser Ala Tyr Ala Asp Leu Leu Ser Asp Asn Leu Asp Val Leu
                250                 255                 260

gac gct atc cca gac tcc gcg ttc tcc tcc ttc gag gac gag ctc tct   931
Asp Ala Ile Pro Asp Ser Ala Phe Ser Ser Phe Glu Asp Glu Leu Ser
            265                 270                 275

ggc cgt tcc atc aac cag cct tcc gct gtg ttc cag tcc ttc acc atc   979
Gly Arg Ser Ile Asn Gln Pro Ser Ala Val Phe Gln Ser Phe Thr Ile
        280                 285                 290

ccg gag agc ctt gag cac ttc tcc ggc gaa gaa ggc gtg ctg cgt cgc   1027
Pro Glu Ser Leu Glu His Phe Ser Gly Glu Glu Gly Val Leu Arg Arg
    295                 300                 305

cag gcc atc tcc ttg gcc gtc aac cgc gac gag atc acc caa acc atc   1075
Gln Ala Ile Ser Leu Ala Val Asn Arg Asp Glu Ile Thr Gln Thr Ile
310                 315                 320                 325

ttc gaa ggc acc cgc acc cca gcg acg gac ttc acc tcc cct gtc atc   1123
Phe Glu Gly Thr Arg Thr Pro Ala Thr Asp Phe Thr Ser Pro Val Ile
                330                 335                 340

gac gga cac tct gat tcc ctc cag ggc gca gat gtc ttg acc tac gat   1171
Asp Gly His Ser Asp Ser Leu Gln Gly Ala Asp Val Leu Thr Tyr Asp
            345                 350                 355
```

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cca gag cgc gct cag gaa ctg tgg gca cag gca gac gag atc agc cct   1219
Pro Glu Arg Ala Gln Glu Leu Trp Ala Gln Ala Asp Glu Ile Ser Pro
        360                 365                 370

tgg tcc ggc gag ttc tcc atc tcc tac aac gca gac ggt gga cac cag   1267
Trp Ser Gly Glu Phe Ser Ile Ser Tyr Asn Ala Asp Gly Gly His Gln
    375                 380                 385

gca tgg gtg gac gca acc gcc aat tcc atc cgc aac acc ctg ggt atc   1315
Ala Trp Val Asp Ala Thr Ala Asn Ser Ile Arg Asn Thr Leu Gly Ile
390                 395                 400                 405

gac gcc atc ggc aac cca tac cca gac ttc aag tcc ctg cgt gac gat   1363
Asp Ala Ile Gly Asn Pro Tyr Pro Asp Phe Lys Ser Leu Arg Asp Asp
                410                 415                 420

gtc acc aac cgc acc atc aac ggc gca ttc cgc acc ggc tgg cag gca   1411
Val Thr Asn Arg Thr Ile Asn Gly Ala Phe Arg Thr Gly Trp Gln Ala
            425                 430                 435

gac tac ccg tcc ttg ggc aac ttc ctc gga cct ttg tac ggc acc ggt   1459
Asp Tyr Pro Ser Leu Gly Asn Phe Leu Gly Pro Leu Tyr Gly Thr Gly
        440                 445                 450

gca ggc tcc aac gat ggt gac tac tcc aac cca gat ttc gat gcc aag   1507
Ala Gly Ser Asn Asp Gly Asp Tyr Ser Asn Pro Asp Phe Asp Ala Lys
    455                 460                 465

ctc gcc gaa gca gca aac gcg gcc gat gtt gac gca tca acc ccg cta   1555
Leu Ala Glu Ala Ala Asn Ala Ala Asp Val Asp Ala Ser Thr Pro Leu
470                 475                 480                 485

tac aac gaa gca cag gaa atc ctg ctc cag gat ctc cca gcg atc cca   1603
Tyr Asn Glu Ala Gln Glu Ile Leu Leu Gln Asp Leu Pro Ala Ile Pro
                490                 495                 500

act tgg tac tcc aac gca gtt ggt gga tac tcc acc aac gtg gac aac   1651
Thr Trp Tyr Ser Asn Ala Val Gly Gly Tyr Ser Thr Asn Val Asp Asn
            505                 510                 515

gtg gaa ttc cag tgg aac tcg caa cct gcg tac tac cag atc acc aag   1699
Val Glu Phe Gln Trp Asn Ser Gln Pro Ala Tyr Tyr Gln Ile Thr Lys
        520                 525                 530

aac tagtagcttc gcaccacccg ctc                                    1725
Asn
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<210> 348
<211> 534
<212> PRT
<213> Corynebacterium glutamicum

<400> 348

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Met Thr Leu Lys Lys Ser Leu Ala Val Thr Thr Ala Ala Ala Leu Ala
  1               5                  10                  15

Leu Ser Leu Ala Ala Cys Ser Ser Asp Ser Ser Ser Asp Ser Ser Ser
             20                  25                  30
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Ser Ser Ser Gly Ser Glu Gly Gly Asp Asn Tyr Val Leu Val Asn Gly
35 40 45

Thr Glu Pro Gln Asn Pro Leu Val Pro Gly Asn Thr Asn Glu Val Gly
50 55 60

Gly Gly Arg Ile Val Asp Ser Ile Phe Ser Gly Leu Val Tyr Tyr Asp
65 70 75 80

Val Asp Gly Ser Pro Val Asn Asp Val Ala Glu Ser Ile Glu Leu Glu
85 90 95

Gly Asp Lys Thr Tyr Arg Ile Thr Ile Lys Asp Gly Gln Thr Phe Thr
100 105 110

Asp Gly Thr Pro Val Thr Ala Glu Ser Phe Val Asn Ala Trp Asn Tyr
115 120 125

Asn Val Ala Asn Ser Thr Leu Ser Ser Tyr Phe Phe Glu Ser Ile Leu
130 135 140

Gly Tyr Glu Glu Gly Val Glu Ser Met Glu Gly Leu Gln Val Val Asp
145 150 155 160

Asp Thr Thr Phe Thr Val Glu Leu Thr Gln Pro Glu Ser Asp Phe Pro
165 170 175

Leu Arg Leu Gly Tyr Ser Ala Phe Phe Pro Leu Pro Glu Ser Ala Phe
180 185 190

Asp Asp Met Asp Ala Phe Gly Glu Asn Pro Ile Gly Asn Gly Pro Tyr
195 200 205

Lys Leu Gln Glu Trp Asn His Asn Gln Asp Ala Thr Ile Val Pro Asn
210 215 220

Ala Asp Tyr Thr Gly Gly Arg Gln Ala Gln Asn Asp Gly Val Lys Phe
225 230 235 240

Ile Phe Tyr Pro Thr Phe Asp Ser Ala Tyr Ala Asp Leu Leu Ser Asp
245 250 255

Asn Leu Asp Val Leu Asp Ala Ile Pro Asp Ser Ala Phe Ser Ser Phe
260 265 270

Glu Asp Glu Leu Ser Gly Arg Ser Ile Asn Gln Pro Ser Ala Val Phe
275 280 285

Gln Ser Phe Thr Ile Pro Glu Ser Leu Glu His Phe Ser Gly Glu Glu
290 295 300

Gly Val Leu Arg Arg Gln Ala Ile Ser Leu Ala Val Asn Arg Asp Glu
305 310 315 320

Ile Thr Gln Thr Ile Phe Glu Gly Thr Arg Thr Pro Ala Thr Asp Phe
325 330 335

Thr Ser Pro Val Ile Asp Gly His Ser Asp Ser Leu Gln Gly Ala Asp
340 345 350

Val Leu Thr Tyr Asp Pro Glu Arg Ala Gln Glu Leu Trp Ala Gln Ala

```
        355                 360                 365

Asp Glu Ile Ser Pro Trp Ser Gly Glu Phe Ser Ile Ser Tyr Asn Ala
    370                 375                 380

Asp Gly Gly His Gln Ala Trp Val Asp Ala Thr Ala Asn Ser Ile Arg
385                 390                 395                 400

Asn Thr Leu Gly Ile Asp Ala Ile Gly Asn Pro Tyr Pro Asp Phe Lys
                405                 410                 415

Ser Leu Arg Asp Asp Val Thr Asn Arg Thr Ile Asn Gly Ala Phe Arg
            420                 425                 430

Thr Gly Trp Gln Ala Asp Tyr Pro Ser Leu Gly Asn Phe Leu Gly Pro
        435                 440                 445

Leu Tyr Gly Thr Gly Ala Gly Ser Asn Asp Gly Asp Tyr Ser Asn Pro
    450                 455                 460

Asp Phe Asp Ala Lys Leu Ala Glu Ala Ala Asn Ala Ala Asp Val Asp
465                 470                 475                 480

Ala Ser Thr Pro Leu Tyr Asn Glu Ala Gln Glu Ile Leu Leu Gln Asp
                485                 490                 495

Leu Pro Ala Ile Pro Thr Trp Tyr Ser Asn Ala Val Gly Gly Tyr Ser
            500                 505                 510

Thr Asn Val Asp Asn Val Glu Phe Gln Trp Asn Ser Gln Pro Ala Tyr
        515                 520                 525

Tyr Gln Ile Thr Lys Asn
    530


<210> 349
<211> 1698
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1675)
<223> RXS01346

<400> 349
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ggcacgttgc aaacagcaac gctcacccat aggagattta atg cgc aca gcc aca   115
                                            Met Arg Thr Ala Thr
                                              1               5

aaa gtc atc gca aca gtg atg gcc tca acc ctg gct atc ggg ctg gca   163
Lys Val Ile Ala Thr Val Met Ala Ser Thr Leu Ala Ile Gly Leu Ala
                  10                  15                  20

tct tgt tcc agc tct agt ggc acc cca gac gtg aat tac gta tcc gtc   211
Ser Cys Ser Ser Ser Ser Gly Thr Pro Asp Val Asn Tyr Val Ser Val
              25                  30                  35
```

```
aac ggc acc gaa cct cag cgc gga ctc atc ccg ggc gac acc aat gaa   259
Asn Gly Thr Glu Pro Gln Arg Gly Leu Ile Pro Gly Asp Thr Asn Glu
         40                  45                  50

aac ggc ggt ggg cga gtg gtg gac atg ctg tac tct ggg ctc gtc tac   307
Asn Gly Gly Gly Arg Val Val Asp Met Leu Tyr Ser Gly Leu Val Tyr
     55                  60                  65

ttt gat gaa gct ggc gtt gct caa aat gac ctg gcg gca tca att gac   355
Phe Asp Glu Ala Gly Val Ala Gln Asn Asp Leu Ala Ala Ser Ile Asp
 70                  75                  80                  85

cag gaa aca gac acc acc tac aaa atc act ttg cgt gat ggc atc aaa   403
Gln Glu Thr Asp Thr Thr Tyr Lys Ile Thr Leu Arg Asp Gly Ile Lys
                 90                  95                 100

ttc agt gac gga tcg gat att act gcc act gat ttt gtg gat acc tgg   451
Phe Ser Asp Gly Ser Asp Ile Thr Ala Thr Asp Phe Val Asp Thr Trp
            105                 110                 115

aat ttt gta gtg gaa aat gga ctg ctc aac act tct ttc ttc tca ccg   499
Asn Phe Val Val Glu Asn Gly Leu Leu Asn Thr Ser Phe Phe Ser Pro
        120                 125                 130

att aaa ggg tat gag gag ggc gtg gaa acg ctc gag ggt ttg aat gtg   547
Ile Lys Gly Tyr Glu Glu Gly Val Glu Thr Leu Glu Gly Leu Asn Val
    135                 140                 145

gtg gat gat cgc aca ttt acc atc gag ctt gcc caa ccg gat tct gag   595
Val Asp Asp Arg Thr Phe Thr Ile Glu Leu Ala Gln Pro Asp Ser Glu
150                 155                 160                 165

ttc acc caa cgc att ggc tac tac ggt ttt gca ccg atg cca gct tcg   643
Phe Thr Gln Arg Ile Gly Tyr Tyr Gly Phe Ala Pro Met Pro Ala Ser
                170                 175                 180

gct cgc gat gat att gac gcc ttt ggt gaa aac ccc gtg tcc tct ggc   691
Ala Arg Asp Asp Ile Asp Ala Phe Gly Glu Asn Pro Val Ser Ser Gly
            185                 190                 195

cct tac aaa cta gag cag tgg gat cac aac gca gaa ctg aaa gtg gtg   739
Pro Tyr Lys Leu Glu Gln Trp Asp His Asn Ala Glu Leu Lys Val Val
        200                 205                 210

gcc aat gaa cac tac gat ggc ccg cgc gca gcc aac aac gat ggc ttg   787
Ala Asn Glu His Tyr Asp Gly Pro Arg Ala Ala Asn Asn Asp Gly Leu
    215                 220                 225

aag tac gtg ttc tac gcc caa aat gat gca gct tat tca gat ctg ttg   835
Lys Tyr Val Phe Tyr Ala Gln Asn Asp Ala Ala Tyr Ser Asp Leu Leu
230                 235                 240                 245

gct gga aac cta gat gtg ctg gat ctc att cca cca tcg gcg tac acc   883
Ala Gly Asn Leu Asp Val Leu Asp Leu Ile Pro Pro Ser Ala Tyr Thr
                250                 255                 260

acc tat gaa gag gaa ctg tcg ggt cga tcc att aat caa cct gcg gcc   931
Thr Tyr Glu Glu Glu Leu Ser Gly Arg Ser Ile Asn Gln Pro Ala Ala
            265                 270                 275

tcc tat ctg gaa ctc tcc att cgc atg gaa tcc ccc aac ttt gaa ggg   979
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Ser Tyr Leu Glu Leu Ser Ile Arg Met Glu Ser Pro Asn Phe Glu Gly
        280                 285                 290

caa cag gga cag ttg cgt cga caa gca att tct atg gcg att aac cgt   1027
Gln Gln Gly Gln Leu Arg Arg Gln Ala Ile Ser Met Ala Ile Asn Arg
    295                 300                 305

gaa gaa atc gct gag cag atc ttc gcc ggc acc tac acg cct gcg ctc   1075
Glu Glu Ile Ala Glu Gln Ile Phe Ala Gly Thr Tyr Thr Pro Ala Leu
310                 315                 320                 325

gac ttc acc gcg ccc gtg ctc gac ggc tgg cgc gat gat ttg aac ggc   1123
Asp Phe Thr Ala Pro Val Leu Asp Gly Trp Arg Asp Asp Leu Asn Gly
                330                 335                 340

aat gac gtg ctg act ttc cag cct gac aag gcc cgt gag ctg tgg gaa   1171
Asn Asp Val Leu Thr Phe Gln Pro Asp Lys Ala Arg Glu Leu Trp Glu
            345                 350                 355

gac gct gag gag atc gca cct ttt gag ggc gaa ttg cag atc agt tac   1219
Asp Ala Glu Glu Ile Ala Pro Phe Glu Gly Glu Leu Gln Ile Ser Tyr
        360                 365                 370

aac gcg gat gtt ccc aac cgg gaa tgg gtg gat gcg gta gca aac agc   1267
Asn Ala Asp Val Pro Asn Arg Glu Trp Val Asp Ala Val Ala Asn Ser
    375                 380                 385

atc agc aac gaa tta gac gtc aac gcc act ggc aat cct ttc ccc gat   1315
Ile Ser Asn Glu Leu Asp Val Asn Ala Thr Gly Asn Pro Phe Pro Asp
390                 395                 400                 405

ttt aaa tcc ttc cgc gac aca tac cgc acc acc gga ttg gat ggc gcc   1363
Phe Lys Ser Phe Arg Asp Thr Tyr Arg Thr Thr Gly Leu Asp Gly Ala
                410                 415                 420

tac cgc acc gcg tgg ttt gcg gac tac cca agc atc ggc aac ttc ctt   1411
Tyr Arg Thr Ala Trp Phe Ala Asp Tyr Pro Ser Ile Gly Asn Phe Leu
            425                 430                 435

gga cct aac tac acc tcg ggc gtg gcc tcc aac gat gcc aag tac gaa   1459
Gly Pro Asn Tyr Thr Ser Gly Val Ala Ser Asn Asp Ala Lys Tyr Glu
        440                 445                 450

aac cca gaa ttt gat caa ttg att gcc gac gcc gca gca gcc tcc acc   1507
Asn Pro Glu Phe Asp Gln Leu Ile Ala Asp Ala Ala Ala Ala Ser Thr
    455                 460                 465

aag gag gaa acc ttc cag gca tat gcg cag gcc cag gaa atg ttg ttg   1555
Lys Glu Glu Thr Phe Gln Ala Tyr Ala Gln Ala Gln Glu Met Leu Leu
470                 475                 480                 485

cgc gat ctt ccc gca atc cca ctg tgg tac ccg aat gtg gtt ggc ggc   1603
Arg Asp Leu Pro Ala Ile Pro Leu Trp Tyr Pro Asn Val Val Gly Gly
                490                 495                 500

tac tca gaa tcc gtg gac aac gtc tcc gta aac tgg aag gcc ata cct   1651
Tyr Ser Glu Ser Val Asp Asn Val Ser Val Asn Trp Lys Ala Ile Pro
            505                 510                 515

gtt tat tgg gca att aca aag caa taaactcatt aacctaaatc cgg         1698
Val Tyr Trp Ala Ile Thr Lys Gln
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520 525

<210> 350
<211> 525
<212> PRT
<213> Corynebacterium glutamicum

<400> 350
Met Arg Thr Ala Thr Lys Val Ile Ala Thr Val Met Ala Ser Thr Leu
1 5 10 15

Ala Ile Gly Leu Ala Ser Cys Ser Ser Ser Ser Gly Thr Pro Asp Val
20 25 30

Asn Tyr Val Ser Val Asn Gly Thr Glu Pro Gln Arg Gly Leu Ile Pro
35 40 45

Gly Asp Thr Asn Glu Asn Gly Gly Gly Arg Val Val Asp Met Leu Tyr
50 55 60

Ser Gly Leu Val Tyr Phe Asp Glu Ala Gly Val Ala Gln Asn Asp Leu
65 70 75 80

Ala Ala Ser Ile Asp Gln Glu Thr Asp Thr Thr Tyr Lys Ile Thr Leu
85 90 95

Arg Asp Gly Ile Lys Phe Ser Asp Gly Ser Asp Ile Thr Ala Thr Asp
100 105 110

Phe Val Asp Thr Trp Asn Phe Val Val Glu Asn Gly Leu Leu Asn Thr
115 120 125

Ser Phe Phe Ser Pro Ile Lys Gly Tyr Glu Glu Gly Val Glu Thr Leu
130 135 140

Glu Gly Leu Asn Val Val Asp Asp Arg Thr Phe Thr Ile Glu Leu Ala
145 150 155 160

Gln Pro Asp Ser Glu Phe Thr Gln Arg Ile Gly Tyr Tyr Gly Phe Ala
165 170 175

Pro Met Pro Ala Ser Ala Arg Asp Asp Ile Asp Ala Phe Gly Glu Asn
180 185 190

Pro Val Ser Ser Gly Pro Tyr Lys Leu Glu Gln Trp Asp His Asn Ala
195 200 205

Glu Leu Lys Val Val Ala Asn Glu His Tyr Asp Gly Pro Arg Ala Ala
210 215 220

Asn Asn Asp Gly Leu Lys Tyr Val Phe Tyr Ala Gln Asn Asp Ala Ala
225 230 235 240

Tyr Ser Asp Leu Leu Ala Gly Asn Leu Asp Val Leu Asp Leu Ile Pro
245 250 255

Pro Ser Ala Tyr Thr Thr Tyr Glu Glu Glu Leu Ser Gly Arg Ser Ile
260 265 270

Asn Gln Pro Ala Ala Ser Tyr Leu Glu Leu Ser Ile Arg Met Glu Ser

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        275                 280                 285

Pro Asn Phe Glu Gly Gln Gln Gly Gln Leu Arg Arg Gln Ala Ile Ser
    290                 295                 300

Met Ala Ile Asn Arg Glu Glu Ile Ala Glu Gln Ile Phe Ala Gly Thr
305                 310                 315                 320

Tyr Thr Pro Ala Leu Asp Phe Thr Ala Pro Val Leu Asp Gly Trp Arg
                325                 330                 335

Asp Asp Leu Asn Gly Asn Asp Val Leu Thr Phe Gln Pro Asp Lys Ala
            340                 345                 350

Arg Glu Leu Trp Glu Asp Ala Glu Glu Ile Ala Pro Phe Glu Gly Glu
        355                 360                 365

Leu Gln Ile Ser Tyr Asn Ala Asp Val Pro Asn Arg Glu Trp Val Asp
    370                 375                 380

Ala Val Ala Asn Ser Ile Ser Asn Glu Leu Asp Val Asn Ala Thr Gly
385                 390                 395                 400

Asn Pro Phe Pro Asp Phe Lys Ser Phe Arg Asp Thr Tyr Arg Thr Thr
                405                 410                 415

Gly Leu Asp Gly Ala Tyr Arg Thr Ala Trp Phe Ala Asp Tyr Pro Ser
            420                 425                 430

Ile Gly Asn Phe Leu Gly Pro Asn Tyr Thr Ser Gly Val Ala Ser Asn
        435                 440                 445

Asp Ala Lys Tyr Glu Asn Pro Glu Phe Asp Gln Leu Ile Ala Asp Ala
    450                 455                 460

Ala Ala Ala Ser Thr Lys Glu Glu Thr Phe Gln Ala Tyr Ala Gln Ala
465                 470                 475                 480

Gln Glu Met Leu Leu Arg Asp Leu Pro Ala Ile Pro Leu Trp Tyr Pro
                485                 490                 495

Asn Val Val Gly Gly Tyr Ser Glu Ser Val Asp Asn Val Ser Val Asn
            500                 505                 510

Trp Lys Ala Ile Pro Val Tyr Trp Ala Ile Thr Lys Gln
        515                 520                 525
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<210> 351
<211> 321
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (26)..(298)
<223> RXS00912

<400> 351
ccacaccttt gaaaggagct aagcgatg gac aac acc ctc tac aca gca ggc 52
Met Asp Asn Thr Leu Tyr Thr Ala Gly

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                                    1               5

ctc aca atc gca gct gcc ttt ttc atg ctg tcg ttc atc ttc acc atc   100
Leu Thr Ile Ala Ala Ala Phe Phe Met Leu Ser Phe Ile Phe Thr Ile
 10                  15                  20                  25

tac cgc atc atc gtc ggg ccc aac tcc atc gat cgc cta ctc ggc ctg   148
Tyr Arg Ile Ile Val Gly Pro Asn Ser Ile Asp Arg Leu Leu Gly Leu
                 30                  35                  40

gac gga acc gtc tcc atg att caa tgc tcc atg gcc acc tac atc tgc   196
Asp Gly Thr Val Ser Met Ile Gln Cys Ser Met Ala Thr Tyr Ile Cys
             45                  50                  55

tgg aca ctc gac acc acc gtc acc aac ttc atg atg gtc atc gca ctc   244
Trp Thr Leu Asp Thr Thr Val Thr Asn Phe Met Met Val Ile Ala Leu
         60                  65                  70

tta gga ttc atc agc tct gta tcc gta gcc cgc ttc cgc aag agg gat   292
Leu Gly Phe Ile Ser Ser Val Ser Val Ala Arg Phe Arg Lys Arg Asp
     75                  80                  85

ggt gcc taaatgaccc tgcaactatt cac                                 321
Gly Ala
 90
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09e4a93 : 4e8e5e5d

<210> 352
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

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<400> 352
Met Asp Asn Thr Leu Tyr Thr Ala Gly Leu Thr Ile Ala Ala Ala Phe
  1               5                  10                  15

Phe Met Leu Ser Phe Ile Phe Thr Ile Tyr Arg Ile Ile Val Gly Pro
             20                  25                  30

Asn Ser Ile Asp Arg Leu Leu Gly Leu Asp Gly Thr Val Ser Met Ile
         35                  40                  45

Gln Cys Ser Met Ala Thr Tyr Ile Cys Trp Thr Leu Asp Thr Thr Val
     50                  55                  60

Thr Asn Phe Met Met Val Ile Ala Leu Leu Gly Phe Ile Ser Ser Val
 65                  70                  75                  80

Ser Val Ala Arg Phe Arg Lys Arg Asp Gly Ala
                 85                  90
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<210> 353
<211> 2472
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2449)
<223> RXS00453

<400> 353
tagtggggcg tgaaaaaata gctcatttaa gaggagaagc aaccccgtgg cgaaattgct 60

attcaggttg gggcgatggt cctataatcg caagtggatt gtg att tcg gca tgg 115
Val Ile Ser Ala Trp
1 5

cta ctt att ttg gcc att gtt ggt ggt ctg gcc ctg acg atg cag aag 163
Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala Leu Thr Met Gln Lys
10 15 20

ggg ttc agt aac tct ttc act att gaa gac acc cct tcg att gat gcc 211
Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr Pro Ser Ile Asp Ala
25 30 35

act gtt tct ctg gtt gaa aat ttc cct gat cag acg aac ccg gtg acg 259
Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln Thr Asn Pro Val Thr
40 45 50

gcc gcc gga gtt aac gtg gtt ttc caa tcc ccg gaa gga acc acg ctt 307
Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro Glu Gly Thr Thr Leu
55 60 65

gat gat cct cag atg atg act gcg atg gat gca gtc gtt gat tac att 355
Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala Val Val Asp Tyr Ile
70 75 80 85

gag gac aat ttg cct gat ttt ggt ggg gga gag cgc ttc ggc aat cct 403
Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu Arg Phe Gly Asn Pro
90 95 100

gtt gag gtg tct cct gcg ttg gaa gag atg gtc atc gag cag atg acc 451
Val Glu Val Ser Pro Ala Leu Glu Glu Met Val Ile Glu Gln Met Thr
105 110 115

agc atg ggg ctt cct gag gaa acc gct gca aag gat gct gcc aat ctg 499
Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys Asp Ala Ala Asn Leu
120 125 130

gcg gtg ttg agc gaa gac aaa acc att ggc tac acc tct ttc aac att 547
Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr Thr Ser Phe Asn Ile
135 140 145

gat gtt gag gcc gca gaa tat gtg gag caa aaa cac cgc gat gtg atc 595
Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys His Arg Asp Val Ile
150 155 160 165

aac gaa gcg atg caa atc ggt gaa gat tta ggt gtc cgg gtg gaa gcc 643
Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly Val Arg Val Glu Ala
170 175 180

ggt gga cct gct ttc ggt gat cca att cag att gaa acc acc agt gag 691
Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile Glu Thr Thr Ser Glu
185 190 195

atc atc ggt att ggc atc gcg ttc atc gtg ttg att ttc acc ttt ggt 739
Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu Ile Phe Thr Phe Gly
200 205 210

tct ttg att gct gca ggc ttg cct ttg att acc gcg gtg atc ggc gtg 787

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Ser Leu Ile Ala Ala Gly Leu Pro Leu Ile Thr Ala Val Ile Gly Val
    215                 220                 225

ggc att ggt gcg ctg gca att gtg ctg gcc acg gcg ttt act gat ctc   835
Gly Ile Gly Ala Leu Ala Ile Val Leu Ala Thr Ala Phe Thr Asp Leu
230                 235                 240                 245

aac aat gtg act cca gtg ctc gca gtg atg att ggc ctg gcc gtg ggc   883
Asn Asn Val Thr Pro Val Leu Ala Val Met Ile Gly Leu Ala Val Gly
                250                 255                 260

att gac tac gcg ctg ttt att ttg tct agg tac cgt gcg gag tat aag   931
Ile Asp Tyr Ala Leu Phe Ile Leu Ser Arg Tyr Arg Ala Glu Tyr Lys
            265                 270                 275

cgc atg cca cgt gcc gat gct gcc gga atg gcg gtg ggc aca gct ggt   979
Arg Met Pro Arg Ala Asp Ala Ala Gly Met Ala Val Gly Thr Ala Gly
        280                 285                 290

agt gcg gtg gtg ttt gct ggc gcg acg gtg att atc gcg ctg gta gcc   1027
Ser Ala Val Val Phe Ala Gly Ala Thr Val Ile Ile Ala Leu Val Ala
    295                 300                 305

ctc atc att gcg gat atc gga ttc ctc acg gcc atg ggt att tct gcg   1075
Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala Met Gly Ile Ser Ala
310                 315                 320                 325

gcg ttt acg gtg ttc gtg gct gtg ctc att gcg ttg acg ttt atc ccg   1123
Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala Leu Thr Phe Ile Pro
                330                 335                 340

gcg ctg ttg ggt gtg ttt ggt ggt cat gcg ttc aag ggc aag atc cct   1171
Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe Lys Gly Lys Ile Pro
            345                 350                 355

gga att ggt gga aac cca acg cca aag cag acg tgg gag caa gcg ctt   1219
Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr Trp Glu Gln Ala Leu
        360                 365                 370

aat cgt cgt tcc aag ggt cgc tca tgg gtc aag ctt gta cag aaa gca   1267
Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys Leu Val Gln Lys Ala
    375                 380                 385

ccg ggt ctt gtg gtg gca gtg gtg gtc ttg ggt ctt ggt gcc ttg acc   1315
Pro Gly Leu Val Val Ala Val Val Val Leu Gly Leu Gly Ala Leu Thr
390                 395                 400                 405

att cct gca atg aac ctg cag ttg tca ctg cct tct gac tcc acc tcc   1363
Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro Ser Asp Ser Thr Ser
                410                 415                 420

aat att gat acc act cag cgt cag tcg gct gat ttg atg gca gag ggc   1411
Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp Leu Met Ala Glu Gly
            425                 430                 435

ttt ggc gcg ggc gtt aat gcg ccg ttc ttg gtc atc gtc gat acg cat   1459
Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val Ile Val Asp Thr His
        440                 445                 450

gag gtc aat gct gat tcc acc gca ttg cag cca ctg att gag gca cag   1507
Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro Leu Ile Glu Ala Gln
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    455                 460                 465

gag cct gaa gag ggc gag ttc gat cgg gag cag gcg gct cgt ttt gct   1555
Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln Ala Ala Arg Phe Ala
470                 475                 480                 485

acc tat atg tat gtc acc cag acc tac aat tcc aac atc gat gtg aag   1603
Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser Asn Ile Asp Val Lys
                490                 495                 500

aat gcg cag atc atc agc gtc aat gat gat ttc act gcg gcg cag att   1651
Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe Thr Ala Ala Gln Ile
            505                 510                 515

ctc gtg act cca tac acc gga cct gcg gat aaa gag acc cct gag ttg   1699
Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys Glu Thr Pro Glu Leu
        520                 525                 530

atg cac gtg ctg cgt gcg cag gaa gct cag att gag gat gtt acg gga   1747
Met His Val Leu Arg Ala Gln Glu Ala Gln Ile Glu Asp Val Thr Gly
    535                 540                 545

act gaa ctg ggt acc act ggg ttt acg gcg gtt cag ttg gac att act   1795
Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val Gln Leu Asp Ile Thr
550                 555                 560                 565

gag cag ctg gaa gac gca atg ccg gtt tac ctc gct gtg gtt gtt ggt   1843
Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu Ala Val Val Val Gly
                570                 575                 580

ttg gct att ttc ctc ctc att ctg gtg ttc cgt tcc ctg ctt gtt ccg   1891
Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg Ser Leu Leu Val Pro
            585                 590                 595

ctg gtt gct ggc ctt ggc ttc ttg ttg tct gtg ggt gcg gcc ttc ggt   1939
Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val Gly Ala Ala Phe Gly
        600                 605                 610

gcg acg gtg ttg gtc tgg cag gag ggc ttc ggt ggc ttt gtg aac acc   1987
Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly Gly Phe Val Asn Thr
    615                 620                 625

cct ggt ccg ctg att tcc ttc atg ccg atc ttc ctc atc ggc gtg acc   2035
Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe Leu Ile Gly Val Thr
630                 635                 640                 645

ttc ggt ttg gcc atg gac tat cag gtg ttc ctt gtg act cgc atg cgc   2083
Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu Val Thr Arg Met Arg
                650                 655                 660

gag cac tac acc cac cac aat ggc aag gga cag cct ggt tcc aag tac   2131
Glu His Tyr Thr His His Asn Gly Lys Gly Gln Pro Gly Ser Lys Tyr
            665                 670                 675

acc ccg gtt gag cag tca gtg att gaa ggc ttc acg cag ggc tcc cgc   2179
Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe Thr Gln Gly Ser Arg
        680                 685                 690

gtg gtt aca gca gcg gca ctg atc atg att gcc gtg ttc gtg gcg ttt   2227
Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala Val Phe Val Ala Phe
    695                 700                 705
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att gat cag ccg ttg cca ttt att aag atc ttc ggt ttc gcg ttg ggt   2275
Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe Gly Phe Ala Leu Gly
710                 715                 720                 725

gcg ggc gtg ttt ttc gat gct ttc ttc att cgc atg ggt ctg gtc ccc   2323
Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg Met Gly Leu Val Pro
                730                 735                 740

gcg tcg atg ttc ctg atg ggc aag gcc acg tgg tgg atg cct aag tgg   2371
Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp Trp Met Pro Lys Trp
            745                 750                 755

ctg gat cga att ctg cca agt ttg gac att gaa ggc acc gca ctg gag   2419
Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu Gly Thr Ala Leu Glu
        760                 765                 770

aag gaa tgg gag gag aag cag gct gca cgt tagacttggc acctatgtca     2469
Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg
    775                 780

gat                                                               2472


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Leu Thr Met Gln Lys Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr
            20                  25                  30

Pro Ser Ile Asp Ala Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln
        35                  40                  45

Thr Asn Pro Val Thr Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro
    50                  55                  60

Glu Gly Thr Thr Leu Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala
65                  70                  75                  80

Val Val Asp Tyr Ile Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu
                85                  90                  95

Arg Phe Gly Asn Pro Val Glu Val Ser Pro Ala Leu Glu Glu Met Val
            100                 105                 110

Ile Glu Gln Met Thr Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys
        115                 120                 125

Asp Ala Ala Asn Leu Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr
    130                 135                 140

Thr Ser Phe Asn Ile Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys
145                 150                 155                 160

His Arg Asp Val Ile Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly
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165 170 175

Val Arg Val Glu Ala Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile
180 185 190

Glu Thr Thr Ser Glu Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu
195 200 205

Ile Phe Thr Phe Gly Ser Leu Ile Ala Ala Gly Leu Pro Leu Ile Thr
210 215 220

Ala Val Ile Gly Val Gly Ile Gly Ala Leu Ala Ile Val Leu Ala Thr
225 230 235 240

Ala Phe Thr Asp Leu Asn Asn Val Thr Pro Val Leu Ala Val Met Ile
245 250 255

Gly Leu Ala Val Gly Ile Asp Tyr Ala Leu Phe Ile Leu Ser Arg Tyr
260 265 270

Arg Ala Glu Tyr Lys Arg Met Pro Arg Ala Asp Ala Ala Gly Met Ala
275 280 285

Val Gly Thr Ala Gly Ser Ala Val Val Phe Ala Gly Ala Thr Val Ile
290 295 300

Ile Ala Leu Val Ala Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala
305 310 315 320

Met Gly Ile Ser Ala Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala
325 330 335

Leu Thr Phe Ile Pro Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe
340 345 350

Lys Gly Lys Ile Pro Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr
355 360 365

Trp Glu Gln Ala Leu Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys
370 375 380

Leu Val Gln Lys Ala Pro Gly Leu Val Val Ala Val Val Val Leu Gly
385 390 395 400

Leu Gly Ala Leu Thr Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro
405 410 415

Ser Asp Ser Thr Ser Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp
420 425 430

Leu Met Ala Glu Gly Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val
435 440 445

Ile Val Asp Thr His Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro
450 455 460

Leu Ile Glu Ala Gln Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln
465 470 475 480

Ala Ala Arg Phe Ala Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser
485 490 495

DUPLICATA - nouveau

Asn Ile Asp Val Lys Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe
500 505 510

Thr Ala Ala Gln Ile Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys
515 520 525

Glu Thr Pro Glu Leu Met His Val Leu Arg Ala Gln Glu Ala Gln Ile
530 535 540

Glu Asp Val Thr Gly Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val
545 550 555 560

Gln Leu Asp Ile Thr Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu
565 570 575

Ala Val Val Val Gly Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg
580 585 590

Ser Leu Leu Val Pro Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val
595 600 605

Gly Ala Ala Phe Gly Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly
610 615 620

Gly Phe Val Asn Thr Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe
625 630 635 640

Leu Ile Gly Val Thr Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu
645 650 655

Val Thr Arg Met Arg Glu His Tyr Thr His His Asn Gly Lys Gly Gln
660 665 670

Pro Gly Ser Lys Tyr Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe
675 680 685

Thr Gln Gly Ser Arg Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala
690 695 700

Val Phe Val Ala Phe Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe
705 710 715 720

Gly Phe Ala Leu Gly Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg
725 730 735

Met Gly Leu Val Pro Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp
740 745 750

Trp Met Pro Lys Trp Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu
755 760 765

Gly Thr Ala Leu Glu Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg
770 775 780

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<223> RXS00932

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aataaggtga tgtttcaacg attaggttac ggtaggggcc atg acg cca cag aaa 115
Met Thr Pro Gln Lys
1 5

ctt cac cgt ttt gca gcc ctt tta gaa atg ggt acc tgg acc ctg ctg 163
Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly Thr Trp Thr Leu Leu
10 15 20

atc atc ggc atg atc tta aaa tac agt gga gtg aca gac gcc gta acc 211
Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val Thr Asp Ala Val Thr
25 30 35

cct att gcc ggc ggt atc cac ggc ttt ggc ttc ctc tgt ttt gca gcc 259
Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe Leu Cys Phe Ala Ala
40 45 50

atc acc atc acc gtg tgg atc aat aat aag tgg aca ttc ccg cag ggt 307
Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp Thr Phe Pro Gln Gly
55 60 65

atc gca ggt ttg atc gtc tct gtt atc ccg tgg gct gca ttg cca ttt 355
Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp Ala Ala Leu Pro Phe
70 75 80 85

gca ttg tgg gca gac aag aag ggc ctc gtt gcc ggc gga tgg cgc ttt 403
Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala Gly Gly Trp Arg Phe
90 95 100

tca gat ccg tcc gaa aag cca cac act ttc ttt gac aag atc ttg gct 451
Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe Asp Lys Ile Leu Ala
105 110 115

caa ttg gtc agg cac cca atc cga tcc att tta att ctg ctg gtg att 499
Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu Ile Leu Leu Val Ile
120 125 130

atc gcc gtc gtc ttc tct atc ttg ctg gcg atg gga cca cct tat gat 547
Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met Gly Pro Pro Tyr Asp
135 140 145

cca gat gcc atc gca aac act gtg gat taaacaacag cctccttcac 594
Pro Asp Ala Ile Ala Asn Thr Val Asp
150 155

atg 597

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<213> Corynebacterium glutamicum

<400> 356

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Thr Trp Thr Leu Leu Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val
             20                  25                  30

Thr Asp Ala Val Thr Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe
         35                  40                  45

Leu Cys Phe Ala Ala Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp
     50                  55                  60

Thr Phe Pro Gln Gly Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp
 65                  70                  75                  80

Ala Ala Leu Pro Phe Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala
                 85                  90                  95

Gly Gly Trp Arg Phe Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe
            100                 105                 110

Asp Lys Ile Leu Ala Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu
        115                 120                 125

Ile Leu Leu Val Ile Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met
    130                 135                 140

Gly Pro Pro Tyr Asp Pro Asp Ala Ile Ala Asn Thr Val Asp
145                 150                 155


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                                          Met Ser Thr Ser Ile
                                            1               5

aca aca gag aac aag aag aaa tct ggt cct cct cgc ttg atg aga atc   163
Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro Arg Leu Met Arg Ile
                10                  15                  20

ttt ctg ccc gcc ttg cta att tta gtt tgg ctt gta gga gct gga gtc   211
Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu Val Gly Ala Gly Val
            25                  30                  35

ggc ggt cct tat ttt ggc aag gtt agt gag gtc tcc tcc aac agc cag   259
Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val Ser Ser Asn Ser Gln
        40                  45                  50

acc aca tat ctg cca gaa tct gcc gat gcc act caa gta cag gaa cag   307
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Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr Gln Val Gln Glu Gln
     55                  60                  65

ttg gga gat ttt act gat tct gaa tcc atc cca gcc att gtc gta atg   355
Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro Ala Ile Val Val Met
 70                  75                  80                  85

gtc agc gat gaa ccc tta aca cag caa gac atc aca caa ctc aat gaa   403
Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile Thr Gln Leu Asn Glu
                 90                  95                 100

gtt gtt gct ggg ctt tca gaa tta gac ata gtt tcc gat gaa gtc tcc   451
Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val Ser Asp Glu Val Ser
            105                 110                 115

cct gct att cca tcc gag gac ggc aga gct gtc caa gtg ttt gtc ccc   499
Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val Gln Val Phe Val Pro
        120                 125                 130

ctc aat cca tca gcg gag ctg acg gaa agc gtc gag aag ctc tct gag   547
Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val Glu Lys Leu Ser Glu
    135                 140                 145

acc ttg acc cag caa acg ccg gac tat gtg agc acc tat gtg acc gga   595
Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser Thr Tyr Val Thr Gly
150                 155                 160                 165

ccg gct ggg ttt acc gct gat ctc agc gca gct ttc gcg ggt att gat   643
Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala Phe Ala Gly Ile Asp
                170                 175                 180

ggg cta ctc cta gca gtc gcc ttg gct gcc gtc ctt gtc att ctt gtc   691
Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val Leu Val Ile Leu Val
            185                 190                 195

atc gtc tat cgc tcc ttc att ctg ccc atc gcc gtg ctt gcc acc agt   739
Ile Val Tyr Arg Ser Phe Ile Leu Pro Ile Ala Val Leu Ala Thr Ser
        200                 205                 210

ttg ttt gcg ctg act gta gct cta ttg gtg gtg tgg tgg cta gct aag   787
Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val Trp Trp Leu Ala Lys
    215                 220                 225

tgg gac atc ctg ctg ctt tcg ggt cag act caa ggc atc ctc ttc att   835
Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln Gly Ile Leu Phe Ile
230                 235                 240                 245

ctg gtc att ggc gcc gcc acc gac tac tca ttg cta tac gtt gct cgt   883
Leu Val Ile Gly Ala Ala Thr Asp Tyr Ser Leu Leu Tyr Val Ala Arg
                250                 255                 260

ttc cgt gaa gag tta cgc gtt caa caa gat aaa ggg ata gcc aca ggg   931
Phe Arg Glu Glu Leu Arg Val Gln Gln Asp Lys Gly Ile Ala Thr Gly
            265                 270                 275

aaa gcc atc cgg gca tcg gtg gaa ccc att ctt gcc tcg ggc agc act   979
Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu Ala Ser Gly Ser Thr
        280                 285                 290

gtt att gcg ggc ctc ctt tgt ttg cta ttt agt gat ttg aaa tct aac  1027
Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser Asp Leu Lys Ser Asn
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    295                 300                 305

tcc acg cta ggt cca gta gct tcg gtg ggc att att ttt gca atg ctt   1075
Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile Ile Phe Ala Met Leu
310                 315                 320                 325

tct gct ctt act ctg cta cca gcc ctg ctg ttt gta ttc ggt cgg gtg   1123
Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe Val Phe Gly Arg Val
                330                 335                 340

gcc ttt tgg ccc aag cga cca aaa tac gaa cct gaa aaa gcc cgt gcg   1171
Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro Glu Lys Ala Arg Ala
            345                 350                 355

aaa aac gac atc ccc gcc agc ggg atc tgg tca aaa gtg gct gat tta   1219
Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser Lys Val Ala Asp Leu
        360                 365                 370

gtg gag cag cat cct cgt gca atc tgg gta tct aca ctt att gtg ctt   1267
Val Glu Gln His Pro Arg Ala Ile Trp Val Ser Thr Leu Ile Val Leu
    375                 380                 385

ctc ttg ggt gcg gct ttc gtt ccc aca cta aaa gcg gac ggt gtg tcc   1315
Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys Ala Asp Gly Val Ser
390                 395                 400                 405

caa tcc gac cta gtt ctg ggt tcc tct gaa gca cgt gat ggc cag cag   1363
Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala Arg Asp Gly Gln Gln
                410                 415                 420

gct tta ggc gaa cac ttc ccc ggt gga tcc ggc agt cct gct tat att   1411
Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly Ser Pro Ala Tyr Ile
            425                 430                 435

atc gtt gat gaa aca cag gca gca cag gct gct gac gta gtc ctt aac   1459
Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala Asp Val Val Leu Asn
        440                 445                 450

aac gac aat ttc gag act gta act gta act agt gct gac tcc ccc tct   1507
Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser Ala Asp Ser Pro Ser
    455                 460                 465

ggc tca gcc cca atc acc gct gac ggt att gtg ccg tta ggt tct ggt   1555
Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val Pro Leu Gly Ser Gly
470                 475                 480                 485

aca gct cca ggc ccg gta gtt gta gaa ggg caa gtc ctt tta caa gca   1603
Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln Val Leu Leu Gln Ala
                490                 495                 500

aca ctt gtc gaa gca cca gat tcc gaa gaa gct caa aaa gct att cgc   1651
Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala Gln Lys Ala Ile Arg
            505                 510                 515

agt atc cgc caa act ttt gca gat gaa aat ata tca gcg gta gta ggc   1699
Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile Ser Ala Val Val Gly
        520                 525                 530

ggt gtc act gca act tcc gta gac act aac gat gcc tcc atc cat gac   1747
Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp Ala Ser Ile His Asp
    535                 540                 545
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cgc aac ctg atc atc cca att gta ttg ctg gtc att ttg gtt att ctc   1795
Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val Ile Leu Val Ile Leu
550                 555                 560                 565

atg ctg ttg ctg cgg tct att gtc gca cca ctc ctg cta gta gtc acc   1843
Met Leu Leu Leu Arg Ser Ile Val Ala Pro Leu Leu Leu Val Val Thr
                570                 575                 580

acc gtg gtg tct ttt gct act gct tta ggc gtg gct gct tta ctt ttc   1891
Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val Ala Ala Leu Leu Phe
            585                 590                 595

aat cac gtt ttc agt ttc cca gga gca gac ccc gca gta cct ctc tac   1939
Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro Ala Val Pro Leu Tyr
        600                 605                 610

gga ttt gta ttt tta gta gcc ttg ggc atc gac tac aac att ttc tta   1987
Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp Tyr Asn Ile Phe Leu
    615                 620                 625

gtc acc cga atc cgt gaa gaa acc aaa acc cac ggc aca aga ctt gga   2035
Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His Gly Thr Arg Leu Gly
630                 635                 640                 645

att ctt cga ggc ctg aca gta acc ggc gga gta att acc tca gct gga   2083
Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val Ile Thr Ser Ala Gly
                650                 655                 660

gta gtt ctc gcc gca acg ttc gca gca ctc tat gtc atc cca att cta   2131
Val Val Leu Ala Ala Thr Phe Ala Ala Leu Tyr Val Ile Pro Ile Leu
            665                 670                 675

ttc ctg gca caa att gcc ttc att gtc gct ttt gga gtt ctt att gat   2179
Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe Gly Val Leu Ile Asp
        680                 685                 690

acc ctg ctc gtt cgc gcc ttc ttg gtg cct gct ttg ttc tac gac atc   2227
Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala Leu Phe Tyr Asp Ile
    695                 700                 705

gga ccg aaa atc tgg tgg ccg tca aaa ttg tcc aat cag aaa tac cag   2275
Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser Asn Gln Lys Tyr Gln
710                 715                 720                 725

aag cag cct cag cta tgacacacca aaattcgcct ctc                     2313
Lys Gln Pro Gln Leu
                730
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<210> 358
<211> 730
<212> PRT
<213> Corynebacterium glutamicum

<400> 358

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Met Ser Thr Ser Ile Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro
  1               5                  10                  15

Arg Leu Met Arg Ile Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu
             20                  25                  30
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Val Gly Ala Gly Val Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val
35 40 45

Ser Ser Asn Ser Gln Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr
50 55 60

Gln Val Gln Glu Gln Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro
65 70 75 80

Ala Ile Val Val Met Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile
85 90 95

Thr Gln Leu Asn Glu Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val
100 105 110

Ser Asp Glu Val Ser Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val
115 120 125

Gln Val Phe Val Pro Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val
130 135 140

Glu Lys Leu Ser Glu Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser
145 150 155 160

Thr Tyr Val Thr Gly Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala
165 170 175

Phe Ala Gly Ile Asp Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val
180 185 190

Leu Val Ile Leu Val Ile Val Tyr Arg Ser Phe Ile Leu Pro Ile Ala
195 200 205

Val Leu Ala Thr Ser Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val
210 215 220

Trp Trp Leu Ala Lys Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln
225 230 235 240

Gly Ile Leu Phe Ile Leu Val Ile Gly Ala Ala Thr Asp Tyr Ser Leu
245 250 255

Leu Tyr Val Ala Arg Phe Arg Glu Glu Leu Arg Val Gln Gln Asp Lys
260 265 270

Gly Ile Ala Thr Gly Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu
275 280 285

Ala Ser Gly Ser Thr Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser
290 295 300

Asp Leu Lys Ser Asn Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile
305 310 315 320

Ile Phe Ala Met Leu Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe
325 330 335

Val Phe Gly Arg Val Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro
340 345 350

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Glu Lys Ala Arg Ala Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser
355 360 365

Lys Val Ala Asp Leu Val Glu Gln His Pro Arg Ala Ile Trp Val Ser
370 375 380

Thr Leu Ile Val Leu Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys
385 390 395 400

Ala Asp Gly Val Ser Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala
405 410 415

Arg Asp Gly Gln Gln Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly
420 425 430

Ser Pro Ala Tyr Ile Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala
435 440 445

Asp Val Val Leu Asn Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser
450 455 460

Ala Asp Ser Pro Ser Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val
465 470 475 480

Pro Leu Gly Ser Gly Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln
485 490 495

Val Leu Leu Gln Ala Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala
500 505 510

Gln Lys Ala Ile Arg Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile
515 520 525

Ser Ala Val Val Gly Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp
530 535 540

Ala Ser Ile His Asp Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val
545 550 555 560

Ile Leu Val Ile Leu Met Leu Leu Leu Arg Ser Ile Val Ala Pro Leu
565 570 575

Leu Leu Val Val Thr Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val
580 585 590

Ala Ala Leu Leu Phe Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro
595 600 605

Ala Val Pro Leu Tyr Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp
610 615 620

Tyr Asn Ile Phe Leu Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His
625 630 635 640

Gly Thr Arg Leu Gly Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val
645 650 655

Ile Thr Ser Ala Gly Val Val Leu Ala Ala Thr Phe Ala Ala Leu Tyr
660 665 670

Val Ile Pro Ile Leu Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe

675 680 685

Gly Val Leu Ile Asp Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala
690 695 700

Leu Phe Tyr Asp Ile Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser
705 710 715 720

Asn Gln Lys Tyr Gln Lys Gln Pro Gln Leu
725 730

<210> 359
<211> 393
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> RXS02586

<400> 359
ttctctgaga tcgtcatgat gaagtacatc gcgttcggca tgatcgcagc gctgattctg 60

gatgccacca tcatccgcat gctgcttgtc ccccgccgtg atg cac ctg ctt cgc 115
Met His Leu Leu Arg
1 5

gac gac aac tgg tgg gca ccc ggc ttc gtt aaa aag gcc tac acc gtc 163
Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys Lys Ala Tyr Thr Val
10 15 20

atg ggt cac ggc tct gag gtg gag gaa gca cct cgc cca acc acc cgt 211
Met Gly His Gly Ser Glu Val Glu Glu Ala Pro Arg Pro Thr Thr Arg
25 30 35

cgc ctc aac gac gat gag gaa gtc acc gtg cat gaa gca gtt gtc gct 259
Arg Leu Asn Asp Asp Glu Glu Val Thr Val His Glu Ala Val Val Ala
40 45 50

ggc gat acc gtg gca tct cgc ggt ggt ttg agc acg cag gaa aac cgt 307
Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser Thr Gln Glu Asn Arg
55 60 65

gat ctg gtg tcc ttc gtg gaa ctt aag gct cgt ttg gaa aag cgc agg 355
Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg Leu Glu Lys Arg Arg
70 75 80 85

ctt gag gat cta gat taaatctatg cgaggatttt tca 393
Leu Glu Asp Leu Asp
90

<210> 360
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 360
Met His Leu Leu Arg Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys

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  1               5                  10                  15

Lys Ala Tyr Thr Val Met Gly His Gly Ser Glu Val Glu Glu Ala Pro
            20                  25                  30

Arg Pro Thr Thr Arg Arg Leu Asn Asp Asp Glu Glu Val Thr Val His
        35                  40                  45

Glu Ala Val Val Ala Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser
    50                  55                  60

Thr Gln Glu Asn Arg Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg
65                  70                  75                  80

Leu Glu Lys Arg Arg Leu Glu Asp Leu Asp
                85                  90
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<210> 361
<211> 2214
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2191)
<223> RXS02587

<400> 361

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agcctggata acctgccaga cggtggcgca tggctgcagc cgttccgccc tctgactgcc 60

ttgttatcca accgccacaa ttcccaggag taatccaccc gtg ttt tct aaa tgg   115
                                            Val Phe Ser Lys Trp
                                              1               5

ggc cac ttt gct tac aga ttt agg cgc att gtt ccg tta gtc gtc atc   163
Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val Pro Leu Val Val Ile
                  10                  15                  20

gcc gcg att ttg gct ttg ttt gtc att ttc ggc acc aag ctg ggc gac   211
Ala Ala Ile Leu Ala Leu Phe Val Ile Phe Gly Thr Lys Leu Gly Asp
              25                  30                  35

cgc atg agc cag gaa gga tgg gat gat cct ggt tct tcc tcg acc gct   259
Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly Ser Ser Ser Thr Ala
          40                  45                  50

gcg gcg cgc atc gag ttg gag acc ttt ggg cgt gac aat gac ggc gat   307
Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg Asp Asn Asp Gly Asp
      55                  60                  65

gtc gtg ttg ctg ttt act gcg cct gaa ggc act tct ttc gat gat gca   355
Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr Ser Phe Asp Asp Ala
 70                  75                  80                  85

gag gtg ttc tcc agc atc tct ggc tac tta gat ggg cta atc gag aac   403
Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp Gly Leu Ile Glu Asn
                  90                  95                 100

aac cct gat gaa gtc agc cac atc aac agc tac ttt gac act cgt aat   451
Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr Phe Asp Thr Arg Asn
```

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                105                 110                 115

caa aat ctc ctc agc aaa gac ggc acc caa acc ttt gca gct ctc ggg   499
Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr Phe Ala Ala Leu Gly
        120                 125                 130

ctc aaa ggt gac ggc gag caa acg ctg aag gac ttc cgg gag att gaa   547
Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp Phe Arg Glu Ile Glu
    135                 140                 145

gat cag ctc cat ccg gac aac ctt gcc ggt ggc gtc acc act gag gtc   595
Asp Gln Leu His Pro Asp Asn Leu Ala Gly Gly Val Thr Thr Glu Val
150                 155                 160                 165

gcg ggt gcc acc gct gta gcc gac gca ctc gat gag ggc atg gct ggc   643
Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp Glu Gly Met Ala Gly
                170                 175                 180

gat att tca cgc gcc gaa gtt ttt gcg ctg cct ttc gtg gct atc ttg   691
Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro Phe Val Ala Ile Leu
            185                 190                 195

ctg ctc atc gtg ttt ggc tca gtt gtt gcc gcg gcg atg cca ttg atc   739
Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala Ala Met Pro Leu Ile
        200                 205                 210

gtg ggc att ttg tcc atc ttg ggt tcg ctg ggc atc ttg gca att ttg   787
Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly Ile Leu Ala Ile Leu
    215                 220                 225

gct gga ttc ttc cag gtc aac gta ttt gca caa tct gtt gtg acc ctt   835
Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln Ser Val Val Thr Leu
230                 235                 240                 245

ctg ggc ttg ggt ctt gcc att gac tat ggc tta ttc atg gtc tct cgt   883
Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu Phe Met Val Ser Arg
                250                 255                 260

ttc cgt gag gaa atg gat aag ggc acc ccg gtt gaa cag gct gtt gcc   931
Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val Glu Gln Ala Val Ala
            265                 270                 275

acc act acg gcg acc gcg ggt aag act gtg gtg ttc tct gca gcg atg   979
Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val Phe Ser Ala Ala Met
        280                 285                 290

gtg gct gtg gcg ctg tcc ggg ttg ttt gtt ttc cca cag gct ttc ttg  1027
Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe Pro Gln Ala Phe Leu
    295                 300                 305

aag tcg gtg gca ttc ggt gcg att tcc gcg gtt ggc ctt gct gct ttg  1075
Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val Gly Leu Ala Ala Leu
310                 315                 320                 325

atg tcg gtg acg gtg ttg ccg tcg ctg ttc agc atg ttg ggt aag aat  1123
Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser Met Leu Gly Lys Asn
                330                 335                 340

atc gat aag tgg agt ttg cgt cgc act gct cga aca gcg cgc cgt ttg  1171
Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg Thr Ala Arg Arg Leu
            345                 350                 355
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09536365.030905

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gaa gac acc att tgg tac cgc gtg ccg gca tgg gca atg cgc cat gcc   1219
Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp Ala Met Arg His Ala
        360                 365                 370

aag gca gtg acc gtg ggc gtc gta ttg ctc ttg ctt gct ctt aca gtg   1267
Lys Ala Val Thr Val Gly Val Val Leu Leu Leu Leu Ala Leu Thr Val
    375                 380                 385

ccg ttg acg ggc gtg aaa ttc ggc ggc atc aat gaa acg tat ctg cca   1315
Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn Glu Thr Tyr Leu Pro
390                 395                 400                 405

cca gct aac gac acc cgc gtc gcc caa gag cgt ttc gac gag gcg ttt   1363
Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg Phe Asp Glu Ala Phe
                410                 415                 420

ccc gcc ttc cgc acc gag ccg gtc aag ctt gtg gtc acc ggg gcg gac   1411
Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val Val Thr Gly Ala Asp
            425                 430                 435

aac aac cag ctg atc gat atc tat gtt cag gcc aac gaa gtt gag gga   1459
Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala Asn Glu Val Glu Gly
        440                 445                 450

ctg aca gat cgt ttc acc gca ggt gcg act acc gat gat ggc acc acg   1507
Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr Asp Asp Gly Thr Thr
    455                 460                 465

gtg ttg tct act ggt att cag gat cgt tcc ctc aat gag cag gta gtg   1555
Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu Asn Glu Gln Val Val
470                 475                 480                 485

gag cag ctt cgc gct att tcc gtc cct gag ggc gtt gag gtg cag atc   1603
Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly Val Glu Val Gln Ile
                490                 495                 500

ggt ggc act cca gcc atg gag atc gaa tcc att gag gcg ctc ttt gaa   1651
Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile Glu Ala Leu Phe Glu
            505                 510                 515

aag ctc ctc tgg atg gct ctc tac att gtg ctg gcc act ttc atc ctc   1699
Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu Ala Thr Phe Ile Leu
        520                 525                 530

atg gca ttg gta ttt ggt tcg gtg att ttg ccg gcg aag gcc atc atc   1747
Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro Ala Lys Ala Ile Ile
    535                 540                 545

atg acc att ctg ggt atg ggt gcc acc ttg ggt att ctc acc ttg atg   1795
Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly Ile Leu Thr Leu Met
550                 555                 560                 565

ttc gtc gat ggc gtg ggt gcc agc gca ttg aac ttc tcc cct ggc cca   1843
Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn Phe Ser Pro Gly Pro
                570                 575                 580

ctg atg agt cca gtg ctg gtg ctg atc atg gct att att tac gga ctt   1891
Leu Met Ser Pro Val Leu Val Leu Ile Met Ala Ile Ile Tyr Gly Leu
            585                 590                 595
```

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tcc acc gac tat gag gtg ttc ctg gta tct cgc atg gtg gag gcc cgc   1939
Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg Met Val Glu Ala Arg
        600                 605                 610

gat aaa ggc gaa tcc acc gac gac gcc atc aga tac ggc act gca cac   1987
Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg Tyr Gly Thr Ala His
    615                 620                 625

acc gga tct atc atc acc gcg gcc gca ctg atc atg att gtg gtc tgt   2035
Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile Met Ile Val Val Cys
630                 635                 640                 645

gga gcg ttt ggt ttc tct gag atc gtc atg atg aag tac atc gcg ttc   2083
Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met Lys Tyr Ile Ala Phe
                650                 655                 660

ggc atg atc gca gcg ctg att ctg gat gcc acc atc atc cgc atg ctg   2131
Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr Ile Ile Arg Met Leu
            665                 670                 675

ctt gtc ccc cgc cgt gat gca cct gct tcg cga cga caa ctg gtg ggc   2179
Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg Arg Gln Leu Val Gly
        680                 685                 690

acc cgg ctt cgt taaaaaggcc tacaccgtca tgg                        2214
Thr Arg Leu Arg
    695
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DE102005028936.9

<210> 362
<211> 697
<212> PRT
<213> Corynebacterium glutamicum

<400> 362

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Val Phe Ser Lys Trp Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val
  1               5                  10                  15

Pro Leu Val Val Ile Ala Ala Ile Leu Ala Leu Phe Val Ile Phe Gly
            20                  25                  30

Thr Lys Leu Gly Asp Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly
        35                  40                  45

Ser Ser Ser Thr Ala Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg
    50                  55                  60

Asp Asn Asp Gly Asp Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr
65                  70                  75                  80

Ser Phe Asp Asp Ala Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp
                85                  90                  95

Gly Leu Ile Glu Asn Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr
            100                 105                 110

Phe Asp Thr Arg Asn Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr
        115                 120                 125

Phe Ala Ala Leu Gly Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp
    130                 135                 140
```

Phe Arg Glu Ile Glu Asp Gln Leu His Pro Asp Asn Leu Ala Gly Gly
145 150 155 160

Val Thr Thr Glu Val Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp
165 170 175

Glu Gly Met Ala Gly Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro
180 185 190

Phe Val Ala Ile Leu Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala
195 200 205

Ala Met Pro Leu Ile Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly
210 215 220

Ile Leu Ala Ile Leu Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln
225 230 235 240

Ser Val Val Thr Leu Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu
245 250 255

Phe Met Val Ser Arg Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val
260 265 270

Glu Gln Ala Val Ala Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val
275 280 285

Phe Ser Ala Ala Met Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe
290 295 300

Pro Gln Ala Phe Leu Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val
305 310 315 320

Gly Leu Ala Ala Leu Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser
325 330 335

Met Leu Gly Lys Asn Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg
340 345 350

Thr Ala Arg Arg Leu Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp
355 360 365

Ala Met Arg His Ala Lys Ala Val Thr Val Gly Val Val Leu Leu Leu
370 375 380

Leu Ala Leu Thr Val Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn
385 390 395 400

Glu Thr Tyr Leu Pro Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg
405 410 415

Phe Asp Glu Ala Phe Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val
420 425 430

Val Thr Gly Ala Asp Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala
435 440 445

Asn Glu Val Glu Gly Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr
450 455 460

Asp Asp Gly Thr Thr Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu
465 470 475 480

Asn Glu Gln Val Val Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly
485 490 495

Val Glu Val Gln Ile Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile
500 505 510

Glu Ala Leu Phe Glu Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu
515 520 525

Ala Thr Phe Ile Leu Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro
530 535 540

Ala Lys Ala Ile Ile Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly
545 550 555 560

Ile Leu Thr Leu Met Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn
565 570 575

Phe Ser Pro Gly Pro Leu Met Ser Pro Val Leu Val Leu Ile Met Ala
580 585 590

Ile Ile Tyr Gly Leu Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg
595 600 605

Met Val Glu Ala Arg Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg
610 615 620

Tyr Gly Thr Ala His Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile
625 630 635 640

Met Ile Val Val Cys Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met
645 650 655

Lys Tyr Ile Ala Phe Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr
660 665 670

Ile Ile Arg Met Leu Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg
675 680 685

Arg Gln Leu Val Gly Thr Arg Leu Arg
690 695

<210> 363
<211> 729
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(706)
<223> RXS03042

<400> 363
atgacaccgg cgcgacgtat ggcattactg gcgtacccca atttacgatg acatctctgc 60

tcgcctcggc gacgtcctgg ttccttacgt tctgatcgtt ttg gtt cta gcg ttc 115
Leu Val Leu Ala Phe

DO3S3450 <4209> 20050930

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                                                    1               5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg   163
Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
                10                  15                  20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg   211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
            25                  30                  35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca   259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
        40                  45                  50

ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg   307
Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu
    55                  60                  65

gcc atg gat tac cag atc ttc ctc gtt act cgt atg cgt gag ggc ttc   355
Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe
70                  75                  80                  85

acc aag ggc aag act gcg ggc aac gca acg tcg aat ggt ttc aag cac   403
Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His
                90                  95                  100

ggt gcc cgc gtg gtc act gct gcg gcg ctg atc atg gtg tct gtg ttc   451
Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe
            105                 110                 115

gcg gca ttc ata gcg cag gac atg gcg ttt att aag acc atg ggc ttt   499
Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile Lys Thr Met Gly Phe
        120                 125                 130

gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg   547
Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met
    135                 140                 145

att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta   595
Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu
150                 155                 160                 165

cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag   643
Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu
                170                 175                 180

ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat   691
Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn
            185                 190                 195

gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta                    729
Val Gly Val Gly Ala
        200
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<210> 364
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 364

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Leu Val Leu Ala Phe Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp
  1               5                  10                  15

Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
             20                  25                  30

Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
         35                  40                  45

Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly
     50                  55                  60

Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg
 65                  70                  75                  80

Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser
                 85                  90                  95

Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile
            100                 105                 110

Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile
        115                 120                 125

Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe
    130                 135                 140

Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp
145                 150                 155                 160

Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val
                165                 170                 175

Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu
            180                 185                 190

Glu Leu Lys Glu Asn Val Gly Val Gly Ala
        195                 200
```

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<210> 365
<211> 826
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> RXS03075

<400> 365
tgtgcaaaat tgcattcagg ctgaaaaatt cctaaaggga ctccgtccga ataattggaa 60

agcccagaag aacagtcaac tcctagatta aaggataatc gtg gcg aaa ttc ctg 115
                                              Val Ala Lys Phe Leu
                                                1               5

tat aag tta ggc tcc acg gcc tat caa aag aaa tgg ccg ttt ctt gcg 163
Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys Trp Pro Phe Leu Ala
            10                  15                  20

```
gtc tgg ctc gtg att ctc ata ggt atc acg acg ctg gcg ggg ctg tat   211
Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr Leu Ala Gly Leu Tyr
            25                  30                  35

gcc aag cca acg tcg agt agc ttc tct atc cct ggt ctt gat tct gtc   259
Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val
        40                  45                  50

acg acc atg gag aag atg cag gag cgt ttc cct ggt tcg gat gat gca   307
Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala
    55                  60                  65

aca tcg gct ccc act ggt tct gtc gtc att cag gca ccg gaa ggc aag   355
Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln Ala Pro Glu Gly Lys
70                  75                  80                  85

acc ctc act gat cct gag gtt ggg gct gaa gta aac cag atg ctt gat   403
Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp
                90                  95                  100

gag gtt cgg gcg act ggt gtg ctg aag gat gct gat tcc gtt gtg gat   451
Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala Asp Ser Val Val Asp
            105                 110                 115

cct gtg ttg gct gcg cag ggt gtg gct gct cag atg acc cca gcc ctg   499
Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln Met Thr Pro Ala Leu
        120                 125                 130

gag gct cag ggt gta cct gcg gag aag atc gcc gca gat att gag tcg   547
Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala Ala Asp Ile Glu Ser
    135                 140                 145

att agt cca ctg agt gca gat gag act acc ggc atc atc tcg atg act   595
Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly Ile Ile Ser Met Thr
150                 155                 160                 165

ttt gat gca gat tct gcc atg gat ata tcc gca gag gat cgt gag aag   643
Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys
                170                 175                 180

gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc   691
Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val
            185                 190                 195

tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc   739
Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr Ser Leu Asp Met Thr
        200                 205                 210

tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc   787
Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr
    215                 220                 225

ttc ggt tcg ttc atc gct gcc ggt atg ccg ctg atc tct               826
Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser
230                 235                 240
```

<210> 366
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 366

```
Val Ala Lys Phe Leu Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys
  1               5                  10                  15

Trp Pro Phe Leu Ala Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr
             20                  25                  30

Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro
         35                  40                  45

Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro
     50                  55                  60

Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
 65                  70                  75                  80

Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
                 85                  90                  95

Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
            100                 105                 110

Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
        115                 120                 125

Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
    130                 135                 140

Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
145                 150                 155                 160

Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala
                165                 170                 175

Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
            180                 185                 190

Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr
        195                 200                 205

Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
    210                 215                 220

Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu
225                 230                 235                 240

Ile Ser
```

<210> 367
<211> 983
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(960)
<223> RXS03124

<400> 367

```
atg act cct acc ctg gcg tcg atg att ggt ctg gct gtc ggt atc gac   48
Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
  1               5                  10                  15

tac gcg cta ttt atc gtg tcc cgt ttc cgc aat gag ttg att tct cag   96
Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
            20                  25                  30

act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc   144
Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
        35                  40                  45

acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc   192
Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
    50                  55                  60

act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct   240
Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
65                  70                  75                  80

ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc   288
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
                85                  90                  95

att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc   336
Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
            100                 105                 110

ttc ctc cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca   384
Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
        115                 120                 125

cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg   432
Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
    130                 135                 140

atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac   480
Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
145                 150                 155                 160

ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc   528
Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
                165                 170                 175

aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc   576
Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
            180                 185                 190

gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc   624
Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
        195                 200                 205

cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag   672
Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
    210                 215                 220

gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac   720
Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
225                 230                 235                 240
```

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```
act gat ggt gtg aag aat gct cag atc act cag acc acg gag aat ttc   768
Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe
                245                 250                 255

gat acc gcg cag atc ctg tta ccc cag aat ttg atg cga tcg atg agc   816
Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser
            260                 265                 270

gca cct ctg aga ctc tcg caa ctc ttc gtg cag atg ctg aga cct tcg   864
Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
        275                 280                 285

ctg atg aca ccg gcg cga cgt atg gca tta ctg gcg tca ccc caa ttt   912
Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
    290                 295                 300

acg atg aca tct ctg ctc gcc tcg gcg acg tcc tgg ttc ctt acg ttc   960
Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
305                 310                 315                 320

tgatcgtttt ggttctagcg ttc                                        983
```

<210> 368
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

<400> 368

```
Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
  1               5                  10                  15

Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
             20                  25                  30

Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
         35                  40                  45

Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
     50                  55                  60

Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
 65                  70                  75                  80

Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
                 85                  90                  95

Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
            100                 105                 110

Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
        115                 120                 125

Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
    130                 135                 140

Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
145                 150                 155                 160

Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
                165                 170                 175
```

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```
Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
            180                 185                 190

Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
        195                 200                 205

Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
    210                 215                 220

Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
225                 230                 235                 240

Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe
                245                 250                 255

Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser
            260                 265                 270

Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
        275                 280                 285

Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
    290                 295                 300

Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
305                 310                 315                 320
```

09/12/2005 09:56:05

<210> 369
<211> 271
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> RXS03125

<400> 369

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tgacaccggc gcgacgtatg gcattactgg cgtcacccca atttacgatg acatctctgc 60

tcgcctcggc gacgtcctgg ttccttacgt tctgatcgtt ttg gtt cta gcg ttc   115
                                              Leu Val Leu Ala Phe
                                                1               5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg   163
Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
                10                  15                  20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg   211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
            25                  30                  35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca   259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
        40                  45                  50
```

```
ctg ctg tgc ttc                                                    271
Leu Leu Cys Phe
     55
```

<210> 370
<211> 57
<212> PRT
<213> Corynebacterium glutamicum

<400> 370

```
Leu Val Leu Ala Phe Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp
  1               5                  10                  15

Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
             20                  25                  30

Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
         35                  40                  45

Asp Asp Pro Gln Pro Leu Leu Cys Phe
     50                  55
```

<210> 371
<211> 576
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXA00596

<400> 371

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ccgccaccga cggcctcttg aacaccgatg cataccaaca ggctgtgctc ggtgaaaatg 60

ccatcggagt gccaagccct agctaccagg gaggaaacta atg ctt aac gcc ctg   115
                                               Met Leu Asn Ala Leu
                                                 1               5

aaa ttc atc cca tgg ctg atc ggc cag att ttc ctc tct ggc ttc agc   163
Lys Phe Ile Pro Trp Leu Ile Gly Gln Ile Phe Leu Ser Gly Phe Ser
                 10                  15                  20

gtg atc acc gct gcg gta aaa aag gac acc ggc ttc aac ccc gtt gtt   211
Val Ile Thr Ala Ala Val Lys Lys Asp Thr Gly Phe Asn Pro Val Val
             25                  30                  35

atc cgc tac cca ctt cga gtg acc acg gac ttc cag atc gca gcc ctg   259
Ile Arg Tyr Pro Leu Arg Val Thr Thr Asp Phe Gln Ile Ala Ala Leu
         40                  45                  50

tca acg tgc atc acc gcg act cct tcc acc ctg tcc ctt ggc cta cgc   307
Ser Thr Cys Ile Thr Ala Thr Pro Ser Thr Leu Ser Leu Gly Leu Arg
     55                  60                  65

gaa ccc cgc aag ccc ggc gac ccc acc att ttg ctg atc caa gca gtg   355
Glu Pro Arg Lys Pro Gly Asp Pro Thr Ile Leu Leu Ile Gln Ala Val
 70                  75                  80                  85
```

```
ttt ggt tcc gat cca gta gaa gtt ttt gaa tcc atc gcc gat atg gaa   403
Phe Gly Ser Asp Pro Val Glu Val Phe Glu Ser Ile Ala Asp Met Glu
                 90                  95                 100

caa cgc ctc gtc cct tcg gtc gct tca att gac cac ggc gtc cca ggc   451
Gln Arg Leu Val Pro Ser Val Ala Ser Ile Asp His Gly Val Pro Gly
            105                 110                 115

caa ggc cct tac aag gag atc cgc ccc agc gat gct gag tgg cca agt   499
Gln Gly Pro Tyr Lys Glu Ile Arg Pro Ser Asp Ala Glu Trp Pro Ser
        120                 125                 130

cgc gag atc gct gac acc gcc caa aac acc gtc agc caa gac aag agg   547
Arg Glu Ile Ala Asp Thr Ala Gln Asn Thr Val Ser Gln Asp Lys Arg
    135                 140                 145

gag ttt taaaacaaca tgactgcttt tgg                                576
Glu Phe
150
```

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<210> 372
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 372

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Met Leu Asn Ala Leu Lys Phe Ile Pro Trp Leu Ile Gly Gln Ile Phe
  1               5                  10                  15

Leu Ser Gly Phe Ser Val Ile Thr Ala Ala Val Lys Lys Asp Thr Gly
            20                  25                  30

Phe Asn Pro Val Val Ile Arg Tyr Pro Leu Arg Val Thr Thr Asp Phe
        35                  40                  45

Gln Ile Ala Ala Leu Ser Thr Cys Ile Thr Ala Thr Pro Ser Thr Leu
    50                  55                  60

Ser Leu Gly Leu Arg Glu Pro Arg Lys Pro Gly Asp Pro Thr Ile Leu
65                  70                  75                  80

Leu Ile Gln Ala Val Phe Gly Ser Asp Pro Val Glu Val Phe Glu Ser
                85                  90                  95

Ile Ala Asp Met Glu Gln Arg Leu Val Pro Ser Val Ala Ser Ile Asp
            100                 105                 110

His Gly Val Pro Gly Gln Gly Pro Tyr Lys Glu Ile Arg Pro Ser Asp
        115                 120                 125

Ala Glu Trp Pro Ser Arg Glu Ile Ala Asp Thr Ala Gln Asn Thr Val
    130                 135                 140

Ser Gln Asp Lys Arg Glu Phe
145                 150
```

<210> 373
<211> 738
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> RXA02079

<400> 373
cggggagccg tgcggacgct gcggaacatt aatcatccgg gagagtttca tgaaccgcgg 60

```
ctcccactac tgcccaaact gccagaagcg gcgctagctg atg agc gaa gct ttt   115
                                              Met Ser Glu Ala Phe
                                                1               5

gat gca acc aaa gtg cgc aaa gct gtg ctc acc gtc gcg ctg ctt aac   163
Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr Val Ala Leu Leu Asn
               10                  15                  20

ttc gct tat ttc ttt gta gaa ttc ttt att gca tta agc gca ggc tcc   211
Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala Leu Ser Ala Gly Ser
           25                  30                  35

gtt tct cta ctg gct gac agt gtc gat ttt ctt gaa gac acc tcc atc   259
Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu Glu Asp Thr Ser Ile
       40                  45                  50

aac ctg ctc att ttc att gcc cta gga tgg ccg ttg gcg agg cgc gca   307
Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro Leu Ala Arg Arg Ala
   55                  60                  65

gtg atg ggc aaa ctt atg gcg att gtg att ctt gca cct gct gct ttt   355
Val Met Gly Lys Leu Met Ala Ile Val Ile Leu Ala Pro Ala Ala Phe
70                  75                  80                  85

gct gcg tgg gca gcg att caa cgg ttt tcc gca ccg caa gcg ccc gaa   403
Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala Pro Gln Ala Pro Glu
               90                  95                 100

gtg ttt ccg atc atc gtc gct tct ctg ggc gcc gtc gtg atc aac ggc   451
Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala Val Val Ile Asn Gly
           105                 110                 115

gcg agt gcc atc att att tct cga gtg cga caa cat ggt ggc tcg ctt   499
Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln His Gly Gly Ser Leu
       120                 125                 130

ggc caa gct gcc ttc cta tcc gcc cga aat gac gtc ctg atc aac att   547
Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp Val Leu Ile Asn Ile
   135                 140                 145

gcc atc atc atg atg gcc tta att acc gca tgg acg acg tct gga tgg   595
Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp Thr Thr Ser Gly Trp
150                 155                 160                 165

cca gat ttg atc cta ggt tgt ttc atc att ctg ctc gca ctg cac gcc   643
Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu Leu Ala Leu His Ala
               170                 175                 180

gct cac gag gtg tgg gaa gtc agt gag gaa gaa cgc ctc gcc tcc aaa   691
Ala His Glu Val Trp Glu Val Ser Glu Glu Glu Arg Leu Ala Ser Lys
           185                 190                 195
```

gcc ctt gct ggg gaa gcc atc gat taggggagca gtatgagctt ttc 738
Ala Leu Ala Gly Glu Ala Ile Asp
200 205

<210> 374
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 374
Met Ser Glu Ala Phe Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr
1 5 10 15

Val Ala Leu Leu Asn Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala
20 25 30

Leu Ser Ala Gly Ser Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu
35 40 45

Glu Asp Thr Ser Ile Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro
50 55 60

Leu Ala Arg Arg Ala Val Met Gly Lys Leu Met Ala Ile Val Ile Leu
65 70 75 80

Ala Pro Ala Ala Phe Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala
85 90 95

Pro Gln Ala Pro Glu Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala
100 105 110

Val Val Ile Asn Gly Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln
115 120 125

His Gly Gly Ser Leu Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp
130 135 140

Val Leu Ile Asn Ile Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp
145 150 155 160

Thr Thr Ser Gly Trp Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu
165 170 175

Leu Ala Leu His Ala Ala His Glu Val Trp Glu Val Ser Glu Glu Glu
180 185 190

Arg Leu Ala Ser Lys Ala Leu Ala Gly Glu Ala Ile Asp
195 200 205

<210> 375
<211> 1458
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1435)
<223> RXA01303

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<400> 375
aacatgcggg cgcaggtcag agctgttatc ttagtactta tcacagccat agggcgggct 60

tgacggaaag cctttccgcg taaccatgaa gaggcatcac gtg aca caa ctc aac 115
Val Thr Gln Leu Asn
1 5

acc aaa ggc gtt gtt ctg caa ggg tgg gat cca gaa gat cct gaa cat 163
Thr Lys Gly Val Val Leu Gln Gly Trp Asp Pro Glu Asp Pro Glu His
10 15 20

tgg gac tcg aaa att gca tgg cga acc ctg tgg att acc acc ttc tcc 211
Trp Asp Ser Lys Ile Ala Trp Arg Thr Leu Trp Ile Thr Thr Phe Ser
25 30 35

atg att att ggg ttc tgc gtg tgg tat ttg gtt tct gcc atc gct ccc 259
Met Ile Ile Gly Phe Cys Val Trp Tyr Leu Val Ser Ala Ile Ala Pro
40 45 50

cta ctc aat cga att gga ttt gat ctc tca gca ggt cag ctt tat tgg 307
Leu Leu Asn Arg Ile Gly Phe Asp Leu Ser Ala Gly Gln Leu Tyr Trp
55 60 65

ctc gca tct atc ccc ggt ttg gcc ggc gga tta atc cga ttg att tac 355
Leu Ala Ser Ile Pro Gly Leu Ala Gly Gly Leu Ile Arg Leu Ile Tyr
70 75 80 85

atg ttc ctt cca ccg att ctt gga acc cgc aaa ttg gtc gga att tcc 403
Met Phe Leu Pro Pro Ile Leu Gly Thr Arg Lys Leu Val Gly Ile Ser
90 95 100

tcc ggt cta ttt ttg atc ccc atg ttt ggg tgg ttc ctg gct gtc caa 451
Ser Gly Leu Phe Leu Ile Pro Met Phe Gly Trp Phe Leu Ala Val Gln
105 110 115

gat tca agc act ccc tac tgg tgg ctt ctc aca ctc gct gca ctc act 499
Asp Ser Ser Thr Pro Tyr Trp Trp Leu Leu Thr Leu Ala Ala Leu Thr
120 125 130

ggc att ggt ggt ggc gtg ttc tct gga tat atg ccg tcc acg gga tac 547
Gly Ile Gly Gly Gly Val Phe Ser Gly Tyr Met Pro Ser Thr Gly Tyr
135 140 145

ttc ttc ccc aag gca aaa tcg ggc act gcg ctg ggc att cag gca ggt 595
Phe Phe Pro Lys Ala Lys Ser Gly Thr Ala Leu Gly Ile Gln Ala Gly
150 155 160 165

atc ggc aac ctc ggc gtc tcg ata att cag ttc atg ggc cca tgg gtc 643
Ile Gly Asn Leu Gly Val Ser Ile Ile Gln Phe Met Gly Pro Trp Val
170 175 180

atg ggt ttc ggt ctg ctg ggc att ggt ttc ctc acc ccg cag cgc acc 691
Met Gly Phe Gly Leu Leu Gly Ile Gly Phe Leu Thr Pro Gln Arg Thr
185 190 195

att gaa ggc acc acg gtg ttt gtg cac aat gct gcg att gtg ttg gtc 739
Ile Glu Gly Thr Thr Val Phe Val His Asn Ala Ala Ile Val Leu Val
200 205 210

ccg tgg act att ctc gcg gcc gtt tta tcc ttc ctg ttt ctt aaa gat 787

```
Pro Trp Thr Ile Leu Ala Ala Val Leu Ser Phe Leu Phe Leu Lys Asp
    215                 220                 225

gtc cca gtc acc gca aat ttc cgg caa cag atc gat atc ttt ggc aac   835
Val Pro Val Thr Ala Asn Phe Arg Gln Gln Ile Asp Ile Phe Gly Asn
230                 235                 240                 245

aag aac aca tgg att ttg tcc att atc tac ttg atg aca ttc ggt gcc   883
Lys Asn Thr Trp Ile Leu Ser Ile Ile Tyr Leu Met Thr Phe Gly Ala
                250                 255                 260

ttc gcc ggt ttc gcc gcg cag ttc ggt ctg atc atc aac aac aac ttc   931
Phe Ala Gly Phe Ala Ala Gln Phe Gly Leu Ile Ile Asn Asn Asn Phe
            265                 270                 275

ggc atc gct tcc ccg atg gca gag act tat cca gct gag atg ctt cac   979
Gly Ile Ala Ser Pro Met Ala Glu Thr Tyr Pro Ala Glu Met Leu His
        280                 285                 290

gcc ggt gct acg ttc gcg ttt ctt gga cct ttg att ggt gct ttg gtg   1027
Ala Gly Ala Thr Phe Ala Phe Leu Gly Pro Leu Ile Gly Ala Leu Val
    295                 300                 305

cgt gct gca tgg ggt cca ctg tgt gac aga ttc ggt gga gct atc tgg   1075
Arg Ala Ala Trp Gly Pro Leu Cys Asp Arg Phe Gly Gly Ala Ile Trp
310                 315                 320                 325

acc ttt gtc ggt ggc atc gga atg act atc gcc act gca gct gcc gca   1123
Thr Phe Val Gly Gly Ile Gly Met Thr Ile Ala Thr Ala Ala Ala Ala
                330                 335                 340

atc ttc cta agc aga gcg gag aca cct gat gat ttc tgg cca ttc ctg   1171
Ile Phe Leu Ser Arg Ala Glu Thr Pro Asp Asp Phe Trp Pro Phe Leu
            345                 350                 355

tgg tcc atg ctt gcc ctg ttc ttc ttc acc ggt ctg ggc aat gct ggc   1219
Trp Ser Met Leu Ala Leu Phe Phe Phe Thr Gly Leu Gly Asn Ala Gly
        360                 365                 370

acc ttc aaa caa atg ccc atg att ttg cct aaa cgc caa gca ggt ggc   1267
Thr Phe Lys Gln Met Pro Met Ile Leu Pro Lys Arg Gln Ala Gly Gly
    375                 380                 385

gtg atc ggc tgg acc ggt gcc att ggt gcc ttc ggc ccc ttc att gtc   1315
Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe Gly Pro Phe Ile Val
390                 395                 400                 405

ggt gtc ttg ctc tcc ttc act cca act gtc gcg ttc ttc tgg ggc tgc   1363
Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala Phe Phe Trp Gly Cys
                410                 415                 420

gtg gtg ttc ttc atc atc gcc acc gct ttg acc tgg atc tac tac gcc   1411
Val Val Phe Phe Ile Ile Ala Thr Ala Leu Thr Trp Ile Tyr Tyr Ala
            425                 430                 435

cgc ccg aac gct cca ttc ccg gga taaaccgaaa ggccaatcca tga         1458
Arg Pro Asn Ala Pro Phe Pro Gly
        440                 445
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<210> 376

<211> 445
<212> PRT
<213> Corynebacterium glutamicum

<400> 376

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Val Thr Gln Leu Asn Thr Lys Gly Val Val Leu Gln Gly Trp Asp Pro
  1               5                  10                  15

Glu Asp Pro Glu His Trp Asp Ser Lys Ile Ala Trp Arg Thr Leu Trp
            20                  25                  30

Ile Thr Thr Phe Ser Met Ile Ile Gly Phe Cys Val Trp Tyr Leu Val
        35                  40                  45

Ser Ala Ile Ala Pro Leu Leu Asn Arg Ile Gly Phe Asp Leu Ser Ala
    50                  55                  60

Gly Gln Leu Tyr Trp Leu Ala Ser Ile Pro Gly Leu Ala Gly Gly Leu
65                  70                  75                  80

Ile Arg Leu Ile Tyr Met Phe Leu Pro Pro Ile Leu Gly Thr Arg Lys
                85                  90                  95

Leu Val Gly Ile Ser Ser Gly Leu Phe Leu Ile Pro Met Phe Gly Trp
            100                 105                 110

Phe Leu Ala Val Gln Asp Ser Ser Thr Pro Tyr Trp Trp Leu Leu Thr
        115                 120                 125

Leu Ala Ala Leu Thr Gly Ile Gly Gly Gly Val Phe Ser Gly Tyr Met
    130                 135                 140

Pro Ser Thr Gly Tyr Phe Phe Pro Lys Ala Lys Ser Gly Thr Ala Leu
145                 150                 155                 160

Gly Ile Gln Ala Gly Ile Gly Asn Leu Gly Val Ser Ile Ile Gln Phe
                165                 170                 175

Met Gly Pro Trp Val Met Gly Phe Gly Leu Leu Gly Ile Gly Phe Leu
            180                 185                 190

Thr Pro Gln Arg Thr Ile Glu Gly Thr Thr Val Phe Val His Asn Ala
        195                 200                 205

Ala Ile Val Leu Val Pro Trp Thr Ile Leu Ala Ala Val Leu Ser Phe
    210                 215                 220

Leu Phe Leu Lys Asp Val Pro Val Thr Ala Asn Phe Arg Gln Gln Ile
225                 230                 235                 240

Asp Ile Phe Gly Asn Lys Asn Thr Trp Ile Leu Ser Ile Ile Tyr Leu
                245                 250                 255

Met Thr Phe Gly Ala Phe Ala Gly Phe Ala Ala Gln Phe Gly Leu Ile
            260                 265                 270

Ile Asn Asn Asn Phe Gly Ile Ala Ser Pro Met Ala Glu Thr Tyr Pro
        275                 280                 285

Ala Glu Met Leu His Ala Gly Ala Thr Phe Ala Phe Leu Gly Pro Leu
    290                 295                 300
```

```
Ile Gly Ala Leu Val Arg Ala Ala Trp Gly Pro Leu Cys Asp Arg Phe
305                 310                 315                 320

Gly Gly Ala Ile Trp Thr Phe Val Gly Gly Ile Gly Met Thr Ile Ala
                325                 330                 335

Thr Ala Ala Ala Ala Ile Phe Leu Ser Arg Ala Glu Thr Pro Asp Asp
            340                 345                 350

Phe Trp Pro Phe Leu Trp Ser Met Leu Ala Leu Phe Phe Phe Thr Gly
        355                 360                 365

Leu Gly Asn Ala Gly Thr Phe Lys Gln Met Pro Met Ile Leu Pro Lys
    370                 375                 380

Arg Gln Ala Gly Gly Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe
385                 390                 395                 400

Gly Pro Phe Ile Val Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala
                405                 410                 415

Phe Phe Trp Gly Cys Val Val Phe Phe Ile Ile Ala Thr Ala Leu Thr
            420                 425                 430

Trp Ile Tyr Tyr Ala Arg Pro Asn Ala Pro Phe Pro Gly
        435                 440                 445
```

US 2004/0259190 A1

<210> 377
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> RXA02079

<400> 377
cggggagccg tgcggacgct gcggaacatt aatcatccgg gagagtttca tgaaccgcgg 60

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ctcccactac tgcccaaact gccagaagcg gcgctagctg atg agc gaa gct ttt   115
                                              Met Ser Glu Ala Phe
                                                1               5

gat gca acc aaa gtg cgc aaa gct gtg ctc acc gtc gcg ctg ctt aac   163
Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr Val Ala Leu Leu Asn
                  10                  15                  20

ttc gct tat ttc ttt gta gaa ttc ttt att gca tta agc gca ggc tcc   211
Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala Leu Ser Ala Gly Ser
              25                  30                  35

gtt tct cta ctg gct gac agt gtc gat ttt ctt gaa gac acc tcc atc   259
Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu Glu Asp Thr Ser Ile
          40                  45                  50

aac ctg ctc att ttc att gcc cta gga tgg ccg ttg gcg agg cgc gca   307
Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro Leu Ala Arg Arg Ala
      55                  60                  65
```

```
gtg atg ggc aaa ctt atg gcg att gtg att ctt gca cct gct gct ttt   355
Val Met Gly Lys Leu Met Ala Ile Val Ile Leu Ala Pro Ala Ala Phe
 70                  75                  80                  85

gct gcg tgg gca gcg att caa cgg ttt tcc gca ccg caa gcg ccc gaa   403
Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala Pro Gln Ala Pro Glu
                90                  95                 100

gtg ttt ccg atc atc gtc gct tct ctg ggc gcc gtc gtg atc aac ggc   451
Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala Val Val Ile Asn Gly
            105                 110                 115

gcg agt gcc atc att att tct cga gtg cga caa cat ggt ggc tcg ctt   499
Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln His Gly Gly Ser Leu
        120                 125                 130

ggc caa gct gcc ttc cta tcc gcc cga aat gac gtc ctg atc aac att   547
Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp Val Leu Ile Asn Ile
    135                 140                 145

gcc atc atc atg atg gcc tta att acc gca tgg acg acg tct gga tgg   595
Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp Thr Thr Ser Gly Trp
150                 155                 160                 165

cca gat ttg atc cta ggt tgt ttc atc att ctg ctc gca ctg cac gcc   643
Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu Leu Ala Leu His Ala
                170                 175                 180

gct cac gag gtg tgg gaa gtc agt gag gaa gaa cgc ctc gcc tcc aaa   691
Ala His Glu Val Trp Glu Val Ser Glu Glu Glu Arg Leu Ala Ser Lys
            185                 190                 195

gcc ctt gct ggg gaa gcc atc gat taggggagca gtatgagctt ttc         738
Ala Leu Ala Gly Glu Ala Ile Asp
        200                 205
```

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<210> 378
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 378

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Met Ser Glu Ala Phe Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr
  1               5                  10                  15

Val Ala Leu Leu Asn Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala
             20                  25                  30

Leu Ser Ala Gly Ser Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu
         35                  40                  45

Glu Asp Thr Ser Ile Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro
     50                  55                  60

Leu Ala Arg Arg Ala Val Met Gly Lys Leu Met Ala Ile Val Ile Leu
 65                  70                  75                  80

Ala Pro Ala Ala Phe Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala
                 85                  90                  95
```

```
Pro Gln Ala Pro Glu Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala
            100                 105                 110

Val Val Ile Asn Gly Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln
        115                 120                 125

His Gly Gly Ser Leu Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp
    130                 135                 140

Val Leu Ile Asn Ile Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp
145                 150                 155                 160

Thr Thr Ser Gly Trp Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu
                165                 170                 175

Leu Ala Leu His Ala Ala His Glu Val Trp Glu Val Ser Glu Glu Glu
            180                 185                 190

Arg Leu Ala Ser Lys Ala Leu Ala Gly Glu Ala Ile Asp
        195                 200                 205


<210> 379
<211> 1173
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1150)
<223> RXN00832

<400> 379
gagattgtgc taggttctga tgaggcttcg ggacgacccg aagaaatcta tgacagcctg 60

ggaacggccc agagttctta agaaagtttg actagagaac atg ccg ttt tct tgg   115
                                            Met Pro Phe Ser Trp
                                              1               5

cta aaa cca att gat tat gcc cgc atc ttt gtc ggc tgg gca tcg att   163
Leu Lys Pro Ile Asp Tyr Ala Arg Ile Phe Val Gly Trp Ala Ser Ile
                10                  15                  20

ttt atc atc ccc ctc atc aca ctg cca tca att att gag ttg gcg ctg   211
Phe Ile Ile Pro Leu Ile Thr Leu Pro Ser Ile Ile Glu Leu Ala Leu
            25                  30                  35

atc gtg gca gtc atc cta ttc tgc gca ttt ggc gtg gtg aag atg gcg   259
Ile Val Ala Val Ile Leu Phe Cys Ala Phe Gly Val Val Lys Met Ala
        40                  45                  50

gag cgt ttg gct cat att ttg ggt gat cct ttt gga tcg ttg atc ctt   307
Glu Arg Leu Ala His Ile Leu Gly Asp Pro Phe Gly Ser Leu Ile Leu
    55                  60                  65

acc ttg tcg atc gtg atc att gaa gtg att ttg atc tgt gcg gtg atg   355
Thr Leu Ser Ile Val Ile Ile Glu Val Ile Leu Ile Cys Ala Val Met
70                  75                  80                  85

ctg ggg cct gct gat tca acc act gct ggt cgg gat tcc gtg atg gca   403
```

```
Leu Gly Pro Ala Asp Ser Thr Thr Ala Gly Arg Asp Ser Val Met Ala
                 90                  95                 100

gtg tcc atg atc atc atg ggt ttg gtc gtg gga ttg tgc cta ctc att   451
Val Ser Met Ile Ile Met Gly Leu Val Val Gly Leu Cys Leu Leu Ile
             105                 110                 115

ggt ggt tta agg cat gga agc atg cca cac aat ggg gtg gga act ccg   499
Gly Gly Leu Arg His Gly Ser Met Pro His Asn Gly Val Gly Thr Pro
         120                 125                 130

acc tac ttg gtg ctg atc gca act ttt tcc gta atc gcc ttt gcg gtt   547
Thr Tyr Leu Val Leu Ile Ala Thr Phe Ser Val Ile Ala Phe Ala Val
     135                 140                 145

cca gct ttc agg gga gaa tac tcc act ggg cag gca ctt gtt att tca   595
Pro Ala Phe Arg Gly Glu Tyr Ser Thr Gly Gln Ala Leu Val Ile Ser
150                 155                 160                 165

aca ctg aca gca gtg gtg tac ggg ttc ttc ctg ttt cgc caa atg ggt   643
Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu Phe Arg Gln Met Gly
                 170                 175                 180

gcc caa gct ggt gaa ttt caa gag gtc gag gtc gca gaa aag gca gac   691
Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val Ala Glu Lys Ala Asp
             185                 190                 195

gac gca gca aaa tgg gag gtc cca ttt aga ggc tta atc ttg att atc   739
Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly Leu Ile Leu Ile Ile
         200                 205                 210

act gtg ctc ccc atc gtg ttg ctg tcc cat gac atg gcc acg gtg atg   787
Thr Val Leu Pro Ile Val Leu Leu Ser His Asp Met Ala Thr Val Met
     215                 220                 225

gat gaa gtc ctg gca agc ctt ggt gca ccc gta gca atg gct gga tta   835
Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val Ala Met Ala Gly Leu
230                 235                 240                 245

att att gcc acc att gtc ttc ttg cca gag acc atc acc tcc ttg aaa   883
Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr Ile Thr Ser Leu Lys
                 250                 255                 260

gct gcg tgg aca gga gag att cag cga gta agc aac ctc gcg cat gga   931
Ala Ala Trp Thr Gly Glu Ile Gln Arg Val Ser Asn Leu Ala His Gly
             265                 270                 275

gcc caa gta tca acg gtg ggg ctg aca atc cca gct gtt cta gtg atc   979
Ala Gln Val Ser Thr Val Gly Leu Thr Ile Pro Ala Val Leu Val Ile
         280                 285                 290

ggc gtg atc aca ggt caa gat gta gtt ttg ggg gag acc ccg atc aac   1027
Gly Val Ile Thr Gly Gln Asp Val Val Leu Gly Glu Thr Pro Ile Asn
     295                 300                 305

ttg ttg ctg ctg gga acc acc att gcg gtg aca gcc att gcg ttt agc   1075
Leu Leu Leu Leu Gly Thr Thr Ile Ala Val Thr Ala Ile Ala Phe Ser
310                 315                 320                 325

tcc aag aaa gtc agt gct gtg cat ggc tcg gtg ctg ctc atg ctt ttc   1123
Ser Lys Lys Val Ser Ala Val His Gly Ser Val Leu Leu Met Leu Phe
```

09/09/2003 15:39:39

330 335 340

ggt gtt tac atg atg agc atg ttc gcc tgatttaggt agcctggtgg 1170
Gly Val Tyr Met Met Ser Met Phe Ala
345 350

gaa 1173

<210> 380
<211> 350
<212> PRT
<213> Corynebacterium glutamicum

<400> 380
Met Pro Phe Ser Trp Leu Lys Pro Ile Asp Tyr Ala Arg Ile Phe Val
1 5 10 15

Gly Trp Ala Ser Ile Phe Ile Ile Pro Leu Ile Thr Leu Pro Ser Ile
20 25 30

Ile Glu Leu Ala Leu Ile Val Ala Val Ile Leu Phe Cys Ala Phe Gly
35 40 45

Val Val Lys Met Ala Glu Arg Leu Ala His Ile Leu Gly Asp Pro Phe
50 55 60

Gly Ser Leu Ile Leu Thr Leu Ser Ile Val Ile Ile Glu Val Ile Leu
65 70 75 80

Ile Cys Ala Val Met Leu Gly Pro Ala Asp Ser Thr Thr Ala Gly Arg
85 90 95

Asp Ser Val Met Ala Val Ser Met Ile Ile Met Gly Leu Val Val Gly
100 105 110

Leu Cys Leu Leu Ile Gly Gly Leu Arg His Gly Ser Met Pro His Asn
115 120 125

Gly Val Gly Thr Pro Thr Tyr Leu Val Leu Ile Ala Thr Phe Ser Val
130 135 140

Ile Ala Phe Ala Val Pro Ala Phe Arg Gly Glu Tyr Ser Thr Gly Gln
145 150 155 160

Ala Leu Val Ile Ser Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu
165 170 175

Phe Arg Gln Met Gly Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val
180 185 190

Ala Glu Lys Ala Asp Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly
195 200 205

Leu Ile Leu Ile Ile Thr Val Leu Pro Ile Val Leu Leu Ser His Asp
210 215 220

Met Ala Thr Val Met Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val
225 230 235 240

Ala Met Ala Gly Leu Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr

```
                245                 250                 255

Ile Thr Ser Leu Lys Ala Ala Trp Thr Gly Glu Ile Gln Arg Val Ser
            260                 265                 270

Asn Leu Ala His Gly Ala Gln Val Ser Thr Val Gly Leu Thr Ile Pro
        275                 280                 285

Ala Val Leu Val Ile Gly Val Ile Thr Gly Gln Asp Val Val Leu Gly
    290                 295                 300

Glu Thr Pro Ile Asn Leu Leu Leu Leu Gly Thr Thr Ile Ala Val Thr
305                 310                 315                 320

Ala Ile Ala Phe Ser Ser Lys Lys Val Ser Ala Val His Gly Ser Val
                325                 330                 335

Leu Leu Met Leu Phe Gly Val Tyr Met Met Ser Met Phe Ala
            340                 345                 350
```

09/05/2005 09:59:09

<210> 381
<211> 578
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(555)
<223> FRXA00832

<400> 381

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aca ctg aca gca gtg gtg tac ggg ttc ttc ctg ttt cgc caa atg ggt   48
Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu Phe Arg Gln Met Gly
  1               5                  10                  15

gcc caa gct ggt gaa ttt caa gag gtc gag gtc gca gaa aag gca gac   96
Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val Ala Glu Lys Ala Asp
             20                  25                  30

gac gca gca aaa tgg gag gtc cca ttt aga ggc tta atc ttg att atc  144
Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly Leu Ile Leu Ile Ile
         35                  40                  45

act gtg ctc ccc atc gtg ttg ctg tcc cat gac atg gcc acg gtg atg  192
Thr Val Leu Pro Ile Val Leu Leu Ser His Asp Met Ala Thr Val Met
     50                  55                  60

gat gaa gtc ctg gca agc ctt ggt gca ccc gta gca atg gct gga tta  240
Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val Ala Met Ala Gly Leu
 65                  70                  75                  80

att att gcc acc att gtc ttc ttg cca gag acc atc acc tcc ttg aaa  288
Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr Ile Thr Ser Leu Lys
                 85                  90                  95

gct gcg tgg aca gga gag att cag cga gta agc aac ctc gcg cat gga  336
Ala Ala Trp Thr Gly Glu Ile Gln Arg Val Ser Asn Leu Ala His Gly
            100                 105                 110

gcc caa gta tca acg gtg ggg ctg aca atc cca gct gtt cta gtg atc  384
```

```
Ala Gln Val Ser Thr Val Gly Leu Thr Ile Pro Ala Val Leu Val Ile
        115                 120                 125

ggc gtg atc aca ggt caa gat gta gtt ttg ggg gag acc ccg atc aac   432
Gly Val Ile Thr Gly Gln Asp Val Val Leu Gly Glu Thr Pro Ile Asn
    130                 135                 140

ttg ttg ctg ctg gga acc acc att gcg gtg aca gcc att gcg ttt agc   480
Leu Leu Leu Leu Gly Thr Thr Ile Ala Val Thr Ala Ile Ala Phe Ser
145                 150                 155                 160

tcc aag aaa gtc agt gct gtg cat ggc tcg gtg ctg ctc atg ctt ttc   528
Ser Lys Lys Val Ser Ala Val His Gly Ser Val Leu Leu Met Leu Phe
                165                 170                 175

ggt gtt tac atg atg agc atg ttc gcc tgatttaggt agcctggtgg         575
Gly Val Tyr Met Met Ser Met Phe Ala
            180                 185

gaa                                                               578
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Date Recue/Date Received 2020-12-21

<210> 382
<211> 185
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 382

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Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu Phe Arg Gln Met Gly
  1               5                  10                  15

Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val Ala Glu Lys Ala Asp
            20                  25                  30

Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly Leu Ile Leu Ile Ile
        35                  40                  45

Thr Val Leu Pro Ile Val Leu Leu Ser His Asp Met Ala Thr Val Met
    50                  55                  60

Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val Ala Met Ala Gly Leu
65                  70                  75                  80

Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr Ile Thr Ser Leu Lys
                85                  90                  95

Ala Ala Trp Thr Gly Glu Ile Gln Arg Val Ser Asn Leu Ala His Gly
            100                 105                 110

Ala Gln Val Ser Thr Val Gly Leu Thr Ile Pro Ala Val Leu Val Ile
        115                 120                 125

Gly Val Ile Thr Gly Gln Asp Val Val Leu Gly Glu Thr Pro Ile Asn
    130                 135                 140

Leu Leu Leu Leu Gly Thr Thr Ile Ala Val Thr Ala Ile Ala Phe Ser
145                 150                 155                 160

Ser Lys Lys Val Ser Ala Val His Gly Ser Val Leu Leu Met Leu Phe
                165                 170                 175
```

Gly Val Tyr Met Met Ser Met Phe Ala
180 185

<210> 383
<211> 2733
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2710)
<223> RXN00378

<400> 383
accgtgagcc ttatactgtg aggacattaa aagtgacacc tctttttcta tcttttacaa 60

cccaagaagg tttatcgtga gcacaccgga ttcttcctcg gtg gac aag gcc gta 115
Val Asp Lys Ala Val
1 5

aac act gct atc tct gac gcc aaa aca gcg gcg ctc aag gca ggt gtt 163
Asn Thr Ala Ile Ser Asp Ala Lys Thr Ala Ala Leu Lys Ala Gly Val
10 15 20

gga ttg aac cga gcc acc gcc tca gaa gaa gag gaa gat tta agc tca 211
Gly Leu Asn Arg Ala Thr Ala Ser Glu Glu Glu Glu Asp Leu Ser Ser
25 30 35

agc att aag gtt tct ttg gcc ttt gag ctc gag ggg tta agc aat gca 259
Ser Ile Lys Val Ser Leu Ala Phe Glu Leu Glu Gly Leu Ser Asn Ala
40 45 50

cca tcg ttg atg gtg gtg gaa aaa gcc cta gag aag atc ccc ggt gta 307
Pro Ser Leu Met Val Val Glu Lys Ala Leu Glu Lys Ile Pro Gly Val
55 60 65

tcc gcg gat ctg att tac cct tca caa act gca tgg att aca gca act 355
Ser Ala Asp Leu Ile Tyr Pro Ser Gln Thr Ala Trp Ile Thr Ala Thr
70 75 80 85

gat cgg gta cat ccc gaa acc ctc att gag gtg ttt gag cag ttc ggc 403
Asp Arg Val His Pro Glu Thr Leu Ile Glu Val Phe Glu Gln Phe Gly
90 95 100

atc aaa gca cac ctt tct aat tca tcg ctg ctg cgc agg cat caa cag 451
Ile Lys Ala His Leu Ser Asn Ser Ser Leu Leu Arg Arg His Gln Gln
105 110 115

ctc agc gcg gaa gta aat agg gaa gca cgc ctt gat cgt tac cgc tcc 499
Leu Ser Ala Glu Val Asn Arg Glu Ala Arg Leu Asp Arg Tyr Arg Ser
120 125 130

cga atg gat gcc aag cga atc tcg cct cgt gtg cga agg cat aac cga 547
Arg Met Asp Ala Lys Arg Ile Ser Pro Arg Val Arg Arg His Asn Arg
135 140 145

caa gaa atg gta cat gcg gta cgc gct cgt gaa agt ggt tgg att aaa 595
Gln Glu Met Val His Ala Val Arg Ala Arg Glu Ser Gly Trp Ile Lys
150 155 160 165

```
cgc agg aat cac acc acc tcg cag cat gaa gac cca atg tcg ggc gat   643
Arg Arg Asn His Thr Thr Ser Gln His Glu Asp Pro Met Ser Gly Asp
                170                 175                 180

gtg ctg ttc acc gcc cgc gca ctg att aca cct aag cgt ttg tgg gtg   691
Val Leu Phe Thr Ala Arg Ala Leu Ile Thr Pro Lys Arg Leu Trp Val
            185                 190                 195

tcg ttg ccg ttt gcg ctc atc gta ttg gcg tta tcg ttg aat cct tcg   739
Ser Leu Pro Phe Ala Leu Ile Val Leu Ala Leu Ser Leu Asn Pro Ser
        200                 205                 210

tgg cag ttt gat tat tgg cag tgg ttg tcc gct gtg ttg gct att cct   787
Trp Gln Phe Asp Tyr Trp Gln Trp Leu Ser Ala Val Leu Ala Ile Pro
    215                 220                 225

gtg gtg gtg tgg ggt gcc tgg ccg ttt cac cgc gct gca gca ggc ggt   835
Val Val Val Trp Gly Ala Trp Pro Phe His Arg Ala Ala Ala Gly Gly
230                 235                 240                 245

att cgt cga gga att tcc gct ctt gat gcg acc agc tca atc gct att   883
Ile Arg Arg Gly Ile Ser Ala Leu Asp Ala Thr Ser Ser Ile Ala Ile
                250                 255                 260

gct gct gca tac gcg tgg tct atc gcc atg ctg ttg ttt gaa acc cca   931
Ala Ala Ala Tyr Ala Trp Ser Ile Ala Met Leu Leu Phe Glu Thr Pro
            265                 270                 275

gga ggt aaa tcc tgg cgg tca tat ccg tcc tgg ttc gct ttt gac cac   979
Gly Gly Lys Ser Trp Arg Ser Tyr Pro Ser Trp Phe Ala Phe Asp His
        280                 285                 290

ggc acg ttg acc caa aac gag att tat ttt gat gtg gcc tgc gga atc  1027
Gly Thr Leu Thr Gln Asn Glu Ile Tyr Phe Asp Val Ala Cys Gly Ile
    295                 300                 305

acc gtg ttg ctt ctt gcc gga cgg ctg ctg aca agg cgt cga agc caa  1075
Thr Val Leu Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln
310                 315                 320                 325

tcc agt ttg tta gcg gaa ctt ggt cgc ctc caa atc gat cca cag cgc  1123
Ser Ser Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg
                330                 335                 340

att gtc act gtg gtg cgt aaa cac cga ttg aag cgc gta gtc cag gaa  1171
Ile Val Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu
            345                 350                 355

ctg aac att cca gtg cag gaa gtc cgt gtc aat gac gat gtg aaa gtt  1219
Leu Asn Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val
        360                 365                 370

cca cct aat acc acg atc cct gtg gat ggc act gtc atc ggt ggc ggt  1267
Pro Pro Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Gly
    375                 380                 385

tcg cgg atc gca gct agc atc atc atg gga caa gac cag cgt gat gta  1315
Ser Arg Ile Ala Ala Ser Ile Ile Met Gly Gln Asp Gln Arg Asp Val
390                 395                 400                 405

aaa gta aat gac aaa gtt ttc gcc ggc agc ctc aac ctc gaa tcc gaa  1363
```

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Lys Val Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu
                410                 415                 420

atc aag gtt cgt gtt att cgc act ggt cac cgc acc cgc atc gcc gcg   1411
Ile Lys Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala
            425                 430                 435

gta cat agg tgg gtt aaa gaa gcg acg ttg aag gaa aac cgc cac aat   1459
Val His Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn
        440                 445                 450

agg gca gcg atc cgt tcg gcc ggt aac ctt gtg ccc atc acg ttc acc   1507
Arg Ala Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr
    455                 460                 465

ctt gct gtg gtg gac ttc tgt ctg tgg gca ctg atc tct gga aac atc   1555
Leu Ala Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile
470                 475                 480                 485

aac gct gca ttt acc act acc ttg gct gtc ctt gcg tgc gtg gct ccg   1603
Asn Ala Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro
                490                 495                 500

gtg gcc tta gcg ttg tct gct cca ctt gcc acg agg aat tcc atc gaa   1651
Val Ala Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu
            505                 510                 515

gct gca gca cga cac ggt att ttg gtc cgc tct ggt gaa att ttc cga   1699
Ala Ala Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg
        520                 525                 530

gtt ctc gat gat gtg gat act gcc gta ttt aat cgt gtg ggc aca cta   1747
Val Leu Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu
    535                 540                 545

acc gat ggc gaa atg aca gtg gaa acc gtc aca gca gac aaa ggc gag   1795
Thr Asp Gly Glu Met Thr Val Glu Thr Val Thr Ala Asp Lys Gly Glu
550                 555                 560                 565

gac cca gaa cta gtg ctg cgt gtc gcc ggg gcg ttg gcc atg gaa tcc   1843
Asp Pro Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser
                570                 575                 580

cac cac gcg att tcc aaa gca ctg gtg aaa gca tcc cgt gaa gct cgt   1891
His His Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg
            585                 590                 595

gat acc ggc gcc ggt ggt gaa gat gtc cca cac tgg att gaa gta ggc   1939
Asp Thr Gly Ala Gly Gly Glu Asp Val Pro His Trp Ile Glu Val Gly
        600                 605                 610

aac gtg gaa atc acc gaa gcc ggc tca ttc caa gca acc atc gag ctg   1987
Asn Val Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu
    615                 620                 625

cca ctg atc aaa cca tct ggc gaa aaa atc atg cgc acc aca gaa gca   2035
Pro Leu Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala
630                 635                 640                 645

ctc ctg tgg cga cca cga tcc atg aca gaa gtc cgt gag cac tta agc   2083
Leu Leu Trp Arg Pro Arg Ser Met Thr Glu Val Arg Glu His Leu Ser
```

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                650                 655                 660

ccc cga cta gtg gca gca gca acc tca ggt ggc gca cca ctg atc gtg   2131
Pro Arg Leu Val Ala Ala Ala Thr Ser Gly Gly Ala Pro Leu Ile Val
            665                 670                 675

cga tgg aaa ggc aaa gac cgc gga gtt atc act cta agt gac cac gtg   2179
Arg Trp Lys Gly Lys Asp Arg Gly Val Ile Thr Leu Ser Asp His Val
        680                 685                 690

aga tca gat tcc tcc gat gcg att att gcg att gaa gaa caa ggc atc   2227
Arg Ser Asp Ser Ser Asp Ala Ile Ile Ala Ile Glu Glu Gln Gly Ile
    695                 700                 705

gag acc atg atg ctt tca cgt gat act tac ccg gtg gca cgt cga tac   2275
Glu Thr Met Met Leu Ser Arg Asp Thr Tyr Pro Val Ala Arg Arg Tyr
710                 715                 720                 725

gca gac agc tta ggc atc acc cac gtc ttg gcc ggc atc gcg ccg ggc   2323
Ala Asp Ser Leu Gly Ile Thr His Val Leu Ala Gly Ile Ala Pro Gly
                730                 735                 740

aag aaa gcc cag gtc gtc cgt gca gtc cac acc cgc gga tcc act gtc   2371
Lys Lys Ala Gln Val Val Arg Ala Val His Thr Arg Gly Ser Thr Val
            745                 750                 755

gcg atg atc ggc gat gaa tca gta atg gac tgt ttg aaa gtc gct gac   2419
Ala Met Ile Gly Asp Glu Ser Val Met Asp Cys Leu Lys Val Ala Asp
        760                 765                 770

gtg ggt gta ctg atg ggc gtc gat cgt ccc tca gat ctg cgt gat gat   2467
Val Gly Val Leu Met Gly Val Asp Arg Pro Ser Asp Leu Arg Asp Asp
    775                 780                 785

tcc gat gac ccg gca gct gac gtt gtg gtc atg cgc gaa gag gtc atg   2515
Ser Asp Asp Pro Ala Ala Asp Val Val Val Met Arg Glu Glu Val Met
790                 795                 800                 805

agc gtg ccg acg ctg ttt aaa ctg gct cga cgc tac gcc aag ttg gtc   2563
Ser Val Pro Thr Leu Phe Lys Leu Ala Arg Arg Tyr Ala Lys Leu Val
                810                 815                 820

aat ggc aat att gct ctg gcc tgg atc tat aac ggt gtt gcc atg gtg   2611
Asn Gly Asn Ile Ala Leu Ala Trp Ile Tyr Asn Gly Val Ala Met Val
            825                 830                 835

ctt gca gtg tct ggc ttg ctg cat cca atg gct gcg acc gtg gct atg   2659
Leu Ala Val Ser Gly Leu Leu His Pro Met Ala Ala Thr Val Ala Met
        840                 845                 850

ctg gcg tct tcg ctg ctt att gaa tgg cgc tcg ggc agg gcg cgc aag   2707
Leu Ala Ser Ser Leu Leu Ile Glu Trp Arg Ser Gly Arg Ala Arg Lys
    855                 860                 865

tac taaccagcaa ttcccaagcc caa                                    2733
Tyr
870
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<210> 384
<211> 870

<212> PRT
<213> Corynebacterium glutamicum

<400> 384

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Val Asp Lys Ala Val Asn Thr Ala Ile Ser Asp Ala Lys Thr Ala Ala
  1               5                  10                  15

Leu Lys Ala Gly Val Gly Leu Asn Arg Ala Thr Ala Ser Glu Glu Glu
             20                  25                  30

Glu Asp Leu Ser Ser Ser Ile Lys Val Ser Leu Ala Phe Glu Leu Glu
         35                  40                  45

Gly Leu Ser Asn Ala Pro Ser Leu Met Val Val Glu Lys Ala Leu Glu
     50                  55                  60

Lys Ile Pro Gly Val Ser Ala Asp Leu Ile Tyr Pro Ser Gln Thr Ala
 65                  70                  75                  80

Trp Ile Thr Ala Thr Asp Arg Val His Pro Glu Thr Leu Ile Glu Val
                 85                  90                  95

Phe Glu Gln Phe Gly Ile Lys Ala His Leu Ser Asn Ser Ser Leu Leu
            100                 105                 110

Arg Arg His Gln Gln Leu Ser Ala Glu Val Asn Arg Glu Ala Arg Leu
        115                 120                 125

Asp Arg Tyr Arg Ser Arg Met Asp Ala Lys Arg Ile Ser Pro Arg Val
    130                 135                 140

Arg Arg His Asn Arg Gln Glu Met Val His Ala Val Arg Ala Arg Glu
145                 150                 155                 160

Ser Gly Trp Ile Lys Arg Arg Asn His Thr Thr Ser Gln His Glu Asp
                165                 170                 175

Pro Met Ser Gly Asp Val Leu Phe Thr Ala Arg Ala Leu Ile Thr Pro
            180                 185                 190

Lys Arg Leu Trp Val Ser Leu Pro Phe Ala Leu Ile Val Leu Ala Leu
        195                 200                 205

Ser Leu Asn Pro Ser Trp Gln Phe Asp Tyr Trp Gln Trp Leu Ser Ala
    210                 215                 220

Val Leu Ala Ile Pro Val Val Val Trp Gly Ala Trp Pro Phe His Arg
225                 230                 235                 240

Ala Ala Ala Gly Gly Ile Arg Arg Gly Ile Ser Ala Leu Asp Ala Thr
                245                 250                 255

Ser Ser Ile Ala Ile Ala Ala Ala Tyr Ala Trp Ser Ile Ala Met Leu
            260                 265                 270

Leu Phe Glu Thr Pro Gly Gly Lys Ser Trp Arg Ser Tyr Pro Ser Trp
        275                 280                 285

Phe Ala Phe Asp His Gly Thr Leu Thr Gln Asn Glu Ile Tyr Phe Asp
    290                 295                 300
```

Val Ala Cys Gly Ile Thr Val Leu Leu Leu Ala Gly Arg Leu Leu Thr
305 310 315 320

Arg Arg Arg Ser Gln Ser Ser Leu Leu Ala Glu Leu Gly Arg Leu Gln
325 330 335

Ile Asp Pro Gln Arg Ile Val Thr Val Val Arg Lys His Arg Leu Lys
340 345 350

Arg Val Val Gln Glu Leu Asn Ile Pro Val Gln Glu Val Arg Val Asn
355 360 365

Asp Asp Val Lys Val Pro Pro Asn Thr Thr Ile Pro Val Asp Gly Thr
370 375 380

Val Ile Gly Gly Gly Ser Arg Ile Ala Ala Ser Ile Ile Met Gly Gln
385 390 395 400

Asp Gln Arg Asp Val Lys Val Asn Asp Lys Val Phe Ala Gly Ser Leu
405 410 415

Asn Leu Glu Ser Glu Ile Lys Val Arg Val Ile Arg Thr Gly His Arg
420 425 430

Thr Arg Ile Ala Ala Val His Arg Trp Val Lys Glu Ala Thr Leu Lys
435 440 445

Glu Asn Arg His Asn Arg Ala Ala Ile Arg Ser Ala Gly Asn Leu Val
450 455 460

Pro Ile Thr Phe Thr Leu Ala Val Val Asp Phe Cys Leu Trp Ala Leu
465 470 475 480

Ile Ser Gly Asn Ile Asn Ala Ala Phe Thr Thr Thr Leu Ala Val Leu
485 490 495

Ala Cys Val Ala Pro Val Ala Leu Ala Leu Ser Ala Pro Leu Ala Thr
500 505 510

Arg Asn Ser Ile Glu Ala Ala Ala Arg His Gly Ile Leu Val Arg Ser
515 520 525

Gly Glu Ile Phe Arg Val Leu Asp Asp Val Asp Thr Ala Val Phe Asn
530 535 540

Arg Val Gly Thr Leu Thr Asp Gly Glu Met Thr Val Glu Thr Val Thr
545 550 555 560

Ala Asp Lys Gly Glu Asp Pro Glu Leu Val Leu Arg Val Ala Gly Ala
565 570 575

Leu Ala Met Glu Ser His His Ala Ile Ser Lys Ala Leu Val Lys Ala
580 585 590

Ser Arg Glu Ala Arg Asp Thr Gly Ala Gly Gly Glu Asp Val Pro His
595 600 605

Trp Ile Glu Val Gly Asn Val Glu Ile Thr Glu Ala Gly Ser Phe Gln
610 615 620

Ala Thr Ile Glu Leu Pro Leu Ile Lys Pro Ser Gly Glu Lys Ile Met

625 630 635 640

Arg Thr Thr Glu Ala Leu Leu Trp Arg Pro Arg Ser Met Thr Glu Val
645 650 655

Arg Glu His Leu Ser Pro Arg Leu Val Ala Ala Ala Thr Ser Gly Gly
660 665 670

Ala Pro Leu Ile Val Arg Trp Lys Gly Lys Asp Arg Gly Val Ile Thr
675 680 685

Leu Ser Asp His Val Arg Ser Asp Ser Ser Asp Ala Ile Ile Ala Ile
690 695 700

Glu Glu Gln Gly Ile Glu Thr Met Met Leu Ser Arg Asp Thr Tyr Pro
705 710 715 720

Val Ala Arg Arg Tyr Ala Asp Ser Leu Gly Ile Thr His Val Leu Ala
725 730 735

Gly Ile Ala Pro Gly Lys Lys Ala Gln Val Val Arg Ala Val His Thr
740 745 750

Arg Gly Ser Thr Val Ala Met Ile Gly Asp Glu Ser Val Met Asp Cys
755 760 765

Leu Lys Val Ala Asp Val Gly Val Leu Met Gly Val Asp Arg Pro Ser
770 775 780

Asp Leu Arg Asp Asp Ser Asp Asp Pro Ala Ala Asp Val Val Val Met
785 790 795 800

Arg Glu Glu Val Met Ser Val Pro Thr Leu Phe Lys Leu Ala Arg Arg
805 810 815

Tyr Ala Lys Leu Val Asn Gly Asn Ile Ala Leu Ala Trp Ile Tyr Asn
820 825 830

Gly Val Ala Met Val Leu Ala Val Ser Gly Leu Leu His Pro Met Ala
835 840 845

Ala Thr Val Ala Met Leu Ala Ser Ser Leu Leu Ile Glu Trp Arg Ser
850 855 860

Gly Arg Ala Arg Lys Tyr
865 870

<210> 385
<211> 1796
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1773)
<223> FRXA00378

<400> 385
aaa tcc tgg cgg tca tat ccg tcc tgg ttc gct ttt gac cac ggc acg 48
Lys Ser Trp Arg Ser Tyr Pro Ser Trp Phe Ala Phe Asp His Gly Thr

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1               5                  10                  15

ttg acc caa aac gag att tat ttt gat gtg gcc tgc gga atc acc gtg   96
Leu Thr Gln Asn Glu Ile Tyr Phe Asp Val Ala Cys Gly Ile Thr Val
            20                  25                  30

ttg ctt ctt gcc gga cgg ctg ctg aca agg cgt cga agc caa tcc agt   144
Leu Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln Ser Ser
        35                  40                  45

ttg tta gcg gaa ctt ggt cgc ctc caa atc gat cca cag cgc att gtc   192
Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg Ile Val
    50                  55                  60

act gtg gtg cgt aaa cac cga ttg aag cgc gta gtc cag gaa ctg aac   240
Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu Leu Asn
65                  70                  75                  80

att cca gtg cag gaa gtc cgt gtc aat gac gat gtg aaa gtt cca cct   288
Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val Pro Pro
                85                  90                  95

aat acc acg atc cct gtg gat ggc act gtc atc ggt ggc ggt tcg cgg   336
Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Gly Ser Arg
            100                 105                 110

atc gca gct agc atc atc atg gga caa gac cag cgt gat gta aaa gta   384
Ile Ala Ala Ser Ile Ile Met Gly Gln Asp Gln Arg Asp Val Lys Val
        115                 120                 125

aat gac aaa gtt ttc gcc ggc agc ctc aac ctc gaa tcc gaa atc aag   432
Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu Ile Lys
    130                 135                 140

gtt cgt gtt att cgc act ggt cac cgc acc cgc atc gcc gcg gta cat   480
Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala Val His
145                 150                 155                 160

agg tgg gtt aaa gaa gcg acg ttg aag gaa aac cgc cac aat agg gca   528
Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn Arg Ala
                165                 170                 175

gcg atc cgt tcg gcc ggt aac ctt gtg ccc atc acg ttc acc ctt gct   576
Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr Leu Ala
            180                 185                 190

gtg gtg gac ttc tgt ctg tgg gca ctg atc tct gga aac atc aac gct   624
Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile Asn Ala
        195                 200                 205

gca ttt acc act acc ttg gct gtc ctt gcg tgc gtg gct ccg gtg gcc   672
Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro Val Ala
    210                 215                 220

tta gcg ttg tct gct cca ctt gcc acg agg aat tcc atc gaa gct gca   720
Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu Ala Ala
225                 230                 235                 240

gca cga cac ggt att ttg gtc cgc tct ggt gaa att ttc cga gtt ctc   768
Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg Val Leu
                245                 250                 255
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gat gat gtg gat act gcc gta ttt aat cgt gtg ggc aca cta acc gat   816
Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu Thr Asp
            260                 265                 270

ggc gaa atg aca gtg gaa acc gtc aca gca gac aaa ggc gag gac cca   864
Gly Glu Met Thr Val Glu Thr Val Thr Ala Asp Lys Gly Glu Asp Pro
        275                 280                 285

gaa cta gtg ctg cgt gtc gcc ggg gcg ttg gcc atg gaa tcc cac cac   912
Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser His His
    290                 295                 300

gcg att tcc aaa gca ctg gtg aaa gca tcc cgt gaa gct cgt gat acc   960
Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg Asp Thr
305                 310                 315                 320

ggc gcc ggt ggt gaa gat gtc cca cac tgg att gaa gta ggc aac gtg   1008
Gly Ala Gly Gly Glu Asp Val Pro His Trp Ile Glu Val Gly Asn Val
                325                 330                 335

gaa atc acc gaa gcc ggc tca ttc caa gca acc atc gag ctg cca ctg   1056
Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu Pro Leu
            340                 345                 350

atc aaa cca tct ggc gaa aaa atc atg cgc acc aca gaa gca ctc ctg   1104
Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala Leu Leu
        355                 360                 365

tgg cga cca cga tcc atg aca gaa gtc cgt gag cac tta agc ccc cga   1152
Trp Arg Pro Arg Ser Met Thr Glu Val Arg Glu His Leu Ser Pro Arg
    370                 375                 380

cta gtg gca gca gca acc tca ggt ggc gca cca ctg atc gtg cga tgg   1200
Leu Val Ala Ala Ala Thr Ser Gly Gly Ala Pro Leu Ile Val Arg Trp
385                 390                 395                 400

aaa ggc aaa gac cgc gga gtt atc act cta agt gac cac gtg aga tca   1248
Lys Gly Lys Asp Arg Gly Val Ile Thr Leu Ser Asp His Val Arg Ser
                405                 410                 415

gat tcc tcc gat gcg att att gcg att gaa gaa caa ggc atc gag acc   1296
Asp Ser Ser Asp Ala Ile Ile Ala Ile Glu Glu Gln Gly Ile Glu Thr
            420                 425                 430

atg atg ctt tca cgt gat act tac ccg gtg gca cgt cga tac gca gac   1344
Met Met Leu Ser Arg Asp Thr Tyr Pro Val Ala Arg Arg Tyr Ala Asp
        435                 440                 445

agc tta ggc atc acc cac gtc ttg gcc ggc atc gcg ccg ggc aag aaa   1392
Ser Leu Gly Ile Thr His Val Leu Ala Gly Ile Ala Pro Gly Lys Lys
    450                 455                 460

gcc cag gtc gtc cgt gca gtc cac acc cgc gga tcc act gtc gcg atg   1440
Ala Gln Val Val Arg Ala Val His Thr Arg Gly Ser Thr Val Ala Met
465                 470                 475                 480

atc ggc gat gaa tca gta atg gac tgt ttg aaa gtc gct gac gtg ggt   1488
Ile Gly Asp Glu Ser Val Met Asp Cys Leu Lys Val Ala Asp Val Gly
                485                 490                 495
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gta ctg atg ggc gtc gat cgt ccc tca gat ctg cgt gat gat tcc gat   1536
Val Leu Met Gly Val Asp Arg Pro Ser Asp Leu Arg Asp Asp Ser Asp
            500                 505                 510

gac ccg gca gct gac gtt gtg gtc atg cgc gaa gag gtc atg agc gtg   1584
Asp Pro Ala Ala Asp Val Val Val Met Arg Glu Glu Val Met Ser Val
        515                 520                 525

ccg acg ctg ttt aaa ctg gct cga cgc tac gcc aag ttg gtc aat ggc   1632
Pro Thr Leu Phe Lys Leu Ala Arg Arg Tyr Ala Lys Leu Val Asn Gly
    530                 535                 540

aat att gct ctg gcc tgg atc tat aac ggt gtt gcc atg gtg ctt gca   1680
Asn Ile Ala Leu Ala Trp Ile Tyr Asn Gly Val Ala Met Val Leu Ala
545                 550                 555                 560

gtg tct ggc ttg ctg cat cca atg gct gcg acc gtg gct atg ctg gcg   1728
Val Ser Gly Leu Leu His Pro Met Ala Ala Thr Val Ala Met Leu Ala
                565                 570                 575

tct tcg ctg ctt att gaa tgg cgc tcg ggc agg gcg cgc aag tac       1773
Ser Ser Leu Leu Ile Glu Trp Arg Ser Gly Arg Ala Arg Lys Tyr
            580                 585                 590

taaccagcaa ttcccaagcc caa                                        1796
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<210> 386
<211> 591
<212> PRT
<213> Corynebacterium glutamicum

<400> 386

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Lys Ser Trp Arg Ser Tyr Pro Ser Trp Phe Ala Phe Asp His Gly Thr
  1               5                  10                  15

Leu Thr Gln Asn Glu Ile Tyr Phe Asp Val Ala Cys Gly Ile Thr Val
             20                  25                  30

Leu Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln Ser Ser
         35                  40                  45

Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg Ile Val
     50                  55                  60

Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu Leu Asn
 65                  70                  75                  80

Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val Pro Pro
                 85                  90                  95

Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Gly Ser Arg
            100                 105                 110

Ile Ala Ala Ser Ile Ile Met Gly Gln Asp Gln Arg Asp Val Lys Val
        115                 120                 125

Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu Ile Lys
    130                 135                 140

Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala Val His
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09634936.050905

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145                 150                 155                 160

Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn Arg Ala
                165                 170                 175

Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr Leu Ala
            180                 185                 190

Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile Asn Ala
        195                 200                 205

Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro Val Ala
    210                 215                 220

Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu Ala Ala
225                 230                 235                 240

Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg Val Leu
                245                 250                 255

Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu Thr Asp
            260                 265                 270

Gly Glu Met Thr Val Glu Thr Val Thr Ala Asp Lys Gly Glu Asp Pro
        275                 280                 285

Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser His His
    290                 295                 300

Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg Asp Thr
305                 310                 315                 320

Gly Ala Gly Gly Glu Asp Val Pro His Trp Ile Glu Val Gly Asn Val
                325                 330                 335

Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu Pro Leu
            340                 345                 350

Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala Leu Leu
        355                 360                 365

Trp Arg Pro Arg Ser Met Thr Glu Val Arg Glu His Leu Ser Pro Arg
    370                 375                 380

Leu Val Ala Ala Ala Thr Ser Gly Gly Ala Pro Leu Ile Val Arg Trp
385                 390                 395                 400

Lys Gly Lys Asp Arg Gly Val Ile Thr Leu Ser Asp His Val Arg Ser
                405                 410                 415

Asp Ser Ser Asp Ala Ile Ile Ala Ile Glu Glu Gln Gly Ile Glu Thr
            420                 425                 430

Met Met Leu Ser Arg Asp Thr Tyr Pro Val Ala Arg Arg Tyr Ala Asp
        435                 440                 445

Ser Leu Gly Ile Thr His Val Leu Ala Gly Ile Ala Pro Gly Lys Lys
    450                 455                 460

Ala Gln Val Val Arg Ala Val His Thr Arg Gly Ser Thr Val Ala Met
465                 470                 475                 480
```

```
Ile Gly Asp Glu Ser Val Met Asp Cys Leu Lys Val Ala Asp Val Gly
                485                 490                 495

Val Leu Met Gly Val Asp Arg Pro Ser Asp Leu Arg Asp Asp Ser Asp
            500                 505                 510

Asp Pro Ala Ala Asp Val Val Val Met Arg Glu Glu Val Met Ser Val
        515                 520                 525

Pro Thr Leu Phe Lys Leu Ala Arg Arg Tyr Ala Lys Leu Val Asn Gly
    530                 535                 540

Asn Ile Ala Leu Ala Trp Ile Tyr Asn Gly Val Ala Met Val Leu Ala
545                 550                 555                 560

Val Ser Gly Leu Leu His Pro Met Ala Ala Thr Val Ala Met Leu Ala
                565                 570                 575

Ser Ser Leu Leu Ile Glu Trp Arg Ser Gly Arg Ala Arg Lys Tyr
            580                 585                 590
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<210> 387
<211> 327
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(304)
<223> RXA00942

<400> 387

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agagtccgct ggatttcatc acatcggaag gaagagaatt ttg agt acc aaa aat   115
                                              Leu Ser Thr Lys Asn
                                                1               5

tac cac gtc gag ggt ttg acc tgc gca aac ggt gta gct tcc gta gag   163
Tyr His Val Glu Gly Leu Thr Cys Ala Asn Gly Val Ala Ser Val Glu
                  10                  15                  20

gat gaa atc ggc att gtt gcg ggc acc cag ggt gtg gat att gat att   211
Asp Glu Ile Gly Ile Val Ala Gly Thr Gln Gly Val Asp Ile Asp Ile
              25                  30                  35

gag acc ggc cgc gtc acg gtg act ggt gaa ggt ttc act gac gag gaa   259
Glu Thr Gly Arg Val Thr Val Thr Gly Glu Gly Phe Thr Asp Glu Glu
          40                  45                  50

atc att gag gct gtc gcg aac gcg ggc tac aaa gtt tct ggg cgg       304
Ile Ile Glu Ala Val Ala Asn Ala Gly Tyr Lys Val Ser Gly Arg
      55                  60                  65

tagcacaatt acacattcat ctc                                        327
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<210> 388
<211> 68

<212> PRT
<213> Corynebacterium glutamicum

<400> 388
Leu Ser Thr Lys Asn Tyr His Val Glu Gly Leu Thr Cys Ala Asn Gly
1 5 10 15

Val Ala Ser Val Glu Asp Glu Ile Gly Ile Val Ala Gly Thr Gln Gly
20 25 30

Val Asp Ile Asp Ile Glu Thr Gly Arg Val Thr Val Thr Gly Glu Gly
35 40 45

Phe Thr Asp Glu Glu Ile Ile Glu Ala Val Ala Asn Ala Gly Tyr Lys
50 55 60

Val Ser Gly Arg
65

<210> 389
<211> 1925
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1902)
<223> RXN01338

<400> 389
aaa act tat acc cca aat ccc tgg atg tta ttc atc cgc tca ttt gat 48
Lys Thr Tyr Thr Pro Asn Pro Trp Met Leu Phe Ile Arg Ser Phe Asp
1 5 10 15

ggc atc atc act gtc gca gcc ctt gtt gcc atc gca ata cat ctc att 96
Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile His Leu Ile
20 25 30

tta tgg ctg gct cta gat cta gat ggc ctt gct aaa aac tgg cct tta 144
Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn Trp Pro Leu
35 40 45

ata gcc atc gtt atc gta ggt ggc att ccg ttg atg tgg gat gtg ctg 192
Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp Asp Val Leu
50 55 60

aaa tca gcc att aaa act cgc ggt ggc gcg gat act tta gca gca gtc 240
Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu Ala Ala Val
65 70 75 80

tcc atc att act tct gtg ttg tta ggg gag tgg ttg gtt gcc gcg atc 288
Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val Ala Ala Ile
85 90 95

atc gtg ctc atg ctc tct ggt ggt gaa gcg cta gaa gag gca gca tca 336
Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu Ala Ala Ser
100 105 110

cgg cga gcc agt ggc acc ttg gac gca ctt gcc cgg cgc gca cca agt 384
Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg Ala Pro Ser

```
        115                 120                 125

aca gct cac cgc ctg ttg ggt gca acc att ctt gat gga acc gaa gag   432
Thr Ala His Arg Leu Leu Gly Ala Thr Ile Leu Asp Gly Thr Glu Glu
    130                 135                 140

atc gcc gtg gaa gag atc acg gtt ggt gat tta gtg gcg gtg ctc ccg   480
Ile Ala Val Glu Glu Ile Thr Val Gly Asp Leu Val Ala Val Leu Pro
145                 150                 155                 160

cat gaa ctt tgt ccc gtg gat ggt gaa atc gtg gca ggc cac ggc acc   528
His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly His Gly Thr
                165                 170                 175

atg gat gag tct tat ctc acg ggt gag ccc tat gtg gtg agt aaa tct   576
Met Asp Glu Ser Tyr Leu Thr Gly Glu Pro Tyr Val Val Ser Lys Ser
            180                 185                 190

aaa ggt tcg caa gca atg tcg ggt gca gtc aat ggt gat act ccg ctg   624
Lys Gly Ser Gln Ala Met Ser Gly Ala Val Asn Gly Asp Thr Pro Leu
        195                 200                 205

acg att gtt gcc aca aag ctt gcc cat gat tcc aga tac gcc caa att   672
Thr Ile Val Ala Thr Lys Leu Ala His Asp Ser Arg Tyr Ala Gln Ile
    210                 215                 220

gtt ggt gta ctc cat gaa gca gaa aac aac cgc cca gaa atg cgc agg   720
Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu Met Arg Arg
225                 230                 235                 240

atg gct gac cgt ctt ggc gcg tgg tat acg gtg att gca ctt gcc ctc   768
Met Ala Asp Arg Leu Gly Ala Trp Tyr Thr Val Ile Ala Leu Ala Leu
                245                 250                 255

ggt ggt ctt ggc tgg att gtc tcc ggc gac cca gtg agg ttc ttg gct   816
Gly Gly Leu Gly Trp Ile Val Ser Gly Asp Pro Val Arg Phe Leu Ala
            260                 265                 270

gtt gtc gtt gtc gcc acc cca tgt cca ttg ctc att gca gtg cca gtg   864
Val Val Val Val Ala Thr Pro Cys Pro Leu Leu Ile Ala Val Pro Val
        275                 280                 285

gcg atc atc ggt gcg att tct ctt gcg gct cgt cgg ggc atc atc gtg   912
Ala Ile Ile Gly Ala Ile Ser Leu Ala Ala Arg Arg Gly Ile Ile Val
    290                 295                 300

aag aac cct gga atg ctg gaa aac gct tca gga gta aag aca gtg atg   960
Lys Asn Pro Gly Met Leu Glu Asn Ala Ser Gly Val Lys Thr Val Met
305                 310                 315                 320

ttc gat aag act gga acg ctc acc tat ggc agg cca gtg att act gat   1008
Phe Asp Lys Thr Gly Thr Leu Thr Tyr Gly Arg Pro Val Ile Thr Asp
                325                 330                 335

atc cac act gct ccc gga gtt gag gaa gat aca gtc cta gct ttg gct   1056
Ile His Thr Ala Pro Gly Val Glu Glu Asp Thr Val Leu Ala Leu Ala
            340                 345                 350

gct tca gta gag cgc tac tcc aga cac ccg ttg gct gac gcg att cgt   1104
Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp Ala Ile Arg
        355                 360                 365
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gag ggc gca aaa gcc agg gaa ctt cat ctg cct gat gta gtg gaa gta   1152
Glu Gly Ala Lys Ala Arg Glu Leu His Leu Pro Asp Val Val Glu Val
    370                 375                 380

tcg gaa cgt cca gga cag gga cta acc ggc acg gtg ggc gag cac ctg   1200
Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly Glu His Leu
385                 390                 395                 400

gtt cga ata acc aat agg cgc agc aca cta gaa att gat cca gac agc   1248
Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp Pro Asp Ser
                405                 410                 415

aag aac tac att ccg gtg aca agt tcc ggc atg gaa tct gtg gtg ctt   1296
Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser Val Val Leu
            420                 425                 430

gtt gat gat aaa tat gca gca ctc att cgc ctc cgg gat gaa cct cgt   1344
Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp Glu Pro Arg
        435                 440                 445

gca tct gcc agt gag ttc atc gcg cac ttg ccc aag aag cac aaa gtg   1392
Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys His Lys Val
    450                 455                 460

gac aag ctc atg att atc tct ggt gat cgc gca tct gag gtt cgt tac   1440
Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu Val Arg Tyr
465                 470                 475                 480

ctt gcg gac aag gtt ggc att gat gag gta cac gca gag gcc tca ccg   1488
Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu Ala Ser Pro
                485                 490                 495

gaa gac aag ctg aac att gtt aat cgg cat aat gag cac ggc gcc acc   1536
Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His Gly Ala Thr
            500                 505                 510

atg ttc tta ggt gat gga atc aac gat gcg cca gcc atg gcc gtt gcc   1584
Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met Ala Val Ala
        515                 520                 525

acc gtt ggt gtc gcg atg gga gca gac tcc gat gtc acg tcc gaa gca   1632
Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr Ser Glu Ala
    530                 535                 540

gca gat gct gtg att ttg gat tct tcc ctg gaa cgt ctc gac gat ctg   1680
Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu Asp Asp Leu
545                 550                 555                 560

ctc cac atc agt gca cgg atg cgt cga ata gcg ttg caa tct gcg ggc   1728
Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln Ser Ala Gly
                565                 570                 575

ggt ggc atg gcg ttg agt gtc ata gga atg atc ctc gcg gta ttt gga   1776
Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala Val Phe Gly
            580                 585                 590

ttc ttg acg cca ctg atg ggt gcg atc ttc caa gag gtc att gac gtg   1824
Phe Leu Thr Pro Leu Met Gly Ala Ile Phe Gln Glu Val Ile Asp Val
        595                 600                 605
```

```
ctg gct atc ctc aat tcc gct cgg gtc gca ctg cca cgc gga gcg att   1872
Leu Ala Ile Leu Asn Ser Ala Arg Val Ala Leu Pro Arg Gly Ala Ile
    610                 615                 620

agt gat ttt gat acg caa gaa aaa gtt tct tagcagggta acctaaatgt     1922
Ser Asp Phe Asp Thr Gln Glu Lys Val Ser
625                 630

cgt                                                               1925
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<210> 390
<211> 634
<212> PRT
<213> Corynebacterium glutamicum

<400> 390

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Lys Thr Tyr Thr Pro Asn Pro Trp Met Leu Phe Ile Arg Ser Phe Asp
 1               5                  10                  15

Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile His Leu Ile
            20                  25                  30

Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn Trp Pro Leu
        35                  40                  45

Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp Asp Val Leu
    50                  55                  60

Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu Ala Ala Val
65                  70                  75                  80

Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val Ala Ala Ile
                85                  90                  95

Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu Ala Ala Ser
            100                 105                 110

Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg Ala Pro Ser
        115                 120                 125

Thr Ala His Arg Leu Leu Gly Ala Thr Ile Leu Asp Gly Thr Glu Glu
    130                 135                 140

Ile Ala Val Glu Glu Ile Thr Val Gly Asp Leu Val Ala Val Leu Pro
145                 150                 155                 160

His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly His Gly Thr
                165                 170                 175

Met Asp Glu Ser Tyr Leu Thr Gly Glu Pro Tyr Val Val Ser Lys Ser
            180                 185                 190

Lys Gly Ser Gln Ala Met Ser Gly Ala Val Asn Gly Asp Thr Pro Leu
        195                 200                 205

Thr Ile Val Ala Thr Lys Leu Ala His Asp Ser Arg Tyr Ala Gln Ile
    210                 215                 220

Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu Met Arg Arg
225                 230                 235                 240
```

Met Ala Asp Arg Leu Gly Ala Trp Tyr Thr Val Ile Ala Leu Ala Leu
245 250 255

Gly Gly Leu Gly Trp Ile Val Ser Gly Asp Pro Val Arg Phe Leu Ala
260 265 270

Val Val Val Val Ala Thr Pro Cys Pro Leu Leu Ile Ala Val Pro Val
275 280 285

Ala Ile Ile Gly Ala Ile Ser Leu Ala Ala Arg Arg Gly Ile Ile Val
290 295 300

Lys Asn Pro Gly Met Leu Glu Asn Ala Ser Gly Val Lys Thr Val Met
305 310 315 320

Phe Asp Lys Thr Gly Thr Leu Thr Tyr Gly Arg Pro Val Ile Thr Asp
325 330 335

Ile His Thr Ala Pro Gly Val Glu Glu Asp Thr Val Leu Ala Leu Ala
340 345 350

Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp Ala Ile Arg
355 360 365

Glu Gly Ala Lys Ala Arg Glu Leu His Leu Pro Asp Val Val Glu Val
370 375 380

Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly Glu His Leu
385 390 395 400

Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp Pro Asp Ser
405 410 415

Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser Val Val Leu
420 425 430

Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp Glu Pro Arg
435 440 445

Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys His Lys Val
450 455 460

Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu Val Arg Tyr
465 470 475 480

Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu Ala Ser Pro
485 490 495

Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His Gly Ala Thr
500 505 510

Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met Ala Val Ala
515 520 525

Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr Ser Glu Ala
530 535 540

Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu Asp Asp Leu
545 550 555 560

```
Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln Ser Ala Gly
                565                 570                 575

Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala Val Phe Gly
            580                 585                 590

Phe Leu Thr Pro Leu Met Gly Ala Ile Phe Gln Glu Val Ile Asp Val
        595                 600                 605

Leu Ala Ile Leu Asn Ser Ala Arg Val Ala Leu Pro Arg Gly Ala Ile
    610                 615                 620

Ser Asp Phe Asp Thr Gln Glu Lys Val Ser
625                 630
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<210> 391
<211> 2001
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1978)
<223> FRXA01338

<400> 391

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atggggttta tgaataaaaa cttatacccc aaatccctgg atg tta ttc atc cgc   115
                                              Met Leu Phe Ile Arg
                                                1               5

tca ttt gat ggc atc atc act gtc gca gcc ctt gtt gcc atc gca ata   163
Ser Phe Asp Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile
                10                  15                  20

cat ctc att tta tgg ctg gct cta gat cta gat ggc ctt gct aaa aac   211
His Leu Ile Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn
            25                  30                  35

tgg cct tta ata gcc atc gtt atc gta ggt ggc att ccg ttg atg tgg   259
Trp Pro Leu Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp
        40                  45                  50

gat gtg ctg aaa tca gcc att aaa act cgc ggt ggc gcg gat act tta   307
Asp Val Leu Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu
    55                  60                  65

gca gca gtc tcc atc att act tct gtg ttg tta ggg gag tgg ttg gtt   355
Ala Ala Val Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val
70                  75                  80                  85

gcc gcg atc atc gtg ctc atg ctc tct ggt ggt gaa gcg cta gaa gag   403
Ala Ala Ile Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu
                90                  95                  100

gca gca tca cgg cga gcc agt ggc acc ttg gac gca ctt gcc cgg cgc   451
Ala Ala Ser Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg
            105                 110                 115
```

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gca cca agt aca gct cac cgc ctg ttg ggt gca acc att ctt gat gga   499
Ala Pro Ser Thr Ala His Arg Leu Leu Gly Ala Thr Ile Leu Asp Gly
        120                 125                 130

acc gaa gag atc gcc gtg gaa gag atc acg gtt ggt gat tta gtg gcg   547
Thr Glu Glu Ile Ala Val Glu Glu Ile Thr Val Gly Asp Leu Val Ala
    135                 140                 145

gtg ctc ccg cat gaa ctt tgt ccc gtg gat ggt gaa atc gtg gca ggc   595
Val Leu Pro His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly
150                 155                 160                 165

cac ggc acc atg gat gag tct tat ctc acg ggt gag ccc tat gtg gtg   643
His Gly Thr Met Asp Glu Ser Tyr Leu Thr Gly Glu Pro Tyr Val Val
                170                 175                 180

agt aaa tct aaa ggt tcg caa gca atg tcg ggt gca gtc aat ggt gat   691
Ser Lys Ser Lys Gly Ser Gln Ala Met Ser Gly Ala Val Asn Gly Asp
            185                 190                 195

act ccg ctg acg att gtt gcc aca aag ctt gcc cat gat tcc aga tac   739
Thr Pro Leu Thr Ile Val Ala Thr Lys Leu Ala His Asp Ser Arg Tyr
        200                 205                 210

gcc caa att gtt ggt gta ctc cat gaa gca gaa aac aac cgc cca gaa   787
Ala Gln Ile Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu
    215                 220                 225

atg cgc agg atg gct gac cgt ctt ggc gcg tgg tat acg gtg att gca   835
Met Arg Arg Met Ala Asp Arg Leu Gly Ala Trp Tyr Thr Val Ile Ala
230                 235                 240                 245

ctt gcc ctc ggt ggt ctt ggc tgg att gtc tcc ggc gac cca gtg agg   883
Leu Ala Leu Gly Gly Leu Gly Trp Ile Val Ser Gly Asp Pro Val Arg
                250                 255                 260

ttc ttg gct gtt gtc gtt gtc gcc acc cca tgt cca ttg ctc att gca   931
Phe Leu Ala Val Val Val Val Ala Thr Pro Cys Pro Leu Leu Ile Ala
            265                 270                 275

gtg cca gtg gcg atc atc ggt gcg att tct ctt gcg gct cgt cgg ggc   979
Val Pro Val Ala Ile Ile Gly Ala Ile Ser Leu Ala Ala Arg Arg Gly
        280                 285                 290

atc atc gtg aag aac cct gga atg ctg gaa aac gct tca gga gta aag   1027
Ile Ile Val Lys Asn Pro Gly Met Leu Glu Asn Ala Ser Gly Val Lys
    295                 300                 305

aca gtg atg ttc gat aag act gga acg ctc acc tat ggc agg cca gtg   1075
Thr Val Met Phe Asp Lys Thr Gly Thr Leu Thr Tyr Gly Arg Pro Val
310                 315                 320                 325

att act gat atc cac act gct ccc gga gtt gag gaa gat aca gtc cta   1123
Ile Thr Asp Ile His Thr Ala Pro Gly Val Glu Glu Asp Thr Val Leu
                330                 335                 340

gct ttg gct gct tca gta gag cgc tac tcc aga cac ccg ttg gct gac   1171
Ala Leu Ala Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp
            345                 350                 355

gcg att cgt gag ggc gca aaa gcc agg gaa ctt cat ctg cct gat gta   1219
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US 2005/0196848 A1

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Ala Ile Arg Glu Gly Ala Lys Ala Arg Glu Leu His Leu Pro Asp Val
        360                 365                 370

gtg gaa gta tcg gaa cgt cca gga cag gga cta acc ggc acg gtg ggc   1267
Val Glu Val Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly
    375                 380                 385

gag cac ctg gtt cga ata acc aat agg cgc agc aca cta gaa att gat   1315
Glu His Leu Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp
390                 395                 400                 405

cca gac agc aag aac tac att ccg gtg aca agt tcc ggc atg gaa tct   1363
Pro Asp Ser Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser
                410                 415                 420

gtg gtg ctt gtt gat gat aaa tat gca gca ctc att cgc ctc cgg gat   1411
Val Val Leu Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp
            425                 430                 435

gaa cct cgt gca tct gcc agt gag ttc atc gcg cac ttg ccc aag aag   1459
Glu Pro Arg Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys
        440                 445                 450

cac aaa gtg gac aag ctc atg att atc tct ggt gat cgc gca tct gag   1507
His Lys Val Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu
    455                 460                 465

gtt cgt tac ctt gcg gac aag gtt ggc att gat gag gta cac gca gag   1555
Val Arg Tyr Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu
470                 475                 480                 485

gcc tca ccg gaa gac aag ctg aac att gtt aat cgg cat aat gag cac   1603
Ala Ser Pro Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His
                490                 495                 500

ggc gcc acc atg ttc tta ggt gat gga atc aac gat gcg cca gcc atg   1651
Gly Ala Thr Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met
            505                 510                 515

gcc gtt gcc acc gtt ggt gtc gcg atg gga gca gac tcc gat gtc acg   1699
Ala Val Ala Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr
        520                 525                 530

tcc gaa gca gca gat gct gtg att ttg gat tct tcc ctg gaa cgt ctc   1747
Ser Glu Ala Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu
    535                 540                 545

gac gat ctg ctc cac atc agt gca cgg atg cgt cga ata gcg ttg caa   1795
Asp Asp Leu Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln
550                 555                 560                 565

tct gcg ggc ggt ggc atg gcg ttg agt gtc ata gga atg atc ctc gcg   1843
Ser Ala Gly Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala
                570                 575                 580

gta ttt gga ttc ttg acg cca ctg atg ggt gcg atc ttc caa gag gtc   1891
Val Phe Gly Phe Leu Thr Pro Leu Met Gly Ala Ile Phe Gln Glu Val
            585                 590                 595

att gac gtg ctg gct atc ctc aat tcc gct cgg gtc gca ctg cca cgc   1939
Ile Asp Val Leu Ala Ile Leu Asn Ser Ala Arg Val Ala Leu Pro Arg
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600 605 610

gga gcg att agt gat ttt gat acg caa gaa aaa gtt tct tagcagggta 1988
Gly Ala Ile Ser Asp Phe Asp Thr Gln Glu Lys Val Ser
615 620 625

acctaaatgt cgt 2001

<210> 392
<211> 626
<212> PRT
<213> Corynebacterium glutamicum

<400> 392
Met Leu Phe Ile Arg Ser Phe Asp Gly Ile Ile Thr Val Ala Ala Leu
1 5 10 15

Val Ala Ile Ala Ile His Leu Ile Leu Trp Leu Ala Leu Asp Leu Asp
20 25 30

Gly Leu Ala Lys Asn Trp Pro Leu Ile Ala Ile Val Ile Val Gly Gly
35 40 45

Ile Pro Leu Met Trp Asp Val Leu Lys Ser Ala Ile Lys Thr Arg Gly
50 55 60

Gly Ala Asp Thr Leu Ala Ala Val Ser Ile Ile Thr Ser Val Leu Leu
65 70 75 80

Gly Glu Trp Leu Val Ala Ala Ile Ile Val Leu Met Leu Ser Gly Gly
85 90 95

Glu Ala Leu Glu Glu Ala Ala Ser Arg Arg Ala Ser Gly Thr Leu Asp
100 105 110

Ala Leu Ala Arg Arg Ala Pro Ser Thr Ala His Arg Leu Leu Gly Ala
115 120 125

Thr Ile Leu Asp Gly Thr Glu Glu Ile Ala Val Glu Glu Ile Thr Val
130 135 140

Gly Asp Leu Val Ala Val Leu Pro His Glu Leu Cys Pro Val Asp Gly
145 150 155 160

Glu Ile Val Ala Gly His Gly Thr Met Asp Glu Ser Tyr Leu Thr Gly
165 170 175

Glu Pro Tyr Val Val Ser Lys Ser Lys Gly Ser Gln Ala Met Ser Gly
180 185 190

Ala Val Asn Gly Asp Thr Pro Leu Thr Ile Val Ala Thr Lys Leu Ala
195 200 205

His Asp Ser Arg Tyr Ala Gln Ile Val Gly Val Leu His Glu Ala Glu
210 215 220

Asn Asn Arg Pro Glu Met Arg Arg Met Ala Asp Arg Leu Gly Ala Trp
225 230 235 240

Tyr Thr Val Ile Ala Leu Ala Leu Gly Gly Leu Gly Trp Ile Val Ser

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245 250 255

Gly Asp Pro Val Arg Phe Leu Ala Val Val Val Val Ala Thr Pro Cys
260 265 270

Pro Leu Leu Ile Ala Val Pro Val Ala Ile Ile Gly Ala Ile Ser Leu
275 280 285

Ala Ala Arg Arg Gly Ile Ile Val Lys Asn Pro Gly Met Leu Glu Asn
290 295 300

Ala Ser Gly Val Lys Thr Val Met Phe Asp Lys Thr Gly Thr Leu Thr
305 310 315 320

Tyr Gly Arg Pro Val Ile Thr Asp Ile His Thr Ala Pro Gly Val Glu
325 330 335

Glu Asp Thr Val Leu Ala Leu Ala Ala Ser Val Glu Arg Tyr Ser Arg
340 345 350

His Pro Leu Ala Asp Ala Ile Arg Glu Gly Ala Lys Ala Arg Glu Leu
355 360 365

His Leu Pro Asp Val Val Glu Val Ser Glu Arg Pro Gly Gln Gly Leu
370 375 380

Thr Gly Thr Val Gly Glu His Leu Val Arg Ile Thr Asn Arg Arg Ser
385 390 395 400

Thr Leu Glu Ile Asp Pro Asp Ser Lys Asn Tyr Ile Pro Val Thr Ser
405 410 415

Ser Gly Met Glu Ser Val Val Leu Val Asp Asp Lys Tyr Ala Ala Leu
420 425 430

Ile Arg Leu Arg Asp Glu Pro Arg Ala Ser Ala Ser Glu Phe Ile Ala
435 440 445

His Leu Pro Lys Lys His Lys Val Asp Lys Leu Met Ile Ile Ser Gly
450 455 460

Asp Arg Ala Ser Glu Val Arg Tyr Leu Ala Asp Lys Val Gly Ile Asp
465 470 475 480

Glu Val His Ala Glu Ala Ser Pro Glu Asp Lys Leu Asn Ile Val Asn
485 490 495

Arg His Asn Glu His Gly Ala Thr Met Phe Leu Gly Asp Gly Ile Asn
500 505 510

Asp Ala Pro Ala Met Ala Val Ala Thr Val Gly Val Ala Met Gly Ala
515 520 525

Asp Ser Asp Val Thr Ser Glu Ala Ala Asp Ala Val Ile Leu Asp Ser
530 535 540

Ser Leu Glu Arg Leu Asp Asp Leu Leu His Ile Ser Ala Arg Met Arg
545 550 555 560

Arg Ile Ala Leu Gln Ser Ala Gly Gly Gly Met Ala Leu Ser Val Ile
565 570 575

```
Gly Met Ile Leu Ala Val Phe Gly Phe Leu Thr Pro Leu Met Gly Ala
            580                 585                 590

Ile Phe Gln Glu Val Ile Asp Val Leu Ala Ile Leu Asn Ser Ala Arg
        595                 600                 605

Val Ala Leu Pro Arg Gly Ala Ile Ser Asp Phe Asp Thr Gln Glu Lys
    610                 615                 620

Val Ser
625
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<210> 393
<211> 324
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(301)
<223> RXA01625

<400> 393
gggagcgaag ttccctgggt taaattaacc acttgcagta taccctagtg gggtatattg 60

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tctgctgtta gaagataccc gacagaaagg ggccaataat atg gct atc aag aac   115
                                              Met Ala Ile Lys Asn
                                                1               5

tac acc gtc gaa ggc atg act tgt gga cac tgc gtc tcc tcc gta aag   163
Tyr Thr Val Glu Gly Met Thr Cys Gly His Cys Val Ser Ser Val Lys
                10                  15                  20

gaa gag gtc gga gag gtt gct ggc gtc acc gct gtg gac gtc acc cta   211
Glu Glu Val Gly Glu Val Ala Gly Val Thr Ala Val Asp Val Thr Leu
            25                  30                  35

gaa acc ggt gcc gtg cag gtt acc ggc gaa gac ttc acc gac gag gct   259
Glu Thr Gly Ala Val Gln Val Thr Gly Glu Asp Phe Thr Asp Glu Ala
        40                  45                  50

gtc aag gct gct gtc gtt gag gct ggc tac aag gtt gtt gca           301
Val Lys Ala Ala Val Val Glu Ala Gly Tyr Lys Val Val Ala
    55                  60                  65

taaacccctg aaaagtttaa agc                                        324
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<210> 394
<211> 67
<212> PRT
<213> Corynebacterium glutamicum

<400> 394

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Met Ala Ile Lys Asn Tyr Thr Val Glu Gly Met Thr Cys Gly His Cys
  1               5                  10                  15

Val Ser Ser Val Lys Glu Glu Val Gly Glu Val Ala Gly Val Thr Ala
            20                  25                  30
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Val Asp Val Thr Leu Glu Thr Gly Ala Val Gln Val Thr Gly Glu Asp
35 40 45

Phe Thr Asp Glu Ala Val Lys Ala Ala Val Val Glu Ala Gly Tyr Lys
50 55 60

Val Val Ala
65

<210> 395
<211> 2799
<212> DNA
<213> Corynebacterium glutamicum

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<223> RXA02220

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Val Ser Ser Pro Leu
1 5

ccc gct gcc gtc aca tca aaa ccc gcc cac gcg ctt tcc tct gat gag 163
Pro Ala Ala Val Thr Ser Lys Pro Ala His Ala Leu Ser Ser Asp Glu
10 15 20

gtg tta gaa aat ctc ggg gtc cag gac acc gga ttg acc tcc gcg gag 211
Val Leu Glu Asn Leu Gly Val Gln Asp Thr Gly Leu Thr Ser Ala Glu
25 30 35

gca aca cag cgt ttg gaa gca aac ggg cca aac gag ctt cct caa act 259
Ala Thr Gln Arg Leu Glu Ala Asn Gly Pro Asn Glu Leu Pro Gln Thr
40 45 50

cca cct gaa aca gtc tgg caa cgg cta ttc cgc cag gtc aac gat cca 307
Pro Pro Glu Thr Val Trp Gln Arg Leu Phe Arg Gln Val Asn Asp Pro
55 60 65

atg atc tac gtt ctc att gcc gcc gcg gta ctc acg gcg ttt ctt ggg 355
Met Ile Tyr Val Leu Ile Ala Ala Ala Val Leu Thr Ala Phe Leu Gly
70 75 80 85

cat tgg aca gac acc atc gtg atc ggc gcc gtt gtc atc atc aac atg 403
His Trp Thr Asp Thr Ile Val Ile Gly Ala Val Val Ile Ile Asn Met
90 95 100

atg gtt ggg ttc atc caa gag ggc aaa gct gcg gat gcg ttg gca tcg 451
Met Val Gly Phe Ile Gln Glu Gly Lys Ala Ala Asp Ala Leu Ala Ser
105 110 115

atc cgc aac atg ctc tcc ccg gaa tcc gcg gcg ttg cgc gat ggg gtc 499
Ile Arg Asn Met Leu Ser Pro Glu Ser Ala Ala Leu Arg Asp Gly Val
120 125 130

ttc cac aaa att gat gcg gca gag ctg gtg gtc ggt gac gtt gtg aaa 547

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Phe His Lys Ile Asp Ala Ala Glu Leu Val Val Gly Asp Val Val Lys
    135                 140                 145

cta tcc gcc ggc gat aaa gtg ccc gct gac ctg cgc atg ctc gcc gcc   595
Leu Ser Ala Gly Asp Lys Val Pro Ala Asp Leu Arg Met Leu Ala Ala
150                 155                 160                 165

acc aat ctg cac att gag gaa tcc gcg ctc acc ggc gag gcg gaa gca   643
Thr Asn Leu His Ile Glu Glu Ser Ala Leu Thr Gly Glu Ala Glu Ala
                170                 175                 180

gtg gtc aaa ggt act gat cca gtt gag gcc gac gcc gga atc ggc gac   691
Val Val Lys Gly Thr Asp Pro Val Glu Ala Asp Ala Gly Ile Gly Asp
            185                 190                 195

cgc aca tcc atg gcg ttt tca gga acg ctg gtg ctc aca ggc agc ggc   739
Arg Thr Ser Met Ala Phe Ser Gly Thr Leu Val Leu Thr Gly Ser Gly
        200                 205                 210

acc ggc gtg gtc acc gcc acc ggt gca ggc aca gaa atc ggg cac atc   787
Thr Gly Val Val Thr Ala Thr Gly Ala Gly Thr Glu Ile Gly His Ile
    215                 220                 225

acc acc atg ctt gcc gac gtc gac tcc gtg gat acc cca ttg act cgg   835
Thr Thr Met Leu Ala Asp Val Asp Ser Val Asp Thr Pro Leu Thr Arg
230                 235                 240                 245

tcg atg aaa aag ttc tca tcg gcg tta gca atc gtg tgt gta ttc cta   883
Ser Met Lys Lys Phe Ser Ser Ala Leu Ala Ile Val Cys Val Phe Leu
                250                 255                 260

gcg atc ctc atg ctg gtg gtt gcc ggt cta gtc cac cac aca cct ttg   931
Ala Ile Leu Met Leu Val Val Ala Gly Leu Val His His Thr Pro Leu
            265                 270                 275

gaa gag ctc att ctt tcc gcc atc ggc ttt gcg gtg gct gcc att ccg   979
Glu Glu Leu Ile Leu Ser Ala Ile Gly Phe Ala Val Ala Ala Ile Pro
        280                 285                 290

gag ggt cta cct gcg gtt atc gcc atc acg ctg gca ttg ggt gtg caa   1027
Glu Gly Leu Pro Ala Val Ile Ala Ile Thr Leu Ala Leu Gly Val Gln
    295                 300                 305

aag atg gca gct cga aat gcg att acg cgc cgg ttg aat tcc gtg gaa   1075
Lys Met Ala Ala Arg Asn Ala Ile Thr Arg Arg Leu Asn Ser Val Glu
310                 315                 320                 325

aca ctt ggc tct gtc acc acc atc tgc acg gat aaa acc ggc aca ctc   1123
Thr Leu Gly Ser Val Thr Thr Ile Cys Thr Asp Lys Thr Gly Thr Leu
                330                 335                 340

acc cgc aat gag atg aca gtc cgc gca atc gcc acc ggt acg agt ctt   1171
Thr Arg Asn Glu Met Thr Val Arg Ala Ile Ala Thr Gly Thr Ser Leu
            345                 350                 355

tat gac gtc agt gga gca ggc tac gaa cct ctc ggg gaa atc cgc tta   1219
Tyr Asp Val Ser Gly Ala Gly Tyr Glu Pro Leu Gly Glu Ile Arg Leu
        360                 365                 370

aaa gac ggc gag caa gta tcc aag cag gat ttc cca gat ctc tac gcc   1267
Lys Asp Gly Glu Gln Val Ser Lys Gln Asp Phe Pro Asp Leu Tyr Ala
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    375                 380                 385

atg gcg ttg gtc gca gcg aac gtc aac gac gcc gaa att tac caa gaa   1315
Met Ala Leu Val Ala Ala Asn Val Asn Asp Ala Glu Ile Tyr Gln Glu
390                 395                 400                 405

gac ggc atg tgg agg ctt tcc ggc gaa ccc acc gac ggc ggt att cgt   1363
Asp Gly Met Trp Arg Leu Ser Gly Glu Pro Thr Asp Gly Gly Ile Arg
                410                 415                 420

gcc ttt gca atg aaa acc aac gct gaa atc ttg acc cga aca gcc gaa   1411
Ala Phe Ala Met Lys Thr Asn Ala Glu Ile Leu Thr Arg Thr Ala Glu
            425                 430                 435

gtc ccc ttc gat tcc gca tac aaa tac atg gcg acg ctt cac acc atc   1459
Val Pro Phe Asp Ser Ala Tyr Lys Tyr Met Ala Thr Leu His Thr Ile
        440                 445                 450

gat gga gca aac acc atg ctg gtc aag ggc gct ccc gat cgt tta ttg   1507
Asp Gly Ala Asn Thr Met Leu Val Lys Gly Ala Pro Asp Arg Leu Leu
    455                 460                 465

gat aga agt gca cag cag cgc aac ggt gaa cca ctt gac cgg ccg tat   1555
Asp Arg Ser Ala Gln Gln Arg Asn Gly Glu Pro Leu Asp Arg Pro Tyr
470                 475                 480                 485

tgg gaa cag ctc atc gag gac ctc gcg tcc caa ggc ctc cgc gtg ctg   1603
Trp Glu Gln Leu Ile Glu Asp Leu Ala Ser Gln Gly Leu Arg Val Leu
                490                 495                 500

gct gcg gca tat aaa gag ctt ccc cac agc acg tca aca att act cca   1651
Ala Ala Ala Tyr Lys Glu Leu Pro His Ser Thr Ser Thr Ile Thr Pro
            505                 510                 515

gaa gat gtt gac cag ggc gaa ctc acc ttc ctc ggg ctc tac ggc atc   1699
Glu Asp Val Asp Gln Gly Glu Leu Thr Phe Leu Gly Leu Tyr Gly Ile
        520                 525                 530

atg gat ccg cca cgc gaa gaa gtc atc gaa gcc atg aaa gtg gtg caa   1747
Met Asp Pro Pro Arg Glu Glu Val Ile Glu Ala Met Lys Val Val Gln
    535                 540                 545

tcg gca ggc gtt cgc gtc cgc atg atc acc ggc gat cac tcc tcc acg   1795
Ser Ala Gly Val Arg Val Arg Met Ile Thr Gly Asp His Ser Ser Thr
550                 555                 560                 565

gcc cgc gca atc gcc cgc gaa gtg gga atc cgc ggc cag aac gtg ctc   1843
Ala Arg Ala Ile Ala Arg Glu Val Gly Ile Arg Gly Gln Asn Val Leu
                570                 575                 580

acc ggt gcg gaa att act gcg gct act gat gag gag ctg cag gga ctc   1891
Thr Gly Ala Glu Ile Thr Ala Ala Thr Asp Glu Glu Leu Gln Gly Leu
            585                 590                 595

gtc gat aat gct gat ctt ttt gtg cgc acc agc ccc gag cac aag ctg   1939
Val Asp Asn Ala Asp Leu Phe Val Arg Thr Ser Pro Glu His Lys Leu
        600                 605                 610

cgc gtc gtg cgc gca ctg caa gct aac ggc gaa gtc gcg tcc atg acc   1987
Arg Val Val Arg Ala Leu Gln Ala Asn Gly Glu Val Ala Ser Met Thr
    615                 620                 625
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ggc gac ggc gtc aac gat gcg cca gcg cta aaa caa gcc gac gtc ggc   2035
Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Lys Gln Ala Asp Val Gly
630                 635                 640                 645

gtc gcc atg ggc att aag ggc acc gaa gcc acc aaa gac gcg gcc gac   2083
Val Ala Met Gly Ile Lys Gly Thr Glu Ala Thr Lys Asp Ala Ala Asp
                650                 655                 660

atc gtg ctt gcc gac gac aat ttc gcc aca atc gcc ggc gcc gta gaa   2131
Ile Val Leu Ala Asp Asp Asn Phe Ala Thr Ile Ala Gly Ala Val Glu
            665                 670                 675

atg ggt cgc acc atc tac gac aac ctg cgc aaa gcc gtc gtc ttc atg   2179
Met Gly Arg Thr Ile Tyr Asp Asn Leu Arg Lys Ala Val Val Phe Met
        680                 685                 690

ctc ccc acc aac ggc gcc caa ggc ctc gtc att ttc atc gcg atg ctg   2227
Leu Pro Thr Asn Gly Ala Gln Gly Leu Val Ile Phe Ile Ala Met Leu
    695                 700                 705

ctc ggc tgg gaa ctg ccc atc acc gca ctt caa gtg ctg tgg atc aac   2275
Leu Gly Trp Glu Leu Pro Ile Thr Ala Leu Gln Val Leu Trp Ile Asn
710                 715                 720                 725

ctc atc acc gcc atc aca ctg tcc ctg gcg ctg tcc ttc gag ccg gcc   2323
Leu Ile Thr Ala Ile Thr Leu Ser Leu Ala Leu Ser Phe Glu Pro Ala
                730                 735                 740

gag ccc ggc atc atg aac aga aaa ccc aga aac ccc aag agc ggg ctt   2371
Glu Pro Gly Ile Met Asn Arg Lys Pro Arg Asn Pro Lys Ser Gly Leu
            745                 750                 755

atc gac gcc ccc tcc gtg ctt cgc atc gtc tat gtc tcc ctg ctg ctc   2419
Ile Asp Ala Pro Ser Val Leu Arg Ile Val Tyr Val Ser Leu Leu Leu
        760                 765                 770

ggc gga gca acg ttc tgg gct ttc ctt ggc gcc cgc gac gca gga atc   2467
Gly Gly Ala Thr Phe Trp Ala Phe Leu Gly Ala Arg Asp Ala Gly Ile
    775                 780                 785

gac atc gac acc gcc cgc acc atc gcg gtc acc acc ctt gca gtc agc   2515
Asp Ile Asp Thr Ala Arg Thr Ile Ala Val Thr Thr Leu Ala Val Ser
790                 795                 800                 805

caa gtg ttc tac ctt tta agc tcc cga tac ttc gaa gta tcc gcg ctg   2563
Gln Val Phe Tyr Leu Leu Ser Ser Arg Tyr Phe Glu Val Ser Ala Leu
                810                 815                 820

cga aaa gaa ctc ttc acc acc aac ccg att tcc tgg ctg tgc atc gca   2611
Arg Lys Glu Leu Phe Thr Thr Asn Pro Ile Ser Trp Leu Cys Ile Ala
            825                 830                 835

ctc atg ctg atc ctg caa ctg gcc ttt gtc tac ctg ccg ttc atg caa   2659
Leu Met Leu Ile Leu Gln Leu Ala Phe Val Tyr Leu Pro Phe Met Gln
        840                 845                 850

agc acc ttc gac acc gcc gca ctg acg ctt aga gat tgg gtc atg cca   2707
Ser Thr Phe Asp Thr Ala Ala Leu Thr Leu Arg Asp Trp Val Met Pro
    855                 860                 865
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ctg gtg ttt ggt gtt gtt gtc ttt gcg gtc gtt gaa acc gag aaa ttc   2755
Leu Val Phe Gly Val Val Val Phe Ala Val Val Glu Thr Glu Lys Phe
870                 875                 880                 885

atc agg cgc ctt aaa gcg tct taaggtttca gcccctcaag ata            2799
Ile Arg Arg Leu Lys Ala Ser
                890
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<210> 396
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<213> Corynebacterium glutamicum

<400> 396

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            20                  25                  30

Leu Thr Ser Ala Glu Ala Thr Gln Arg Leu Glu Ala Asn Gly Pro Asn
        35                  40                  45

Glu Leu Pro Gln Thr Pro Pro Glu Thr Val Trp Gln Arg Leu Phe Arg
    50                  55                  60

Gln Val Asn Asp Pro Met Ile Tyr Val Leu Ile Ala Ala Ala Val Leu
65                  70                  75                  80

Thr Ala Phe Leu Gly His Trp Thr Asp Thr Ile Val Ile Gly Ala Val
                85                  90                  95

Val Ile Ile Asn Met Met Val Gly Phe Ile Gln Glu Gly Lys Ala Ala
            100                 105                 110

Asp Ala Leu Ala Ser Ile Arg Asn Met Leu Ser Pro Glu Ser Ala Ala
        115                 120                 125

Leu Arg Asp Gly Val Phe His Lys Ile Asp Ala Ala Glu Leu Val Val
    130                 135                 140

Gly Asp Val Val Lys Leu Ser Ala Gly Asp Lys Val Pro Ala Asp Leu
145                 150                 155                 160

Arg Met Leu Ala Ala Thr Asn Leu His Ile Glu Glu Ser Ala Leu Thr
                165                 170                 175

Gly Glu Ala Glu Ala Val Val Lys Gly Thr Asp Pro Val Glu Ala Asp
            180                 185                 190

Ala Gly Ile Gly Asp Arg Thr Ser Met Ala Phe Ser Gly Thr Leu Val
        195                 200                 205

Leu Thr Gly Ser Gly Thr Gly Val Val Thr Ala Thr Gly Ala Gly Thr
    210                 215                 220

Glu Ile Gly His Ile Thr Thr Met Leu Ala Asp Val Asp Ser Val Asp
225                 230                 235                 240

Thr Pro Leu Thr Arg Ser Met Lys Lys Phe Ser Ser Ala Leu Ala Ile
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245 250 255

Val Cys Val Phe Leu Ala Ile Leu Met Leu Val Val Ala Gly Leu Val
260 265 270

His His Thr Pro Leu Glu Glu Leu Ile Leu Ser Ala Ile Gly Phe Ala
275 280 285

Val Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Ala Ile Thr Leu
290 295 300

Ala Leu Gly Val Gln Lys Met Ala Ala Arg Asn Ala Ile Thr Arg Arg
305 310 315 320

Leu Asn Ser Val Glu Thr Leu Gly Ser Val Thr Thr Ile Cys Thr Asp
325 330 335

Lys Thr Gly Thr Leu Thr Arg Asn Glu Met Thr Val Arg Ala Ile Ala
340 345 350

Thr Gly Thr Ser Leu Tyr Asp Val Ser Gly Ala Gly Tyr Glu Pro Leu
355 360 365

Gly Glu Ile Arg Leu Lys Asp Gly Glu Gln Val Ser Lys Gln Asp Phe
370 375 380

Pro Asp Leu Tyr Ala Met Ala Leu Val Ala Ala Asn Val Asn Asp Ala
385 390 395 400

Glu Ile Tyr Gln Glu Asp Gly Met Trp Arg Leu Ser Gly Glu Pro Thr
405 410 415

Asp Gly Gly Ile Arg Ala Phe Ala Met Lys Thr Asn Ala Glu Ile Leu
420 425 430

Thr Arg Thr Ala Glu Val Pro Phe Asp Ser Ala Tyr Lys Tyr Met Ala
435 440 445

Thr Leu His Thr Ile Asp Gly Ala Asn Thr Met Leu Val Lys Gly Ala
450 455 460

Pro Asp Arg Leu Leu Asp Arg Ser Ala Gln Gln Arg Asn Gly Glu Pro
465 470 475 480

Leu Asp Arg Pro Tyr Trp Glu Gln Leu Ile Glu Asp Leu Ala Ser Gln
485 490 495

Gly Leu Arg Val Leu Ala Ala Ala Tyr Lys Glu Leu Pro His Ser Thr
500 505 510

Ser Thr Ile Thr Pro Glu Asp Val Asp Gln Gly Glu Leu Thr Phe Leu
515 520 525

Gly Leu Tyr Gly Ile Met Asp Pro Pro Arg Glu Glu Val Ile Glu Ala
530 535 540

Met Lys Val Val Gln Ser Ala Gly Val Arg Val Arg Met Ile Thr Gly
545 550 555 560

Asp His Ser Ser Thr Ala Arg Ala Ile Ala Arg Glu Val Gly Ile Arg
565 570 575

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Gly Gln Asn Val Leu Thr Gly Ala Glu Ile Thr Ala Ala Thr Asp Glu
580 585 590

Glu Leu Gln Gly Leu Val Asp Asn Ala Asp Leu Phe Val Arg Thr Ser
595 600 605

Pro Glu His Lys Leu Arg Val Val Arg Ala Leu Gln Ala Asn Gly Glu
610 615 620

Val Ala Ser Met Thr Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Lys
625 630 635 640

Gln Ala Asp Val Gly Val Ala Met Gly Ile Lys Gly Thr Glu Ala Thr
645 650 655

Lys Asp Ala Ala Asp Ile Val Leu Ala Asp Asp Asn Phe Ala Thr Ile
660 665 670

Ala Gly Ala Val Glu Met Gly Arg Thr Ile Tyr Asp Asn Leu Arg Lys
675 680 685

Ala Val Val Phe Met Leu Pro Thr Asn Gly Ala Gln Gly Leu Val Ile
690 695 700

Phe Ile Ala Met Leu Leu Gly Trp Glu Leu Pro Ile Thr Ala Leu Gln
705 710 715 720

Val Leu Trp Ile Asn Leu Ile Thr Ala Ile Thr Leu Ser Leu Ala Leu
725 730 735

Ser Phe Glu Pro Ala Glu Pro Gly Ile Met Asn Arg Lys Pro Arg Asn
740 745 750

Pro Lys Ser Gly Leu Ile Asp Ala Pro Ser Val Leu Arg Ile Val Tyr
755 760 765

Val Ser Leu Leu Leu Gly Gly Ala Thr Phe Trp Ala Phe Leu Gly Ala
770 775 780

Arg Asp Ala Gly Ile Asp Ile Asp Thr Ala Arg Thr Ile Ala Val Thr
785 790 795 800

Thr Leu Ala Val Ser Gln Val Phe Tyr Leu Leu Ser Ser Arg Tyr Phe
805 810 815

Glu Val Ser Ala Leu Arg Lys Glu Leu Phe Thr Thr Asn Pro Ile Ser
820 825 830

Trp Leu Cys Ile Ala Leu Met Leu Ile Leu Gln Leu Ala Phe Val Tyr
835 840 845

Leu Pro Phe Met Gln Ser Thr Phe Asp Thr Ala Ala Leu Thr Leu Arg
850 855 860

Asp Trp Val Met Pro Leu Val Phe Gly Val Val Val Phe Ala Val Val
865 870 875 880

Glu Thr Glu Lys Phe Ile Arg Arg Leu Lys Ala Ser
885 890

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<213> Corynebacterium glutamicum

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<222> (101)..(1894)
<223> RXN00980

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                                            Met Leu Ala Asp Ala
                                              1               5

ttc atg atc gcg gct gca att gtt gca ggt tgg ccg atc gcg cag tct   163
Phe Met Ile Ala Ala Ala Ile Val Ala Gly Trp Pro Ile Ala Gln Ser
                  10                  15                  20

gca tat caa gca ctt cgc att cga atg gtg tcg att gac tta ctg gtc   211
Ala Tyr Gln Ala Leu Arg Ile Arg Met Val Ser Ile Asp Leu Leu Val
              25                  30                  35

gtt gtg gct gcc gtt ggt gcc atg ttc atc aac aac tat tgg gag tct   259
Val Val Ala Ala Val Gly Ala Met Phe Ile Asn Asn Tyr Trp Glu Ser
          40                  45                  50

gcg gcg gtg acg ttc ctc ttt gcc ctt ggc aag gca ctg gaa cgc gcg   307
Ala Ala Val Thr Phe Leu Phe Ala Leu Gly Lys Ala Leu Glu Arg Ala
      55                  60                  65

aca atg aac cgc aca cga aaa gca cta tcg gat ctg gtg gat gca gct   355
Thr Met Asn Arg Thr Arg Lys Ala Leu Ser Asp Leu Val Asp Ala Ala
  70                  75                  80                  85

cca gaa act gca aca agg ctc aac gcg gat gac tca aca gag gta gtt   403
Pro Glu Thr Ala Thr Arg Leu Asn Ala Asp Asp Ser Thr Glu Val Val
                  90                  95                 100

gag ctg tgg gag ctt gag ccc ggt gac atc gtc ttg gta cgc aat ggc   451
Glu Leu Trp Glu Leu Glu Pro Gly Asp Ile Val Leu Val Arg Asn Gly
              105                 110                 115

gaa caa att ccc gtc gat gga aac gtg att gcg ggt gtc ggt gga att   499
Glu Gln Ile Pro Val Asp Gly Asn Val Ile Ala Gly Val Gly Gly Ile
          120                 125                 130

gat gaa tcc aac atc acg ggt gaa tca atg ccg gct gaa aag ggt caa   547
Asp Glu Ser Asn Ile Thr Gly Glu Ser Met Pro Ala Glu Lys Gly Gln
      135                 140                 145

ggc tct gat gtg tat gca gga acc tgg ctg cga tct ggt gtt ttg aga   595
Gly Ser Asp Val Tyr Ala Gly Thr Trp Leu Arg Ser Gly Val Leu Arg
150                 155                 160                 165

gtc gag gca aca gga att ggt tca gac tca act ttg gca aaa atc att   643
Val Glu Ala Thr Gly Ile Gly Ser Asp Ser Thr Leu Ala Lys Ile Ile
                170                 175                 180
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cac cgc gtt gaa gac gcc cag gat gac aaa gcc cgc aca caa aca ttc   691
His Arg Val Glu Asp Ala Gln Asp Asp Lys Ala Arg Thr Gln Thr Phe
            185                 190                 195

tta gag aaa ttc tct aag tgg tac acc ccg ggc gtc atg atc gcc gcc   739
Leu Glu Lys Phe Ser Lys Trp Tyr Thr Pro Gly Val Met Ile Ala Ala
        200                 205                 210

gca gtg gtg gga ctt atc acc tgg gac gta gaa cta gca ctg acg ctc   787
Ala Val Val Gly Leu Ile Thr Trp Asp Val Glu Leu Ala Leu Thr Leu
    215                 220                 225

tta gtg atc ggc tgc ccc ggc gcg ttg gtt atc tcc atc ccg gtg tcc   835
Leu Val Ile Gly Cys Pro Gly Ala Leu Val Ile Ser Ile Pro Val Ser
230                 235                 240                 245

atc gtc gca ggc atc ggc cgt gct gca cgc gat ggc gtg ctg atc aag   883
Ile Val Ala Gly Ile Gly Arg Ala Ala Arg Asp Gly Val Leu Ile Lys
                250                 255                 260

ggt gga gaa tac cta gaa acc gcc gcg aaa gtc gac gtc gtt gtc gtg   931
Gly Gly Glu Tyr Leu Glu Thr Ala Ala Lys Val Asp Val Val Val Val
            265                 270                 275

gac aaa act gga acg ctg acc acc ggc cgc cca gaa ctc aca gac gta   979
Asp Lys Thr Gly Thr Leu Thr Thr Gly Arg Pro Glu Leu Thr Asp Val
        280                 285                 290

gaa gtc atc gag ccc gcc tac agc cag ggc gag gtg ctg gag ctc gcc   1027
Glu Val Ile Glu Pro Ala Tyr Ser Gln Gly Glu Val Leu Glu Leu Ala
    295                 300                 305

gcg cgc gcc gag acg gct tca gaa cat ccg ctt gcc gac gcc atc atc   1075
Ala Arg Ala Glu Thr Ala Ser Glu His Pro Leu Ala Asp Ala Ile Ile
310                 315                 320                 325

cgt ggt gcc cag gat cgg ggg ctg tcc aca aca ttg gtg gaa gca gct   1123
Arg Gly Ala Gln Asp Arg Gly Leu Ser Thr Thr Leu Val Glu Ala Ala
                330                 335                 340

gaa aac atc acc ggc cga ggc att atc gca aat gtt gat gga cag gca   1171
Glu Asn Ile Thr Gly Arg Gly Ile Ile Ala Asn Val Asp Gly Gln Ala
            345                 350                 355

gtt gct gtt gga tct gct gag tta ctt gat cat gaa cca gac tcg acc   1219
Val Ala Val Gly Ser Ala Glu Leu Leu Asp His Glu Pro Asp Ser Thr
        360                 365                 370

agg atc ctg gag cta aat gcc gaa gga aag acc gcg atg ttt gtc gga   1267
Arg Ile Leu Glu Leu Asn Ala Glu Gly Lys Thr Ala Met Phe Val Gly
    375                 380                 385

gtg aac gga cac gcc att gga atc gtg gcc gtc gcc gac gcc gtt cgt   1315
Val Asn Gly His Ala Ile Gly Ile Val Ala Val Ala Asp Ala Val Arg
390                 395                 400                 405

tca gat tct gcc tca gca atc gaa tcg ctg cat aag gcg ggc att caa   1363
Ser Asp Ser Ala Ser Ala Ile Glu Ser Leu His Lys Ala Gly Ile Gln
                410                 415                 420
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gtt gtc atg gcg act ggc gac gct cac cgc gtt gca caa aac gtg gcc   1411
Val Val Met Ala Thr Gly Asp Ala His Arg Val Ala Gln Asn Val Ala
            425                 430                 435

tcc aag ctg gga gtg gat gaa gtc tac tca gag cta ctc cct gaa cag   1459
Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu Leu Pro Glu Gln
        440                 445                 450

aaa tta gaa ctg gtg cgt gat ctg caa gct gcc ggc aaa acg gtc gcg   1507
Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala Gly Lys Thr Val Ala
    455                 460                 465

atg gtg ggt gac gga gtc aac gac acc cca gca ttg gca gct gct gat   1555
Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu Ala Ala Ala Asp
470                 475                 480                 485

atc gga gta gcg atg ggc gtg gca ggt tcc cct gca gcc att gaa acc   1603
Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala Ala Ile Glu Thr
                490                 495                 500

gct gat atc gca ctc atg gcg gat cgt ctc cca cgg ctg gca cat gca   1651
Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg Leu Ala His Ala
            505                 510                 515

gtg acc ttg gca aaa cgc acc gta aga acc atg cgc atc aat att ctg   1699
Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg Ile Asn Ile Leu
        520                 525                 530

att gcg ttg gct acc gtg atg gtg tta cta gct ggc gtc cta ttt ggc   1747
Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly Val Leu Phe Gly
    535                 540                 545

gga gtt acc atg tcg gtt ggc atg ctc gtt cac gaa gca agc gtg ctg   1795
Gly Val Thr Met Ser Val Gly Met Leu Val His Glu Ala Ser Val Leu
550                 555                 560                 565

ctt gtt atc agc atc gcc atg ctg ttg ctg cgt cca aca ctt aaa gaa   1843
Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro Thr Leu Lys Glu
                570                 575                 580

gat gct gcg caa gca agt gat att aaa cgc tcg gaa ata caa cag atc   1891
Asp Ala Ala Gln Ala Ser Asp Ile Lys Arg Ser Glu Ile Gln Gln Ile
            585                 590                 595

gca taaccaatgg ctgggtactg atg                                    1917
Ala
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09639449 - 12-06-2009

<210> 398
<211> 598
<212> PRT
<213> Corynebacterium glutamicum

<400> 398

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Ile Asp Leu Leu Val Val Val Ala Ala Val Gly Ala Met Phe Ile Asn
35 40 45

Asn Tyr Trp Glu Ser Ala Ala Val Thr Phe Leu Phe Ala Leu Gly Lys
50 55 60

Ala Leu Glu Arg Ala Thr Met Asn Arg Thr Arg Lys Ala Leu Ser Asp
65 70 75 80

Leu Val Asp Ala Ala Pro Glu Thr Ala Thr Arg Leu Asn Ala Asp Asp
85 90 95

Ser Thr Glu Val Val Glu Leu Trp Glu Leu Glu Pro Gly Asp Ile Val
100 105 110

Leu Val Arg Asn Gly Glu Gln Ile Pro Val Asp Gly Asn Val Ile Ala
115 120 125

Gly Val Gly Gly Ile Asp Glu Ser Asn Ile Thr Gly Glu Ser Met Pro
130 135 140

Ala Glu Lys Gly Gln Gly Ser Asp Val Tyr Ala Gly Thr Trp Leu Arg
145 150 155 160

Ser Gly Val Leu Arg Val Glu Ala Thr Gly Ile Gly Ser Asp Ser Thr
165 170 175

Leu Ala Lys Ile Ile His Arg Val Glu Asp Ala Gln Asp Asp Lys Ala
180 185 190

Arg Thr Gln Thr Phe Leu Glu Lys Phe Ser Lys Trp Tyr Thr Pro Gly
195 200 205

Val Met Ile Ala Ala Ala Val Val Gly Leu Ile Thr Trp Asp Val Glu
210 215 220

Leu Ala Leu Thr Leu Leu Val Ile Gly Cys Pro Gly Ala Leu Val Ile
225 230 235 240

Ser Ile Pro Val Ser Ile Val Ala Gly Ile Gly Arg Ala Ala Arg Asp
245 250 255

Gly Val Leu Ile Lys Gly Gly Glu Tyr Leu Glu Thr Ala Ala Lys Val
260 265 270

Asp Val Val Val Val Asp Lys Thr Gly Thr Leu Thr Thr Gly Arg Pro
275 280 285

Glu Leu Thr Asp Val Glu Val Ile Glu Pro Ala Tyr Ser Gln Gly Glu
290 295 300

Val Leu Glu Leu Ala Ala Arg Ala Glu Thr Ala Ser Glu His Pro Leu
305 310 315 320

Ala Asp Ala Ile Ile Arg Gly Ala Gln Asp Arg Gly Leu Ser Thr Thr
325 330 335

Leu Val Glu Ala Ala Glu Asn Ile Thr Gly Arg Gly Ile Ile Ala Asn
340 345 350

Val Asp Gly Gln Ala Val Ala Val Gly Ser Ala Glu Leu Leu Asp His

```
        355                 360                 365

Glu Pro Asp Ser Thr Arg Ile Leu Glu Leu Asn Ala Glu Gly Lys Thr
    370                 375                 380

Ala Met Phe Val Gly Val Asn Gly His Ala Ile Gly Ile Val Ala Val
385                 390                 395                 400

Ala Asp Ala Val Arg Ser Asp Ser Ala Ser Ala Ile Glu Ser Leu His
                405                 410                 415

Lys Ala Gly Ile Gln Val Val Met Ala Thr Gly Asp Ala His Arg Val
            420                 425                 430

Ala Gln Asn Val Ala Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu
        435                 440                 445

Leu Leu Pro Glu Gln Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala
    450                 455                 460

Gly Lys Thr Val Ala Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala
465                 470                 475                 480

Leu Ala Ala Ala Asp Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro
                485                 490                 495

Ala Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro
            500                 505                 510

Arg Leu Ala His Ala Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met
        515                 520                 525

Arg Ile Asn Ile Leu Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala
    530                 535                 540

Gly Val Leu Phe Gly Gly Val Thr Met Ser Val Gly Met Leu Val His
545                 550                 555                 560

Glu Ala Ser Val Leu Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg
                565                 570                 575

Pro Thr Leu Lys Glu Asp Ala Ala Gln Ala Ser Asp Ile Lys Arg Ser
            580                 585                 590

Glu Ile Gln Gln Ile Ala
        595


<210> 399
<211> 762
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(739)
<223> FRXA00980

<400> 399
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gaccaggatc ctggagctaa atgccgaagg aaagaccgcg atg ttt gtc gga gtg   115
                                              Met Phe Val Gly Val
                                                1               5

aac gga cac gcc att gga atc gtg gcc gtc gcc gac gcc gtt cgt tca   163
Asn Gly His Ala Ile Gly Ile Val Ala Val Ala Asp Ala Val Arg Ser
               10                  15                  20

gat tct gcc tca gca atc gaa tcg ctg cat aag gcg ggc att caa gtt   211
Asp Ser Ala Ser Ala Ile Glu Ser Leu His Lys Ala Gly Ile Gln Val
           25                  30                  35

gtc atg gcg act ggc gac gct cac cgc gtt gca caa aac gtg gcc tcc   259
Val Met Ala Thr Gly Asp Ala His Arg Val Ala Gln Asn Val Ala Ser
       40                  45                  50

aag ctg gga gtg gat gaa gtc tac tca gag cta ctc cct gaa cag aaa   307
Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu Leu Pro Glu Gln Lys
   55                  60                  65

tta gaa ctg gtg cgt gat ctg caa gct gcc ggc aaa acg gtc gcg atg   355
Leu Glu Leu Val Arg Asp Leu Gln Ala Ala Gly Lys Thr Val Ala Met
70                  75                  80                  85

gtg ggt gac gga gtc aac gac acc cca gca ttg gca gct gct gat atc   403
Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu Ala Ala Ala Asp Ile
               90                  95                 100

gga gta gcg atg ggc gtg gca ggt tcc cct gca gcc att gaa acc gct   451
Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala Ala Ile Glu Thr Ala
           105                 110                 115

gat atc gca ctc atg gcg gat cgt ctc cca cgg ctg gca cat gca gtg   499
Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg Leu Ala His Ala Val
       120                 125                 130

acc ttg gca aaa cgc acc gta aga acc atg cgc atc aat att ctg att   547
Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg Ile Asn Ile Leu Ile
   135                 140                 145

gcg ttg gct acc gtg atg gtg tta cta gct ggc gtc cta ttt ggc gga   595
Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly Val Leu Phe Gly Gly
150                 155                 160                 165

gtt acc atg tcg gtt ggc atg ctc gtt cac gaa gca agc gtg ctg ctt   643
Val Thr Met Ser Val Gly Met Leu Val His Glu Ala Ser Val Leu Leu
               170                 175                 180

gtt atc agc atc gcc atg ctg ttg ctg cgt cca aca ctt aaa gaa gat   691
Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro Thr Leu Lys Glu Asp
           185                 190                 195

gct gcg caa gca agt gat att aaa cgc tcg gaa ata caa cag atc gca   739
Ala Ala Gln Ala Ser Asp Ile Lys Arg Ser Glu Ile Gln Gln Ile Ala
       200                 205                 210

taaccaatgg ctgggtactg atg                                        762
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<210> 400
<211> 213

<212> PRT
<213> Corynebacterium glutamicum

<400> 400

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Met Phe Val Gly Val Asn Gly His Ala Ile Gly Ile Val Ala Val Ala
  1               5                  10                  15

Asp Ala Val Arg Ser Asp Ser Ala Ser Ala Ile Glu Ser Leu His Lys
             20                  25                  30

Ala Gly Ile Gln Val Val Met Ala Thr Gly Asp Ala His Arg Val Ala
         35                  40                  45

Gln Asn Val Ala Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu
     50                  55                  60

Leu Pro Glu Gln Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala Gly
 65                  70                  75                  80

Lys Thr Val Ala Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu
                 85                  90                  95

Ala Ala Ala Asp Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala
            100                 105                 110

Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg
        115                 120                 125

Leu Ala His Ala Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg
    130                 135                 140

Ile Asn Ile Leu Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly
145                 150                 155                 160

Val Leu Phe Gly Gly Val Thr Met Ser Val Gly Met Leu Val His Glu
                165                 170                 175

Ala Ser Val Leu Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro
            180                 185                 190

Thr Leu Lys Glu Asp Ala Ala Gln Ala Ser Asp Ile Lys Arg Ser Glu
        195                 200                 205

Ile Gln Gln Ile Ala
    210
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<210> 401
<211> 2007
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1984)
<223> RXN02348

<400> 401

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aaagacccga gccgaagccc tggcctgcgc atacttcctt gtcaacgctc gctgggatta 60

ggtctttttct gagcgctagc atttctccac tcaaaggagc atg ctt aac cgc atg   115
```

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                                                    Met Leu Asn Arg Met
                                                      1               5

aaa agt gcg cgg cca aaa tca gtc gct cca aaa tcc gga caa gct tta   163
Lys Ser Ala Arg Pro Lys Ser Val Ala Pro Lys Ser Gly Gln Ala Leu
                  10                  15                  20

ctc act ctc ggt gcc cta ggt gtt gtg ttc ggc gac atc ggc acc agc   211
Leu Thr Leu Gly Ala Leu Gly Val Val Phe Gly Asp Ile Gly Thr Ser
              25                  30                  35

ccc ctg tac tca ctt cac act gca ttc agc atg cag cac aac aaa gtc   259
Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met Gln His Asn Lys Val
          40                  45                  50

gaa gtc act cag gaa aat gtg tac ggc atc atc tcc atg gtg ttg tgg   307
Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile Ser Met Val Leu Trp
      55                  60                  65

acc atc act ttg atc gtc acc gtc aaa tac gtc atg ctg gtc acc cga   355
Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val Met Leu Val Thr Arg
  70                  75                  80                  85

gct gac aac caa gga caa ggt ggc atc ctg gcg ctc gtt gct ttg ctg   403
Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala Leu Val Ala Leu Leu
                  90                  95                 100

aaa aac cgt ggg cac tgg gga aaa ttc gtg gca gta gcc ggc atg ttg   451
Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala Val Ala Gly Met Leu
              105                 110                 115

ggc gcc gca ttg ttt tat ggc gat gtg gtg atc acc ccg gcg atc tct   499
Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile Thr Pro Ala Ile Ser
          120                 125                 130

gtt ctc agc gca aca gaa ggc ttg acg gtt atc tcc cca agc ttt gag   547
Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile Ser Pro Ser Phe Glu
      135                 140                 145

cgc ttc att ctg ccc gta tct ctc gca gtt ctg atc gct att ttt gca   595
Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu Ile Ala Ile Phe Ala
150                 155                 160                 165

atc caa ccg ctc ggt aca gaa aaa gtc ggc aaa gcc ttc ggc ccc atc   643
Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys Ala Phe Gly Pro Ile
                  170                 175                 180

atg ttg ctg tgg ttt gtc acc ctt gca gga ttg gga att ccg caa atc   691
Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu Gly Ile Pro Gln Ile
              185                 190                 195

atc ggg cac cca gaa atc ttg cag agc ttg tct cca cat tgg gcc ctg   739
Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser Pro His Trp Ala Leu
          200                 205                 210

cgc ttg att gtg gct gag cct ttc caa gca ttt gtg ctg ctt ggt gcc   787
Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe Val Leu Leu Gly Ala
      215                 220                 225

gtt gtc ctg aca gta acg ggt gcg gaa gcg ctc tac gct gat atg ggc   835
Val Val Leu Thr Val Thr Gly Ala Glu Ala Leu Tyr Ala Asp Met Gly
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US 2005/0196785 A1

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230                 235                 240                 245

cat ttt ggg gcg agg cca atc aga gtg gcg tgg ttt tgc gtc gtc atg   883
His Phe Gly Ala Arg Pro Ile Arg Val Ala Trp Phe Cys Val Val Met
                250                 255                 260

cct gct tta atc ttg acg tat ttg ggg cag ggc gcc ttg gtg atc aac   931
Pro Ala Leu Ile Leu Thr Tyr Leu Gly Gln Gly Ala Leu Val Ile Asn
            265                 270                 275

cag cct gaa gcg gtg cgc aac ccc atg ttt tat ctc gcg ccg gaa ggt   979
Gln Pro Glu Ala Val Arg Asn Pro Met Phe Tyr Leu Ala Pro Glu Gly
        280                 285                 290

ctg cgg att ccg ttg gtt att ttg gcg acc atc gct acg gtg atc gca   1027
Leu Arg Ile Pro Leu Val Ile Leu Ala Thr Ile Ala Thr Val Ile Ala
    295                 300                 305

tcg cag gcc gtg att tct ggt gcg tat tca ttg acc aag cag gcc gtg   1075
Ser Gln Ala Val Ile Ser Gly Ala Tyr Ser Leu Thr Lys Gln Ala Val
310                 315                 320                 325

aat ttg aaa ctg ctg cca cgc atg gtg atc cgg cat acc tcc cgc aaa   1123
Asn Leu Lys Leu Leu Pro Arg Met Val Ile Arg His Thr Ser Arg Lys
                330                 335                 340

gag gaa ggc cag atc tat atg cca ctg gtt aat gga ttg ctg ttt gta   1171
Glu Glu Gly Gln Ile Tyr Met Pro Leu Val Asn Gly Leu Leu Phe Val
            345                 350                 355

tcc gtg atg gtt gtg gtg ctg gta ttc cga tcc tct gaa agc ctc gcc   1219
Ser Val Met Val Val Val Leu Val Phe Arg Ser Ser Glu Ser Leu Ala
        360                 365                 370

agc gcg tac gga ctt gca gtg acc gga acc ttg gtg ctg gtc agc gtc   1267
Ser Ala Tyr Gly Leu Ala Val Thr Gly Thr Leu Val Leu Val Ser Val
    375                 380                 385

ctg tat ctg atc tat gtt cac acc aca tgg tgg aaa aca gcg ctg ttc   1315
Leu Tyr Leu Ile Tyr Val His Thr Thr Trp Trp Lys Thr Ala Leu Phe
390                 395                 400                 405

att gtg ctc atc ggt att cca gaa gta ctt cta ttc gcc tcg aac acc   1363
Ile Val Leu Ile Gly Ile Pro Glu Val Leu Leu Phe Ala Ser Asn Thr
                410                 415                 420

acg aaa att cac gac ggt ggc tgg ctt cca cta ctt att gcg gcc gtg   1411
Thr Lys Ile His Asp Gly Gly Trp Leu Pro Leu Leu Ile Ala Ala Val
            425                 430                 435

ctc atc gtg gtg atg cgg acc tgg gag tgg gga agt gac cgc gtc aat   1459
Leu Ile Val Val Met Arg Thr Trp Glu Trp Gly Ser Asp Arg Val Asn
        440                 445                 450

cag gaa cgc gca gag ctg gaa ctt ccc atg gat aag ttc ttg gag aaa   1507
Gln Glu Arg Ala Glu Leu Glu Leu Pro Met Asp Lys Phe Leu Glu Lys
    455                 460                 465

ctc gat cag cca cac aat att ggt ctg cgt aaa gtt gcc gaa gtg gca   1555
Leu Asp Gln Pro His Asn Ile Gly Leu Arg Lys Val Ala Glu Val Ala
470                 475                 480                 485
```

```
gta ttt cca cat ggc acc agc gat act gtc ccg ttg tca ttg gtt cgc   1603
Val Phe Pro His Gly Thr Ser Asp Thr Val Pro Leu Ser Leu Val Arg
                490                 495                 500

tgc gtg aaa gac ctc aag ctt tta tac cga gag atc gtg atc gtt cga   1651
Cys Val Lys Asp Leu Lys Leu Leu Tyr Arg Glu Ile Val Ile Val Arg
            505                 510                 515

atc gtc caa gaa cac gtt ccg cac gtg cca cca gag gaa cgc gcg gaa   1699
Ile Val Gln Glu His Val Pro His Val Pro Pro Glu Glu Arg Ala Glu
        520                 525                 530

atg gaa gtg ctc cat cac gcc ccg atc aga gtc gtg cga gtt gat ctg   1747
Met Glu Val Leu His His Ala Pro Ile Arg Val Val Arg Val Asp Leu
    535                 540                 545

cac ctt ggt tat ttt gat gag cag aac ctg cct gag cat ctc cat gcc   1795
His Leu Gly Tyr Phe Asp Glu Gln Asn Leu Pro Glu His Leu His Ala
550                 555                 560                 565

att gac cca aca tgg gat aac gcc acc tac ttc ctg tct gcc ctg act   1843
Ile Asp Pro Thr Trp Asp Asn Ala Thr Tyr Phe Leu Ser Ala Leu Thr
                570                 575                 580

ctt cgg agc agg ttg cct gga aag att gct ggc tgg cgt gat cgt ttg   1891
Leu Arg Ser Arg Leu Pro Gly Lys Ile Ala Gly Trp Arg Asp Arg Leu
            585                 590                 595

tat ctt tcg atg gaa cgt aat cag gca tct cga act gag tct ttc aaa   1939
Tyr Leu Ser Met Glu Arg Asn Gln Ala Ser Arg Thr Glu Ser Phe Lys
        600                 605                 610

ttg caa cca agc aaa acc atc acg gtt gga aca gag ctg cac ctt       1984
Leu Gln Pro Ser Lys Thr Ile Thr Val Gly Thr Glu Leu His Leu
    615                 620                 625

taatcaggca gttgctggcc aac                                        2007
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<210> 402
<211> 628
<212> PRT
<213> Corynebacterium glutamicum

<400> 402

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Met Leu Asn Arg Met Lys Ser Ala Arg Pro Lys Ser Val Ala Pro Lys
  1               5                  10                  15

Ser Gly Gln Ala Leu Leu Thr Leu Gly Ala Leu Gly Val Val Phe Gly
            20                  25                  30

Asp Ile Gly Thr Ser Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met
        35                  40                  45

Gln His Asn Lys Val Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile
    50                  55                  60

Ser Met Val Leu Trp Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val
65                  70                  75                  80
```

Met Leu Val Thr Arg Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala
85 90 95

Leu Val Ala Leu Leu Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala
100 105 110

Val Ala Gly Met Leu Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile
115 120 125

Thr Pro Ala Ile Ser Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile
130 135 140

Ser Pro Ser Phe Glu Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu
145 150 155 160

Ile Ala Ile Phe Ala Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys
165 170 175

Ala Phe Gly Pro Ile Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu
180 185 190

Gly Ile Pro Gln Ile Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser
195 200 205

Pro His Trp Ala Leu Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe
210 215 220

Val Leu Leu Gly Ala Val Val Leu Thr Val Thr Gly Ala Glu Ala Leu
225 230 235 240

Tyr Ala Asp Met Gly His Phe Gly Ala Arg Pro Ile Arg Val Ala Trp
245 250 255

Phe Cys Val Val Met Pro Ala Leu Ile Leu Thr Tyr Leu Gly Gln Gly
260 265 270

Ala Leu Val Ile Asn Gln Pro Glu Ala Val Arg Asn Pro Met Phe Tyr
275 280 285

Leu Ala Pro Glu Gly Leu Arg Ile Pro Leu Val Ile Leu Ala Thr Ile
290 295 300

Ala Thr Val Ile Ala Ser Gln Ala Val Ile Ser Gly Ala Tyr Ser Leu
305 310 315 320

Thr Lys Gln Ala Val Asn Leu Lys Leu Leu Pro Arg Met Val Ile Arg
325 330 335

His Thr Ser Arg Lys Glu Glu Gly Gln Ile Tyr Met Pro Leu Val Asn
340 345 350

Gly Leu Leu Phe Val Ser Val Met Val Val Val Leu Val Phe Arg Ser
355 360 365

Ser Glu Ser Leu Ala Ser Ala Tyr Gly Leu Ala Val Thr Gly Thr Leu
370 375 380

Val Leu Val Ser Val Leu Tyr Leu Ile Tyr Val His Thr Thr Trp Trp
385 390 395 400

Lys Thr Ala Leu Phe Ile Val Leu Ile Gly Ile Pro Glu Val Leu Leu

```
                405                 410                 415

Phe Ala Ser Asn Thr Thr Lys Ile His Asp Gly Gly Trp Leu Pro Leu
            420                 425                 430

Leu Ile Ala Ala Val Leu Ile Val Val Met Arg Thr Trp Glu Trp Gly
        435                 440                 445

Ser Asp Arg Val Asn Gln Glu Arg Ala Glu Leu Glu Leu Pro Met Asp
    450                 455                 460

Lys Phe Leu Glu Lys Leu Asp Gln Pro His Asn Ile Gly Leu Arg Lys
465                 470                 475                 480

Val Ala Glu Val Ala Val Phe Pro His Gly Thr Ser Asp Thr Val Pro
                485                 490                 495

Leu Ser Leu Val Arg Cys Val Lys Asp Leu Lys Leu Leu Tyr Arg Glu
            500                 505                 510

Ile Val Ile Val Arg Ile Val Gln Glu His Val Pro His Val Pro Pro
        515                 520                 525

Glu Glu Arg Ala Glu Met Glu Val Leu His His Ala Pro Ile Arg Val
    530                 535                 540

Val Arg Val Asp Leu His Leu Gly Tyr Phe Asp Glu Gln Asn Leu Pro
545                 550                 555                 560

Glu His Leu His Ala Ile Asp Pro Thr Trp Asp Asn Ala Thr Tyr Phe
                565                 570                 575

Leu Ser Ala Leu Thr Leu Arg Ser Arg Leu Pro Gly Lys Ile Ala Gly
            580                 585                 590

Trp Arg Asp Arg Leu Tyr Leu Ser Met Glu Arg Asn Gln Ala Ser Arg
        595                 600                 605

Thr Glu Ser Phe Lys Leu Gln Pro Ser Lys Thr Ile Thr Val Gly Thr
    610                 615                 620

Glu Leu His Leu
625
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<210> 403
<211> 1157
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1134)
<223> FRXA02348

<400> 403

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cca atc aga gtg gcg tgg ttt tgc gtc gtc atg cct gct tta atc ttg   48
Pro Ile Arg Val Ala Trp Phe Cys Val Val Met Pro Ala Leu Ile Leu
  1               5                  10                  15

acg tat ttg ggg cag ggc gcc ttg gtg atc aac cag cct gaa gcg gtg   96
```

```
Thr Tyr Leu Gly Gln Gly Ala Leu Val Ile Asn Gln Pro Glu Ala Val
                20                  25                  30

cgc aac ccc atg ttt tat ctc gcg ccg gaa ggt ctg cgg att ccg ttg   144
Arg Asn Pro Met Phe Tyr Leu Ala Pro Glu Gly Leu Arg Ile Pro Leu
            35                  40                  45

gtt att ttg gcg acc atc gct acg gtg atc gca tcg cag gcc gtg att   192
Val Ile Leu Ala Thr Ile Ala Thr Val Ile Ala Ser Gln Ala Val Ile
        50                  55                  60

tct ggt gcg tat tca ttg acc aag cag gcc gtg aat ttg aaa ctg ctg   240
Ser Gly Ala Tyr Ser Leu Thr Lys Gln Ala Val Asn Leu Lys Leu Leu
 65                  70                  75                  80

cca cgc atg gtg atc cgg cat acc tcc cgc aaa gag gaa ggc cag atc   288
Pro Arg Met Val Ile Arg His Thr Ser Arg Lys Glu Glu Gly Gln Ile
                85                  90                  95

tat atg cca ctg gtt aat gga ttg ctg ttt gta tcc gtg atg gtt gtg   336
Tyr Met Pro Leu Val Asn Gly Leu Leu Phe Val Ser Val Met Val Val
            100                 105                 110

gtg ctg gta ttc cga tcc tct gaa agc ctc gcc agc gcg tac gga ctt   384
Val Leu Val Phe Arg Ser Ser Glu Ser Leu Ala Ser Ala Tyr Gly Leu
        115                 120                 125

gca gtg acc gga acc ttg gtg ctg gtc agc gtc ctg tat ctg atc tat   432
Ala Val Thr Gly Thr Leu Val Leu Val Ser Val Leu Tyr Leu Ile Tyr
    130                 135                 140

gtt cac acc aca tgg tgg aaa aca gcg ctg ttc att gtg ctc atc ggt   480
Val His Thr Thr Trp Trp Lys Thr Ala Leu Phe Ile Val Leu Ile Gly
145                 150                 155                 160

att cca gaa gta ctt cta ttc gcc tcg aac acc acg aaa att cac gac   528
Ile Pro Glu Val Leu Leu Phe Ala Ser Asn Thr Thr Lys Ile His Asp
                165                 170                 175

ggt ggc tgg ctt cca cta ctt att gcg gcc gtg ctc atc gtg gtg atg   576
Gly Gly Trp Leu Pro Leu Leu Ile Ala Ala Val Leu Ile Val Val Met
            180                 185                 190

cgg acc tgg gag tgg gga agt gac cgc gtc aat cag gaa cgc gca gag   624
Arg Thr Trp Glu Trp Gly Ser Asp Arg Val Asn Gln Glu Arg Ala Glu
        195                 200                 205

ctg gaa ctt ccc atg gat aag ttc ttg gag aaa ctc gat cag cca cac   672
Leu Glu Leu Pro Met Asp Lys Phe Leu Glu Lys Leu Asp Gln Pro His
    210                 215                 220

aat att ggt ctg cgt aaa gtt gcc gaa gtg gca gta ttt cca cat ggc   720
Asn Ile Gly Leu Arg Lys Val Ala Glu Val Ala Val Phe Pro His Gly
225                 230                 235                 240

acc agc gat act gtc ccg ttg tca ttg gtt cgc tgc gtg aaa gac ctc   768
Thr Ser Asp Thr Val Pro Leu Ser Leu Val Arg Cys Val Lys Asp Leu
                245                 250                 255

aag ctt tta tac cga gag atc gtg atc gtt cga atc gtc caa gaa cac   816
Lys Leu Leu Tyr Arg Glu Ile Val Ile Val Arg Ile Val Gln Glu His
```

```
            260                 265                 270

gtt ccg cac gtg cca cca gag gaa cgc gcg gaa atg gaa gtg ctc cat   864
Val Pro His Val Pro Pro Glu Glu Arg Ala Glu Met Glu Val Leu His
        275                 280                 285

cac gcc ccg atc aga gtc gtg cga gtt gat ctg cac ctt ggt tat ttt   912
His Ala Pro Ile Arg Val Val Arg Val Asp Leu His Leu Gly Tyr Phe
    290                 295                 300

gat gag cag aac ctg cct gag cat ctc cat gcc att gac cca aca tgg   960
Asp Glu Gln Asn Leu Pro Glu His Leu His Ala Ile Asp Pro Thr Trp
305                 310                 315                 320

gat aac gcc acc tac ttc ctg tct gcc ctg act ctt cgg agc agg ttg  1008
Asp Asn Ala Thr Tyr Phe Leu Ser Ala Leu Thr Leu Arg Ser Arg Leu
                325                 330                 335

cct gga aag att gct ggc tgg cgt gat cgt ttg tat ctt tcg atg gaa  1056
Pro Gly Lys Ile Ala Gly Trp Arg Asp Arg Leu Tyr Leu Ser Met Glu
            340                 345                 350

cgt aat cag gca tct cga act gag tct ttc aaa ttg caa cca agc aaa  1104
Arg Asn Gln Ala Ser Arg Thr Glu Ser Phe Lys Leu Gln Pro Ser Lys
        355                 360                 365

acc atc acg gtt gga aca gag ctg cac ctt taatcaggca gttgctggcc    1154
Thr Ile Thr Val Gly Thr Glu Leu His Leu
    370                 375

aac                                                             1157


<210> 404
<211> 378
<212> PRT
<213> Corynebacterium glutamicum

<400> 404
Pro Ile Arg Val Ala Trp Phe Cys Val Val Met Pro Ala Leu Ile Leu
  1               5                  10                  15

Thr Tyr Leu Gly Gln Gly Ala Leu Val Ile Asn Gln Pro Glu Ala Val
             20                  25                  30

Arg Asn Pro Met Phe Tyr Leu Ala Pro Glu Gly Leu Arg Ile Pro Leu
         35                  40                  45

Val Ile Leu Ala Thr Ile Ala Thr Val Ile Ala Ser Gln Ala Val Ile
     50                  55                  60

Ser Gly Ala Tyr Ser Leu Thr Lys Gln Ala Val Asn Leu Lys Leu Leu
 65                  70                  75                  80

Pro Arg Met Val Ile Arg His Thr Ser Arg Lys Glu Glu Gly Gln Ile
                 85                  90                  95

Tyr Met Pro Leu Val Asn Gly Leu Leu Phe Val Ser Val Met Val Val
            100                 105                 110

Val Leu Val Phe Arg Ser Ser Glu Ser Leu Ala Ser Ala Tyr Gly Leu
```

```
        115                 120                 125

Ala Val Thr Gly Thr Leu Val Leu Val Ser Val Leu Tyr Leu Ile Tyr
    130                 135                 140

Val His Thr Thr Trp Trp Lys Thr Ala Leu Phe Ile Val Leu Ile Gly
145                 150                 155                 160

Ile Pro Glu Val Leu Leu Phe Ala Ser Asn Thr Thr Lys Ile His Asp
                165                 170                 175

Gly Gly Trp Leu Pro Leu Leu Ile Ala Ala Val Leu Ile Val Val Met
            180                 185                 190

Arg Thr Trp Glu Trp Gly Ser Asp Arg Val Asn Gln Glu Arg Ala Glu
        195                 200                 205

Leu Glu Leu Pro Met Asp Lys Phe Leu Glu Lys Leu Asp Gln Pro His
    210                 215                 220

Asn Ile Gly Leu Arg Lys Val Ala Glu Val Ala Val Phe Pro His Gly
225                 230                 235                 240

Thr Ser Asp Thr Val Pro Leu Ser Leu Val Arg Cys Val Lys Asp Leu
                245                 250                 255

Lys Leu Leu Tyr Arg Glu Ile Val Ile Val Arg Ile Val Gln Glu His
            260                 265                 270

Val Pro His Val Pro Pro Glu Glu Arg Ala Glu Met Glu Val Leu His
        275                 280                 285

His Ala Pro Ile Arg Val Val Arg Val Asp Leu His Leu Gly Tyr Phe
    290                 295                 300

Asp Glu Gln Asn Leu Pro Glu His Leu His Ala Ile Asp Pro Thr Trp
305                 310                 315                 320

Asp Asn Ala Thr Tyr Phe Leu Ser Ala Leu Thr Leu Arg Ser Arg Leu
                325                 330                 335

Pro Gly Lys Ile Ala Gly Trp Arg Asp Arg Leu Tyr Leu Ser Met Glu
            340                 345                 350

Arg Asn Gln Ala Ser Arg Thr Glu Ser Phe Lys Leu Gln Pro Ser Lys
        355                 360                 365

Thr Ile Thr Val Gly Thr Glu Leu His Leu
    370                 375
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<210> 405
<211> 778
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> FRXA02344

<400> 405
aaagacccga gccgaagccc tggcctgcgc atacttcctt gtcaacgctc gctgggatta 60

ggtctttttct gagcgctagc atttctccac tcaaaggagc atg ctt aac cgc atg 115
Met Leu Asn Arg Met
1 5

aaa agt gcg cgg cca aaa tca gtc gct cca aaa tcc gga caa gct tta 163
Lys Ser Ala Arg Pro Lys Ser Val Ala Pro Lys Ser Gly Gln Ala Leu
10 15 20

ctc act ctc ggt gcc cta ggt gtt gtg ttc ggc gac atc ggc acc agc 211
Leu Thr Leu Gly Ala Leu Gly Val Val Phe Gly Asp Ile Gly Thr Ser
25 30 35

ccc ctg tac tca ctt cac act gca ttc agc atg cag cac aac aaa gtc 259
Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met Gln His Asn Lys Val
40 45 50

gaa gtc act cag gaa aat gtg tac ggc atc atc tcc atg gtg ttg tgg 307
Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile Ser Met Val Leu Trp
55 60 65

acc atc act ttg atc gtc acc gtc aaa tac gtc atg ctg gtc acc cga 355
Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val Met Leu Val Thr Arg
70 75 80 85

gct gac aac caa gga caa ggt ggc atc ctg gcg ctc gtt gct ttg ctg 403
Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala Leu Val Ala Leu Leu
90 95 100

aaa aac cgt ggg cac tgg gga aaa ttc gtg gca gta gcc ggc atg ttg 451
Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala Val Ala Gly Met Leu
105 110 115

ggc gcc gca ttg ttt tat ggc gat gtg gtg atc acc ccg gcg atc tct 499
Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile Thr Pro Ala Ile Ser
120 125 130

gtt ctc agc gca aca gaa ggc ttg acg gtt atc tcc cca agc ttt gag 547
Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile Ser Pro Ser Phe Glu
135 140 145

cgc ttc att ctg ccc gta tct ctc gca gtt ctg atc gct att ttt gca 595
Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu Ile Ala Ile Phe Ala
150 155 160 165

atc caa ccg ctc ggt aca gaa aaa gtc ggc aaa gcc ttc ggc ccc atc 643
Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys Ala Phe Gly Pro Ile
170 175 180

atg ttg ctg tgg ttt gtc acc ctt gca gga ttg gga att ccg caa atc 691
Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu Gly Ile Pro Gln Ile
185 190 195

atc ggg cac cca gaa atc ttg cag agc ttg tct cca cat tgg gcc ctg 739
Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser Pro His Trp Ala Leu
200 205 210

cgc ttg att gtg gct gag cct ttc caa gca ttt gtg ctg 778
Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe Val Leu

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215 220 225

<210> 406
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 406
Met Leu Asn Arg Met Lys Ser Ala Arg Pro Lys Ser Val Ala Pro Lys
1 5 10 15

Ser Gly Gln Ala Leu Leu Thr Leu Gly Ala Leu Gly Val Val Phe Gly
20 25 30

Asp Ile Gly Thr Ser Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met
35 40 45

Gln His Asn Lys Val Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile
50 55 60

Ser Met Val Leu Trp Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val
65 70 75 80

Met Leu Val Thr Arg Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala
85 90 95

Leu Val Ala Leu Leu Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala
100 105 110

Val Ala Gly Met Leu Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile
115 120 125

Thr Pro Ala Ile Ser Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile
130 135 140

Ser Pro Ser Phe Glu Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu
145 150 155 160

Ile Ala Ile Phe Ala Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys
165 170 175

Ala Phe Gly Pro Ile Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu
180 185 190

Gly Ile Pro Gln Ile Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser
195 200 205

Pro His Trp Ala Leu Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe
210 215 220

Val Leu
225

<210> 407
<211> 1058
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (1)..(1035)
<223> RXN00960

<400> 407

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atg gct cgg cat tgt tgc agc aat cgc tac gcg tcc acc gtc ttc tcc   48
Met Ala Arg His Cys Cys Ser Asn Arg Tyr Ala Ser Thr Val Phe Ser
  1               5                  10                  15

ggt ctg atc gcc tac gga gca tcc caa gcg ctc tac cca tgg ctg ctg   96
Gly Leu Ile Ala Tyr Gly Ala Ser Gln Ala Leu Tyr Pro Trp Leu Leu
            20                  25                  30

aaa gac cac caa agc gtc acc gaa atc gac ctt gat gca ggt gcc ctc   144
Lys Asp His Gln Ser Val Thr Glu Ile Asp Leu Asp Ala Gly Ala Leu
        35                  40                  45

cag ccc tac ttc aac atc gag atg cca cca cca ttt gaa gtg atg acc   192
Gln Pro Tyr Phe Asn Ile Glu Met Pro Pro Pro Phe Glu Val Met Thr
    50                  55                  60

gca ctg ctg ctg gca ttc tgc ctc ggc ctg ggc atg gct gta att aaa   240
Ala Leu Leu Leu Ala Phe Cys Leu Gly Leu Gly Met Ala Val Ile Lys
65                  70                  75                  80

tca gac acc ctg ttc aag gta acc cgc gaa ctc gag cgc gta gtc atg   288
Ser Asp Thr Leu Phe Lys Val Thr Arg Glu Leu Glu Arg Val Val Met
                85                  90                  95

aag acc atc acc gcc ttt gtc atc cca ctg ctg cca ctc ttc atc ttc   336
Lys Thr Ile Thr Ala Phe Val Ile Pro Leu Leu Pro Leu Phe Ile Phe
            100                 105                 110

ggc atc ttc ctc ggc atg ggc atg aac ggt ggc ctc ctg gag atc atg   384
Gly Ile Phe Leu Gly Met Gly Met Asn Gly Gly Leu Leu Glu Ile Met
        115                 120                 125

tcc gcc ttt ggc aag gta ctg att ctc gcc gtc gtg gga acc ctg ctc   432
Ser Ala Phe Gly Lys Val Leu Ile Leu Ala Val Val Gly Thr Leu Leu
    130                 135                 140

ttc cta gcc atc cag ttc att atc gct ggt gca gta tcc aag aag aac   480
Phe Leu Ala Ile Gln Phe Ile Ile Ala Gly Ala Val Ser Lys Lys Asn
145                 150                 155                 160

cca tgg aaa ctg ttc aaa aac atg ctc cct gca tac ttc act gca ctg   528
Pro Trp Lys Leu Phe Lys Asn Met Leu Pro Ala Tyr Phe Thr Ala Leu
                165                 170                 175

ggc act tcc tct tca gcg gca acc atc cca gtg acc tac cag cag acc   576
Gly Thr Ser Ser Ser Ala Ala Thr Ile Pro Val Thr Tyr Gln Gln Thr
            180                 185                 190

ctg aaa aac gat gtt gat gtc aac gtc gca ggc ttt gtt gtc cca ctg   624
Leu Lys Asn Asp Val Asp Val Asn Val Ala Gly Phe Val Val Pro Leu
        195                 200                 205

tgc gcc acc atc cac cta gct gga tcg atg atg aag atc ggc ctc ttc   672
Cys Ala Thr Ile His Leu Ala Gly Ser Met Met Lys Ile Gly Leu Phe
    210                 215                 220
```

```
acc ttc gct gtt gtc ttc atg tac gac atg gaa gta ggc gtc ggc ctc   720
Thr Phe Ala Val Val Phe Met Tyr Asp Met Glu Val Gly Val Gly Leu
225                 230                 235                 240

tcc atc gga ttc ctc ctc atg ctg ggc atc acc atg atc gcc gca cca   768
Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro
                245                 250                 255

ggc gtt ccc ggc gga gcc atc atg gca gca acc ggc atg ctg gcc tcc   816
Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser
            260                 265                 270

atg ctc gga ttc aac acc gaa caa gtc gcc ctc atg atc gcc gct tac   864
Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr
        275                 280                 285

atc gcg att gac tcc ttc ggc acc gca gca aac gtc acc ggc gac ggc   912
Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly
    290                 295                 300

gca atc gca gtc atc gtg aac aaa ttc gcc aag ggc cag ctg cac acc   960
Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr
305                 310                 315                 320

act tcc cca gat gaa atc gaa gaa gac gac cgc gtt gcc ttc gac atc   1008
Thr Ser Pro Asp Glu Ile Glu Glu Asp Asp Arg Val Ala Phe Asp Ile
                325                 330                 335

act cca tcg gat gtg gaa cat cac aag tagaaacccg cattttctgt         1055
Thr Pro Ser Asp Val Glu His His Lys
            340                 345

agt                                                              1058
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<210> 408
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 408

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Met Ala Arg His Cys Cys Ser Asn Arg Tyr Ala Ser Thr Val Phe Ser
  1               5                  10                  15

Gly Leu Ile Ala Tyr Gly Ala Ser Gln Ala Leu Tyr Pro Trp Leu Leu
             20                  25                  30

Lys Asp His Gln Ser Val Thr Glu Ile Asp Leu Asp Ala Gly Ala Leu
         35                  40                  45

Gln Pro Tyr Phe Asn Ile Glu Met Pro Pro Pro Phe Glu Val Met Thr
     50                  55                  60

Ala Leu Leu Leu Ala Phe Cys Leu Gly Leu Gly Met Ala Val Ile Lys
 65                  70                  75                  80

Ser Asp Thr Leu Phe Lys Val Thr Arg Glu Leu Glu Arg Val Val Met
                 85                  90                  95

Lys Thr Ile Thr Ala Phe Val Ile Pro Leu Leu Pro Leu Phe Ile Phe
            100                 105                 110
```

Gly Ile Phe Leu Gly Met Gly Met Asn Gly Gly Leu Leu Glu Ile Met
115 120 125

Ser Ala Phe Gly Lys Val Leu Ile Leu Ala Val Val Gly Thr Leu Leu
130 135 140

Phe Leu Ala Ile Gln Phe Ile Ile Ala Gly Ala Val Ser Lys Lys Asn
145 150 155 160

Pro Trp Lys Leu Phe Lys Asn Met Leu Pro Ala Tyr Phe Thr Ala Leu
165 170 175

Gly Thr Ser Ser Ser Ala Ala Thr Ile Pro Val Thr Tyr Gln Gln Thr
180 185 190

Leu Lys Asn Asp Val Asp Val Asn Val Ala Gly Phe Val Val Pro Leu
195 200 205

Cys Ala Thr Ile His Leu Ala Gly Ser Met Met Lys Ile Gly Leu Phe
210 215 220

Thr Phe Ala Val Val Phe Met Tyr Asp Met Glu Val Gly Val Gly Leu
225 230 235 240

Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro
245 250 255

Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser
260 265 270

Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr
275 280 285

Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly
290 295 300

Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr
305 310 315 320

Thr Ser Pro Asp Glu Ile Glu Glu Asp Asp Arg Val Ala Phe Asp Ile
325 330 335

Thr Pro Ser Asp Val Glu His His Lys
340 345

<210> 409
<211> 482
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(459)
<223> FRXA00960

<400> 409
ctg aaa aac gat gtt gat gtc aac gtc gca ggc ttt gtt gtc cca ctg 48
Leu Lys Asn Asp Val Asp Val Asn Val Ala Gly Phe Val Val Pro Leu
1 5 10 15

```
tgc gcc acc atc cac cta gct gga tcg atg atg aag atc ggc ctc ttc   96
Cys Ala Thr Ile His Leu Ala Gly Ser Met Met Lys Ile Gly Leu Phe
             20                  25                  30

acc ttc gct gtt gtc ttc atg tac gac atg gaa gta ggc gtc ggc ctc   144
Thr Phe Ala Val Val Phe Met Tyr Asp Met Glu Val Gly Val Gly Leu
         35                  40                  45

tcc atc gga ttc ctc ctc atg ctg ggc atc acc atg atc gcc gca cca   192
Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro
     50                  55                  60

ggc gtt ccc ggc gga gcc atc atg gca gca acc ggc atg ctg gcc tcc   240
Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser
 65                  70                  75                  80

atg ctc gga ttc aac acc gaa caa gtc gcc ctc atg atc gcc gct tac   288
Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr
                 85                  90                  95

atc gcg att gac tcc ttc ggc acc gca gca aac gtc acc ggc gac ggc   336
Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly
            100                 105                 110

gca atc gca gtc atc gtg aac aaa ttc gcc aag ggc cag ctg cac acc   384
Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr
        115                 120                 125

act tcc cca gat gaa atc gaa gaa gac gac cgc gtt gcc ttc gac atc   432
Thr Ser Pro Asp Glu Ile Glu Glu Asp Asp Arg Val Ala Phe Asp Ile
    130                 135                 140

act cca tcg gat gtg gaa cat cac aag tagaaacccg cattttctgt         479
Thr Pro Ser Asp Val Glu His His Lys
145                 150

agt                                                               482
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09/24/2002 15:36:36

<210> 410
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 410

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Leu Lys Asn Asp Val Asp Val Asn Val Ala Gly Phe Val Val Pro Leu
  1               5                  10                  15

Cys Ala Thr Ile His Leu Ala Gly Ser Met Met Lys Ile Gly Leu Phe
             20                  25                  30

Thr Phe Ala Val Val Phe Met Tyr Asp Met Glu Val Gly Val Gly Leu
         35                  40                  45

Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro
     50                  55                  60

Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser
 65                  70                  75                  80
```

```
Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr
                85                  90                  95

Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly
            100                 105                 110

Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr
        115                 120                 125

Thr Ser Pro Asp Glu Ile Glu Glu Asp Asp Arg Val Ala Phe Asp Ile
    130                 135                 140

Thr Pro Ser Asp Val Glu His His Lys
145                 150
```

<210> 411
<211> 1509
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1486)
<223> RXA01070

<400> 411

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cagcttcggt taatttggtc acactaatgc aataaattcc tgtctacagc gttacagtta 60

atgaattcaa ttcaaccgct aaacgcaagg agtgctaccc atg gct aac gcc acc   115
                                              Met Ala Asn Ala Thr
                                                1               5

gca cag aag ggc cgt ttc ggc ctt ccc ggc tgg atg act ggc ttt ggt   163
Ala Gln Lys Gly Arg Phe Gly Leu Pro Gly Trp Met Thr Gly Phe Gly
                10                  15                  20

gcc cag gtt atc gcc ggc ctc att ctt ggt ctt att ctc ggc ctt gtc   211
Ala Gln Val Ile Ala Gly Leu Ile Leu Gly Leu Ile Leu Gly Leu Val
            25                  30                  35

gcc cga ggc atg gac agc ggc gct gca gac ggt gaa gca agc tgg ctt   259
Ala Arg Gly Met Asp Ser Gly Ala Ala Asp Gly Glu Ala Ser Trp Leu
        40                  45                  50

acc ggt ctt ctt agc ggc gtc ggt tct gct tat gtt tct cta ctt aaa   307
Thr Gly Leu Leu Ser Gly Val Gly Ser Ala Tyr Val Ser Leu Leu Lys
    55                  60                  65

gtt atg gtt cca cca ctg gtg ttc gct gca gtg gtt acc agt gtg gca   355
Val Met Val Pro Pro Leu Val Phe Ala Ala Val Val Thr Ser Val Ala
70                  75                  80                  85

aag ttg cgc gag gta gct aac gct gct cgc ctg gct gtt tcc acc ttg   403
Lys Leu Arg Glu Val Ala Asn Ala Ala Arg Leu Ala Val Ser Thr Leu
                90                  95                  100

gtg tgg ttc gcc att act gca ttc ttc tct gtg ctc gcg ggt atc gcc   451
Val Trp Phe Ala Ile Thr Ala Phe Phe Ser Val Leu Ala Gly Ile Ala
            105                 110                 115
```

```
gta gcg ctg att atg cag cct ggt gtt gga tcc act gtc gac gca tct   499
Val Ala Leu Ile Met Gln Pro Gly Val Gly Ser Thr Val Asp Ala Ser
        120                 125                 130

aat gct gct gat cct tct cgc gtg ggc agc tgg ctg ggc ttt atc cag   547
Asn Ala Ala Asp Pro Ser Arg Val Gly Ser Trp Leu Gly Phe Ile Gln
    135                 140                 145

tcc gtt att cca tca aac att ctg gga ctt tcc ggt tct tac agt gag   595
Ser Val Ile Pro Ser Asn Ile Leu Gly Leu Ser Gly Ser Tyr Ser Glu
150                 155                 160                 165

aac tct ggt gtg aac ctg tcc ttc aac gtg ctg cag atc ctg gtt atc   643
Asn Ser Gly Val Asn Leu Ser Phe Asn Val Leu Gln Ile Leu Val Ile
                170                 175                 180

tcc att gcg att ggt gtt gca gct ctg aag gct ggc aag tcc gcc gag   691
Ser Ile Ala Ile Gly Val Ala Ala Leu Lys Ala Gly Lys Ser Ala Glu
            185                 190                 195

cct ttc ttg aag ttc acc gag tcc ttc ctc aag atc atc cag atc gtg   739
Pro Phe Leu Lys Phe Thr Glu Ser Phe Leu Lys Ile Ile Gln Ile Val
        200                 205                 210

ttg tgg tgg att att cgc ctg gct cca att ggt tcc gct gcg ctg atc   787
Leu Trp Trp Ile Ile Arg Leu Ala Pro Ile Gly Ser Ala Ala Leu Ile
    215                 220                 225

ggt aat gct gtt gct acc tac ggt tgg tct gca ctt gga tcc ctg ggc   835
Gly Asn Ala Val Ala Thr Tyr Gly Trp Ser Ala Leu Gly Ser Leu Gly
230                 235                 240                 245

aag ttt gtt ctt gcg atc tac gtt ggt ctg gca atc gtc atg ttc gtt   883
Lys Phe Val Leu Ala Ile Tyr Val Gly Leu Ala Ile Val Met Phe Val
                250                 255                 260

atc tac cca gtc gtg ctg aag ctc aat gga att cct gtt ctt gga ttc   931
Ile Tyr Pro Val Val Leu Lys Leu Asn Gly Ile Pro Val Leu Gly Phe
            265                 270                 275

ttc aag cgc gtt tgg cct gtc aca agc ctt ggc ttt gtt acc cgt tcc   979
Phe Lys Arg Val Trp Pro Val Thr Ser Leu Gly Phe Val Thr Arg Ser
        280                 285                 290

tcc atg ggc gtt atg cca gtt acc cag cgc gtt act gag cag tcc ttg   1027
Ser Met Gly Val Met Pro Val Thr Gln Arg Val Thr Glu Gln Ser Leu
    295                 300                 305

ggt gtt cca tct gcg tac gct tcc ttt gct atc cca ctg ggt gcg acc   1075
Gly Val Pro Ser Ala Tyr Ala Ser Phe Ala Ile Pro Leu Gly Ala Thr
310                 315                 320                 325

agc aag atg gac ggc tgc gct gct gtc tac cca gct gtt gcc gct atc   1123
Ser Lys Met Asp Gly Cys Ala Ala Val Tyr Pro Ala Val Ala Ala Ile
                330                 335                 340

ttc gtg gca cag ttc tac ggc att gac ttg agc atc atg gat tac gta   1171
Phe Val Ala Gln Phe Tyr Gly Ile Asp Leu Ser Ile Met Asp Tyr Val
            345                 350                 355

ctg atc atg atc gtc tct gtc ctg ggc tct gct gca act gca ggc acc   1219
```

```
Leu Ile Met Ile Val Ser Val Leu Gly Ser Ala Ala Thr Ala Gly Thr
        360                 365                 370

act ggc gca acc gtc atg ctg acc ctg acc cta tcc acc ttg ggt ctg   1267
Thr Gly Ala Thr Val Met Leu Thr Leu Thr Leu Ser Thr Leu Gly Leu
    375                 380                 385

cca ctt gct ggt gtt ggt ctg ctg ctg gct atc gag cca atc atc gac   1315
Pro Leu Ala Gly Val Gly Leu Leu Leu Ala Ile Glu Pro Ile Ile Asp
390                 395                 400                 405

atg gga cgt acc gca acc aac gtc acc ggt cag gca ctg gtt cct gcg   1363
Met Gly Arg Thr Ala Thr Asn Val Thr Gly Gln Ala Leu Val Pro Ala
                410                 415                 420

atc gtt gct aag cgc gag ggc att ctg gat cag gat gtg tgg gat gct   1411
Ile Val Ala Lys Arg Glu Gly Ile Leu Asp Gln Asp Val Trp Asp Ala
            425                 430                 435

gct gaa aag ggt ggc gct gct att gaa atg gca acc gtc tct gag aaa   1459
Ala Glu Lys Gly Gly Ala Ala Ile Glu Met Ala Thr Val Ser Glu Lys
        440                 445                 450

gaa act gag cct gca gag gtt cgc tcc taagctctct tgagtacctg        1506
Glu Thr Glu Pro Ala Glu Val Arg Ser
    455                 460

aga                                                              1509
```

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<210> 412
<211> 462
<212> PRT
<213> Corynebacterium glutamicum

<400> 412

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Met Ala Asn Ala Thr Ala Gln Lys Gly Arg Phe Gly Leu Pro Gly Trp
  1               5                  10                  15

Met Thr Gly Phe Gly Ala Gln Val Ile Ala Gly Leu Ile Leu Gly Leu
            20                  25                  30

Ile Leu Gly Leu Val Ala Arg Gly Met Asp Ser Gly Ala Ala Asp Gly
        35                  40                  45

Glu Ala Ser Trp Leu Thr Gly Leu Leu Ser Gly Val Gly Ser Ala Tyr
    50                  55                  60

Val Ser Leu Leu Lys Val Met Val Pro Pro Leu Val Phe Ala Ala Val
65                  70                  75                  80

Val Thr Ser Val Ala Lys Leu Arg Glu Val Ala Asn Ala Ala Arg Leu
                85                  90                  95

Ala Val Ser Thr Leu Val Trp Phe Ala Ile Thr Ala Phe Phe Ser Val
            100                 105                 110

Leu Ala Gly Ile Ala Val Ala Leu Ile Met Gln Pro Gly Val Gly Ser
        115                 120                 125

Thr Val Asp Ala Ser Asn Ala Ala Asp Pro Ser Arg Val Gly Ser Trp
```

130 135 140

Leu Gly Phe Ile Gln Ser Val Ile Pro Ser Asn Ile Leu Gly Leu Ser
145 150 155 160

Gly Ser Tyr Ser Glu Asn Ser Gly Val Asn Leu Ser Phe Asn Val Leu
165 170 175

Gln Ile Leu Val Ile Ser Ile Ala Ile Gly Val Ala Ala Leu Lys Ala
180 185 190

Gly Lys Ser Ala Glu Pro Phe Leu Lys Phe Thr Glu Ser Phe Leu Lys
195 200 205

Ile Ile Gln Ile Val Leu Trp Trp Ile Ile Arg Leu Ala Pro Ile Gly
210 215 220

Ser Ala Ala Leu Ile Gly Asn Ala Val Ala Thr Tyr Gly Trp Ser Ala
225 230 235 240

Leu Gly Ser Leu Gly Lys Phe Val Leu Ala Ile Tyr Val Gly Leu Ala
245 250 255

Ile Val Met Phe Val Ile Tyr Pro Val Val Leu Lys Leu Asn Gly Ile
260 265 270

Pro Val Leu Gly Phe Phe Lys Arg Val Trp Pro Val Thr Ser Leu Gly
275 280 285

Phe Val Thr Arg Ser Ser Met Gly Val Met Pro Val Thr Gln Arg Val
290 295 300

Thr Glu Gln Ser Leu Gly Val Pro Ser Ala Tyr Ala Ser Phe Ala Ile
305 310 315 320

Pro Leu Gly Ala Thr Ser Lys Met Asp Gly Cys Ala Ala Val Tyr Pro
325 330 335

Ala Val Ala Ala Ile Phe Val Ala Gln Phe Tyr Gly Ile Asp Leu Ser
340 345 350

Ile Met Asp Tyr Val Leu Ile Met Ile Val Ser Val Leu Gly Ser Ala
355 360 365

Ala Thr Ala Gly Thr Thr Gly Ala Thr Val Met Leu Thr Leu Thr Leu
370 375 380

Ser Thr Leu Gly Leu Pro Leu Ala Gly Val Gly Leu Leu Leu Ala Ile
385 390 395 400

Glu Pro Ile Ile Asp Met Gly Arg Thr Ala Thr Asn Val Thr Gly Gln
405 410 415

Ala Leu Val Pro Ala Ile Val Ala Lys Arg Glu Gly Ile Leu Asp Gln
420 425 430

Asp Val Trp Asp Ala Ala Glu Lys Gly Gly Ala Ala Ile Glu Met Ala
435 440 445

Thr Val Ser Glu Lys Glu Thr Glu Pro Ala Glu Val Arg Ser
450 455 460

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<210> 413
<211> 428
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(405)
<223> RXA02628

<400> 413
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atg ctt gaa ggt ttt aga gat ttc gtc ctt cgg gga aat gtc att gaa    48
Met Leu Glu Gly Phe Arg Asp Phe Val Leu Arg Gly Asn Val Ile Glu
  1               5                  10                  15

ctc gca gtt gcc gtg gtc atc ggt act gcc ttc acc gct atc gtg aca    96
Leu Ala Val Ala Val Val Ile Gly Thr Ala Phe Thr Ala Ile Val Thr
             20                  25                  30

gca ttc tcc gag agc atc atc aac cca ttg atc gct tcc atc ggc agc   144
Ala Phe Ser Glu Ser Ile Ile Asn Pro Leu Ile Ala Ser Ile Gly Ser
         35                  40                  45

aca gag gtt gaa ggc ctc ggc ttc cac atc cgc gcc ggc aat gcc gca   192
Thr Glu Val Glu Gly Leu Gly Phe His Ile Arg Ala Gly Asn Ala Ala
     50                  55                  60

aca ttc gtg gat ttt ggt gct gtc atc acc gca gcg atc aac ttc ctc   240
Thr Phe Val Asp Phe Gly Ala Val Ile Thr Ala Ala Ile Asn Phe Leu
 65                  70                  75                  80

atc atc gca gca att gtc tac ttc gtt ctc gtt gct cca atg aac aag   288
Ile Ile Ala Ala Ile Val Tyr Phe Val Leu Val Ala Pro Met Asn Lys
                 85                  90                  95

ctc agc gaa acc ctc gca aag cgc aag ggt gtt gaa gaa gac gag acc   336
Leu Ser Glu Thr Leu Ala Lys Arg Lys Gly Val Glu Glu Asp Glu Thr
            100                 105                 110

cca gct tcc atc gaa gca gaa ctc ctc acc gag atc cgc gat ctc ctg   384
Pro Ala Ser Ile Glu Ala Glu Leu Leu Thr Glu Ile Arg Asp Leu Leu
        115                 120                 125

cag gag caa aag cgc ctt cag tagttaaaag gccctaaaag cac             428
Gln Glu Gln Lys Arg Leu Gln
    130                 135
```

<210> 414
<211> 135
<212> PRT
<213> Corynebacterium glutamicum

<400> 414
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Met Leu Glu Gly Phe Arg Asp Phe Val Leu Arg Gly Asn Val Ile Glu
  1               5                  10                  15

Leu Ala Val Ala Val Val Ile Gly Thr Ala Phe Thr Ala Ile Val Thr
             20                  25                  30
```

```
Ala Phe Ser Glu Ser Ile Ile Asn Pro Leu Ile Ala Ser Ile Gly Ser
          35                  40                  45

Thr Glu Val Glu Gly Leu Gly Phe His Ile Arg Ala Gly Asn Ala Ala
      50                  55                  60

Thr Phe Val Asp Phe Gly Ala Val Ile Thr Ala Ala Ile Asn Phe Leu
 65                  70                  75                  80

Ile Ile Ala Ala Ile Val Tyr Phe Val Leu Val Ala Pro Met Asn Lys
                 85                  90                  95

Leu Ser Glu Thr Leu Ala Lys Arg Lys Gly Val Glu Glu Asp Glu Thr
            100                 105                 110

Pro Ala Ser Ile Glu Ala Glu Leu Leu Thr Glu Ile Arg Asp Leu Leu
        115                 120                 125

Gln Glu Gln Lys Arg Leu Gln
    130                 135
```

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<210> 415
<211> 993
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(970)
<223> RXN03164

<400> 415

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ctttttgca tccagatgca caaagccgtg gcacaaacga gacaaactga gcacaatggc 60

tgtcatggca tatcaaccag cagacaatcg ctatgacgac atg atc tac cgc agg   115
                                          Met Ile Tyr Arg Arg
                                            1               5

gtg gga aat tct ggg ctg aag ctt ccg gca att tcg ctt ggg ctg tgg   163
Val Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile Ser Leu Gly Leu Trp
                10                  15                  20

cac aac ttc ggt gat gac aag ccg ctt tca acg cag cgc agc att att   211
His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln Arg Ser Ile Ile
            25                  30                  35

cac cgc gcg ttt gat agg gga gtc act cac ttc gat ttg gct aat aac   259
His Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp Leu Ala Asn Asn
        40                  45                  50

tat gga cct cca gca ggt tcc gca gag acc aac ttt ggc agg att ttg   307
Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe Gly Arg Ile Leu
    55                  60                  65

cgt gag gat ctc aaa agc cac cgc gat gag ttg atc att tct tcc aag   355
Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile Ile Ser Ser Lys
70                  75                  80                  85

gcg ggt tgg gat atg tgg cct gga cct tat ggt ttt ggt ggt tcc cga   403
```

```
Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe Gly Gly Ser Arg
                 90                  95                 100

aag tat cta gtg agt tcc ctt gat cag tcc ctg act cgc ctc ggc ttg   451
Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr Arg Leu Gly Leu
            105                 110                 115

gat tac gtg gat att ttc tat cat cac cgc ccg gat cca gat act cct   499
Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp Pro Asp Thr Pro
        120                 125                 130

ttg gaa gaa acc atg tac gca ttg cgt gac att gtt gcg tct gga aag   547
Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala Ser Gly Lys
    135                 140                 145

gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc aca gcg gag   595
Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu Thr Ala Glu
150                 155                 160                 165

gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg att cat cag   643
Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu Ile His Gln
                170                 175                 180

cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg ggc gat gac   691
Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro Gly Asp Asp
            185                 190                 195

ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt ggc gtc att   739
Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu Gly Val Ile
        200                 205                 210

gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa tat ctc gat   787
Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys Tyr Leu Asp
    215                 220                 225

gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc ctg tct gag   835
Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser Leu Ser Glu
230                 235                 240                 245

ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag ctc aat gac   883
Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys Leu Asn Asp
                250                 255                 260

atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg ctt gca tgg   931
Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala Leu Ala Trp
            265                 270                 275

gtg ctg cgc gag caa aga gag tac ggc gcc gga tta ccg tgaccagtgc    980
Val Leu Arg Glu Gln Arg Glu Tyr Gly Ala Gly Leu Pro
        280                 285                 290

attgattggt gct                                                   993


<210> 416
<211> 290
<212> PRT
<213> Corynebacterium glutamicum

<400> 416
Met Ile Tyr Arg Arg Val Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile
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1 5 10 15

Ser Leu Gly Leu Trp His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr
20 25 30

Gln Arg Ser Ile Ile His Arg Ala Phe Asp Arg Gly Val Thr His Phe
35 40 45

Asp Leu Ala Asn Asn Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn
50 55 60

Phe Gly Arg Ile Leu Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu
65 70 75 80

Ile Ile Ser Ser Lys Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly
85 90 95

Phe Gly Gly Ser Arg Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu
100 105 110

Thr Arg Leu Gly Leu Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro
115 120 125

Asp Pro Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile
130 135 140

Val Ala Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro
145 150 155 160

Glu Leu Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro
165 170 175

Leu Leu Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu
180 185 190

Glu Pro Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn
195 200 205

Gly Leu Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr
210 215 220

Asp Lys Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly
225 230 235 240

Lys Ser Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val
245 250 255

Arg Lys Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln
260 265 270

Met Ala Leu Ala Trp Val Leu Arg Glu Gln Arg Glu Tyr Gly Ala Gly
275 280 285

Leu Pro
290

<210> 417
<211> 1209
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1186)
<223> FRXA01395

<400> 417
ctcaaaagca ctgataaaag cagtcaaccc acctcgggtt ggctgctttt ttgcatccag 60

atgcacaaag ccgtggcaca aacgagacaa actgagcaca atg gct gtc atg gca 115
Met Ala Val Met Ala
1 5

tat caa cca gca gac aat cgc tat gac gac atg atc tac cgc agg gtg 163
Tyr Gln Pro Ala Asp Asn Arg Tyr Asp Asp Met Ile Tyr Arg Arg Val
10 15 20

gga aat tct ggg ctg aag ctt ccg gca att tcg ctt ggg ctg tgg cac 211
Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile Ser Leu Gly Leu Trp His
25 30 35

aac ttc ggt gat gac aag ccg ctt tca acg cag cgc agc att att cac 259
Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln Arg Ser Ile Ile His
40 45 50

cgc gcg ttt gat agg gga gtc act cac ttc gat ttg gct aat aac tat 307
Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp Leu Ala Asn Asn Tyr
55 60 65

gga cct cca gca ggt tcc gca gag acc aac ttt ggc agg att ttg cgt 355
Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe Gly Arg Ile Leu Arg
70 75 80 85

gag gat ctc aaa agc cac cgc gat gag ttg atc att tct tcc aag gcg 403
Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile Ile Ser Ser Lys Ala
90 95 100

ggt tgg gat atg tgg cct gga cct tat ggt ttt ggt ggt tcc cga aag 451
Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe Gly Gly Ser Arg Lys
105 110 115

tat cta gtg agt tcc ctt gat cag tcc ctg act cgc ctc ggc ttg gat 499
Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr Arg Leu Gly Leu Asp
120 125 130

tac gtg gat att ttc tat cat cac cgc ccg gat cca gat act cct ttg 547
Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp Pro Asp Thr Pro Leu
135 140 145

gaa gaa acc atg tac gca ttg cgt gac att gtt gcg tct gga aag gct 595
Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala Ser Gly Lys Ala
150 155 160 165

ctt tac gtg ggt att tct tcc tac ggt cca gag ctc aca gcg gag gcg 643
Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu Thr Ala Glu Ala
170 175 180

gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg att cat cag cca 691
Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu Ile His Gln Pro
185 190 195

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```
agc tat tcc atc att aat cgt tgg gtg gag gaa ccg ggc gat gac ggt   739
Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro Gly Asp Asp Gly
        200                 205                 210

gag aac ttg ttg cag tca gct gcc aac aat ggt ctt ggc gtc att gct   787
Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu Gly Val Ile Ala
    215                 220                 225

ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa tat ctc gat gga   835
Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys Tyr Leu Asp Gly
230                 235                 240                 245

att cca gag ggt tcc cgc gcc agc cag ggt aag tcc ctk tst kac ggs   883
Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser Xaa Xaa Xaa Xaa
                250                 255                 260

wtg ttg aac gtg aac aat att gat wtg gtc ccm ars ytn awk rsa wtt   931
Xaa Leu Asn Val Asn Asn Ile Asp Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa
            265                 270                 275

tcc mar ram acc ggg cag tcc ttt nnc cna aag gnc ttt tgt tgg gtt   979
Ser Xaa Xaa Thr Gly Gln Ser Phe Xaa Xaa Lys Xaa Phe Cys Trp Val
        280                 285                 290

gtt gcc caa cca agg aaa gta cgg cgc cgg att acc gtg acc agt gca   1027
Val Ala Gln Pro Arg Lys Val Arg Arg Arg Ile Thr Val Thr Ser Ala
    295                 300                 305

ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc ctt gat tca   1075
Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser Leu Asp Ser
310                 315                 320                 325

ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg atc gat gag   1123
Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala Ile Asp Glu
                330                 335                 340

att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc acc gat tcc   1171
Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala Thr Asp Ser
            345                 350                 355

aaa acc cgc gaa aac taacccatca acatcagttt gat                    1209
Lys Thr Arg Glu Asn
        360
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<210> 418
<211> 362
<212> PRT
<213> Corynebacterium glutamicum

<400> 418

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Met Ala Val Met Ala Tyr Gln Pro Ala Asp Asn Arg Tyr Asp Asp Met
  1               5                  10                  15

Ile Tyr Arg Arg Val Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile Ser
             20                  25                  30

Leu Gly Leu Trp His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln
         35                  40                  45

Arg Ser Ile Ile His Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp
```

50 55 60

Leu Ala Asn Asn Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe
65 70 75 80

Gly Arg Ile Leu Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile
85 90 95

Ile Ser Ser Lys Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe
100 105 110

Gly Gly Ser Arg Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr
115 120 125

Arg Leu Gly Leu Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp
130 135 140

Pro Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val
145 150 155 160

Ala Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu
165 170 175

Leu Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu
180 185 190

Leu Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu
195 200 205

Pro Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly
210 215 220

Leu Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp
225 230 235 240

Lys Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys
245 250 255

Ser Xaa Xaa Xaa Xaa Xaa Leu Asn Val Asn Asn Ile Asp Xaa Val Xaa
260 265 270

Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Thr Gly Gln Ser Phe Xaa Xaa Lys
275 280 285

Xaa Phe Cys Trp Val Val Ala Gln Pro Arg Lys Val Arg Arg Arg Ile
290 295 300

Thr Val Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp
305 310 315 320

Asn Ser Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu
325 330 335

Glu Ala Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala
340 345 350

Lys Ala Thr Asp Ser Lys Thr Arg Glu Asn
355 360

<210> 419

<211> 1911
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1888)
<223> RXA02597

<400> 419
atacccactt tgcaagaatt acaaacgggg gcaccctcaa tgacttgaaa cactttatag 60

agtagaaagt gagtcacgac actttttaaa ggaggatgct ttg ccc gaa caa gac 115
Leu Pro Glu Gln Asp
1 5

tta acc acc ttg gcc aat gat tgg ctc caa gct ttt gaa aag gcc act 163
Leu Thr Thr Leu Ala Asn Asp Trp Leu Gln Ala Phe Glu Lys Ala Thr
10 15 20

gct agt tcc agc cct gat gaa gct gcc act gca gtc gtg caa ctt ttt 211
Ala Ser Ser Ser Pro Asp Glu Ala Ala Thr Ala Val Val Gln Leu Phe
25 30 35

gag gat gaa gga tac tgg cga gac ctt ctt gca ttc acg tgg aac ctc 259
Glu Asp Glu Gly Tyr Trp Arg Asp Leu Leu Ala Phe Thr Trp Asn Leu
40 45 50

acc acc gct gaa ggt gca gat gaa atc gcc gag atg att cgc aat acg 307
Thr Thr Ala Glu Gly Ala Asp Glu Ile Ala Glu Met Ile Arg Asn Thr
55 60 65

tgg cca tca agc atc ttc cga aac gtt gag cta aag ggc gaa cca gct 355
Trp Pro Ser Ser Ile Phe Arg Asn Val Glu Leu Lys Gly Glu Pro Ala
70 75 80 85

gat gaa gga gat ggt gtc act cgc gta cat ttc tcc tgc gaa tcc gca 403
Asp Glu Gly Asp Gly Val Thr Arg Val His Phe Ser Cys Glu Ser Ala
90 95 100

gac ttc aag tgc acg ggc att gtc cgc ctt cgt aat ggc aag gcg tgg 451
Asp Phe Lys Cys Thr Gly Ile Val Arg Leu Arg Asn Gly Lys Ala Trp
105 110 115

acg cta ctc acc tca gct cgt gag ctc ctg gag cac cca gag ccc aag 499
Thr Leu Leu Thr Ser Ala Arg Glu Leu Leu Glu His Pro Glu Pro Lys
120 125 130

ggg cgc aac cgt gag atg ggc gtc gtc cat gga caa aat gag gac acc 547
Gly Arg Asn Arg Glu Met Gly Val Val His Gly Gln Asn Glu Asp Thr
135 140 145

cga aat tgg act gac cgc aag aat gat cga caa gca gcg ttg ggt gtc 595
Arg Asn Trp Thr Asp Arg Lys Asn Asp Arg Gln Ala Ala Leu Gly Val
150 155 160 165

acc gag cag cca tac acc ctc atc atc ggt ggt gga cag ggt ggc att 643
Thr Glu Gln Pro Tyr Thr Leu Ile Ile Gly Gly Gly Gln Gly Gly Ile
170 175 180

gcc ttg ggc gca cga ctc aag cga ctt ggt gta ccc gct cta atc att 691

```
Ala Leu Gly Ala Arg Leu Lys Arg Leu Gly Val Pro Ala Leu Ile Ile
                185                 190                 195

gat aaa gca tct cgc ccg ggc gac cag tgg cgt agc cgt tac cat tct   739
Asp Lys Ala Ser Arg Pro Gly Asp Gln Trp Arg Ser Arg Tyr His Ser
        200                 205                 210

ctc tgc ctg cac gat cca gtt tgg tac gac cac ctg cct tac att cca   787
Leu Cys Leu His Asp Pro Val Trp Tyr Asp His Leu Pro Tyr Ile Pro
    215                 220                 225

ttc cca gat cat tgg cca gta ttt act cca aag gac aag atg ggt gac   835
Phe Pro Asp His Trp Pro Val Phe Thr Pro Lys Asp Lys Met Gly Asp
230                 235                 240                 245

tgg ctc gag cac tat gtc ggc atc atg gat ttg gac tat tgg acc aac   883
Trp Leu Glu His Tyr Val Gly Ile Met Asp Leu Asp Tyr Trp Thr Asn
                250                 255                 260

acc gag tgc ctg cgc gcc tca tac aat gag gac acc aag cag tgg gat   931
Thr Glu Cys Leu Arg Ala Ser Tyr Asn Glu Asp Thr Lys Gln Trp Asp
            265                 270                 275

gtg acg gtc aat cgt gat ggc gcg gag tcc acg ctc cac ccc acc caa   979
Val Thr Val Asn Arg Asp Gly Ala Glu Ser Thr Leu His Pro Thr Gln
        280                 285                 290

cta gtc atg gct act gga atg tcg ggc agc ccg aac aaa cca act ttg   1027
Leu Val Met Ala Thr Gly Met Ser Gly Ser Pro Asn Lys Pro Thr Leu
    295                 300                 305

cct ggc cag gat aag ttc cag ggt gaa att cgg cac tct tca gag cac   1075
Pro Gly Gln Asp Lys Phe Gln Gly Glu Ile Arg His Ser Ser Glu His
310                 315                 320                 325

ccc ggc ggc gat gtc gat cgc gat aag aac gtt gta gtt ctg ggc gct   1123
Pro Gly Gly Asp Val Asp Arg Asp Lys Asn Val Val Val Leu Gly Ala
                330                 335                 340

aac aac tca gcc cac gac atc tgc gcg gat ctt tat tcc aat ggt gca   1171
Asn Asn Ser Ala His Asp Ile Cys Ala Asp Leu Tyr Ser Asn Gly Ala
            345                 350                 355

aag ccc gtg atg att cag cgc tcg tct aca cac atc gtg cgt tct gat   1219
Lys Pro Val Met Ile Gln Arg Ser Ser Thr His Ile Val Arg Ser Asp
        360                 365                 370

tcg ctg atg cgc gaa gtc ttc ggg cct ctc tat tct gag gat gcc gtt   1267
Ser Leu Met Arg Glu Val Phe Gly Pro Leu Tyr Ser Glu Asp Ala Val
    375                 380                 385

gaa gcc gga att gat acc gat act gcc gat ctc ctg ttt gcg tcg tgg   1315
Glu Ala Gly Ile Asp Thr Asp Thr Ala Asp Leu Leu Phe Ala Ser Trp
390                 395                 400                 405

cca tat aag gtg ctg cca ggt gtg cag aag cag gct ttc gac aag atc   1363
Pro Tyr Lys Val Leu Pro Gly Val Gln Lys Gln Ala Phe Asp Lys Ile
                410                 415                 420

cgt gag gac gac aag gag ttc tac gac aag ctt gaa aat gct gga ttc   1411
Arg Glu Asp Asp Lys Glu Phe Tyr Asp Lys Leu Glu Asn Ala Gly Phe
```

```
            425                 430                 435

ttg ctt gat ttc ggc gat gac gat tcg ggg ctt ttc tta aag tac ctt   1459
Leu Leu Asp Phe Gly Asp Asp Asp Ser Gly Leu Phe Leu Lys Tyr Leu
        440                 445                 450

cgc cgt ggc tct ggc tac tac atc gat gtc ggc gcc tct gaa ctg gtg   1507
Arg Arg Gly Ser Gly Tyr Tyr Ile Asp Val Gly Ala Ser Glu Leu Val
    455                 460                 465

gct gat gga aag att ccg gtg cgc tcc aat gtc agc att gaa gac gtc   1555
Ala Asp Gly Lys Ile Pro Val Arg Ser Asn Val Ser Ile Glu Asp Val
470                 475                 480                 485

aag gaa aac tct gtg gtg ctc aca gat ggt act gag ctc cca gct gac   1603
Lys Glu Asn Ser Val Val Leu Thr Asp Gly Thr Glu Leu Pro Ala Asp
                490                 495                 500

gtg att gtt cta gcg acc ggc tat gga aac atg aac aac tgg gtt gct   1651
Val Ile Val Leu Ala Thr Gly Tyr Gly Asn Met Asn Asn Trp Val Ala
            505                 510                 515

cag ctg gtt gat cag gaa acc gct gac aag gtc ggc cca tgc tgg ggt   1699
Gln Leu Val Asp Gln Glu Thr Ala Asp Lys Val Gly Pro Cys Trp Gly
        520                 525                 530

ctg ggc tct gaa acc acc aag gat cca ggc cca tgg gaa ggc gag ttg   1747
Leu Gly Ser Glu Thr Thr Lys Asp Pro Gly Pro Trp Glu Gly Glu Leu
    535                 540                 545

cgc aat atg tgg aag ccc aca aac gtg gat tcg ctg tgg ttc cat ggt   1795
Arg Asn Met Trp Lys Pro Thr Asn Val Asp Ser Leu Trp Phe His Gly
550                 555                 560                 565

ggc aac ctt cac cag tca cgc cat tac tca cgg tat ttg tcc atg cag   1843
Gly Asn Leu His Gln Ser Arg His Tyr Ser Arg Tyr Leu Ser Met Gln
                570                 575                 580

ttg aag gcg cgc tac gaa ggt atg aac act ccg gtg tac agc aag       1888
Leu Lys Ala Arg Tyr Glu Gly Met Asn Thr Pro Val Tyr Ser Lys
            585                 590                 595

tagatacaaa gaaaagggca tct                                        1911


<210> 420
<211> 596
<212> PRT
<213> Corynebacterium glutamicum

<400> 420
Leu Pro Glu Gln Asp Leu Thr Thr Leu Ala Asn Asp Trp Leu Gln Ala
  1               5                  10                  15

Phe Glu Lys Ala Thr Ala Ser Ser Ser Pro Asp Glu Ala Ala Thr Ala
             20                  25                  30

Val Val Gln Leu Phe Glu Asp Glu Gly Tyr Trp Arg Asp Leu Leu Ala
         35                  40                  45

Phe Thr Trp Asn Leu Thr Thr Ala Glu Gly Ala Asp Glu Ile Ala Glu
```

```
     50                  55                  60

Met Ile Arg Asn Thr Trp Pro Ser Ser Ile Phe Arg Asn Val Glu Leu
 65                  70                  75                  80

Lys Gly Glu Pro Ala Asp Glu Gly Asp Gly Val Thr Arg Val His Phe
                 85                  90                  95

Ser Cys Glu Ser Ala Asp Phe Lys Cys Thr Gly Ile Val Arg Leu Arg
            100                 105                 110

Asn Gly Lys Ala Trp Thr Leu Leu Thr Ser Ala Arg Glu Leu Leu Glu
        115                 120                 125

His Pro Glu Pro Lys Gly Arg Asn Arg Glu Met Gly Val Val His Gly
    130                 135                 140

Gln Asn Glu Asp Thr Arg Asn Trp Thr Asp Arg Lys Asn Asp Arg Gln
145                 150                 155                 160

Ala Ala Leu Gly Val Thr Glu Gln Pro Tyr Thr Leu Ile Ile Gly Gly
                165                 170                 175

Gly Gln Gly Gly Ile Ala Leu Gly Ala Arg Leu Lys Arg Leu Gly Val
            180                 185                 190

Pro Ala Leu Ile Ile Asp Lys Ala Ser Arg Pro Gly Asp Gln Trp Arg
        195                 200                 205

Ser Arg Tyr His Ser Leu Cys Leu His Asp Pro Val Trp Tyr Asp His
    210                 215                 220

Leu Pro Tyr Ile Pro Phe Pro Asp His Trp Pro Val Phe Thr Pro Lys
225                 230                 235                 240

Asp Lys Met Gly Asp Trp Leu Glu His Tyr Val Gly Ile Met Asp Leu
                245                 250                 255

Asp Tyr Trp Thr Asn Thr Glu Cys Leu Arg Ala Ser Tyr Asn Glu Asp
            260                 265                 270

Thr Lys Gln Trp Asp Val Thr Val Asn Arg Asp Gly Ala Glu Ser Thr
        275                 280                 285

Leu His Pro Thr Gln Leu Val Met Ala Thr Gly Met Ser Gly Ser Pro
    290                 295                 300

Asn Lys Pro Thr Leu Pro Gly Gln Asp Lys Phe Gln Gly Glu Ile Arg
305                 310                 315                 320

His Ser Ser Glu His Pro Gly Gly Asp Val Asp Arg Asp Lys Asn Val
                325                 330                 335

Val Val Leu Gly Ala Asn Asn Ser Ala His Asp Ile Cys Ala Asp Leu
            340                 345                 350

Tyr Ser Asn Gly Ala Lys Pro Val Met Ile Gln Arg Ser Ser Thr His
        355                 360                 365

Ile Val Arg Ser Asp Ser Leu Met Arg Glu Val Phe Gly Pro Leu Tyr
    370                 375                 380
```

Ser Glu Asp Ala Val Glu Ala Gly Ile Asp Thr Asp Thr Ala Asp Leu
385 390 395 400

Leu Phe Ala Ser Trp Pro Tyr Lys Val Leu Pro Gly Val Gln Lys Gln
405 410 415

Ala Phe Asp Lys Ile Arg Glu Asp Asp Lys Glu Phe Tyr Asp Lys Leu
420 425 430

Glu Asn Ala Gly Phe Leu Leu Asp Phe Gly Asp Asp Asp Ser Gly Leu
435 440 445

Phe Leu Lys Tyr Leu Arg Arg Gly Ser Gly Tyr Tyr Ile Asp Val Gly
450 455 460

Ala Ser Glu Leu Val Ala Asp Gly Lys Ile Pro Val Arg Ser Asn Val
465 470 475 480

Ser Ile Glu Asp Val Lys Glu Asn Ser Val Val Leu Thr Asp Gly Thr
485 490 495

Glu Leu Pro Ala Asp Val Ile Val Leu Ala Thr Gly Tyr Gly Asn Met
500 505 510

Asn Asn Trp Val Ala Gln Leu Val Asp Gln Glu Thr Ala Asp Lys Val
515 520 525

Gly Pro Cys Trp Gly Leu Gly Ser Glu Thr Thr Lys Asp Pro Gly Pro
530 535 540

Trp Glu Gly Glu Leu Arg Asn Met Trp Lys Pro Thr Asn Val Asp Ser
545 550 555 560

Leu Trp Phe His Gly Gly Asn Leu His Gln Ser Arg His Tyr Ser Arg
565 570 575

Tyr Leu Ser Met Gln Leu Lys Ala Arg Tyr Glu Gly Met Asn Thr Pro
580 585 590

Val Tyr Ser Lys
595

<210> 421
<211> 367
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(367)
<223> RXA01454

<400> 421
ggccaggact ttggcgtttc ggatcagcag ttcggcttgg attatggatt ctacgcgttt 60

gatcttccga tgcttcgcct catcgcttga ctcactgtcg atg atg ttg atc gtt 115
Met Met Leu Ile Val
1 5

```
gct ttc ctg atc gca ctc gtt ggc cat tac ctc atg ggt ggc att cgc   163
Ala Phe Leu Ile Ala Leu Val Gly His Tyr Leu Met Gly Gly Ile Arg
                 10                  15                  20

gct gga aac cag atg acg ggc cag aag tcc ttt gta tcc cgt ggt gcg   211
Ala Gly Asn Gln Met Thr Gly Gln Lys Ser Phe Val Ser Arg Gly Ala
             25                  30                  35

cgc act cag ctt gcg gta act gct ggt ctg tgg atg ctt gtt aag gtc   259
Arg Thr Gln Leu Ala Val Thr Ala Gly Leu Trp Met Leu Val Lys Val
         40                  45                  50

gct ggc tac tgg ctg gat cgc tat gac ctg ctg act aag gaa aac tca   307
Ala Gly Tyr Trp Leu Asp Arg Tyr Asp Leu Leu Thr Lys Glu Asn Ser
     55                  60                  65

acc ttc aca ggt gca agc tac acc gac atc aat gca cag ctg cca gcg   355
Thr Phe Thr Gly Ala Ser Tyr Thr Asp Ile Asn Ala Gln Leu Pro Ala
 70                  75                  80                  85

aag atc atc ctg                                                  367
Lys Ile Ile Leu
```

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<210> 422
<211> 89
<212> PRT
<213> Corynebacterium glutamicum

<400> 422

```
Met Met Leu Ile Val Ala Phe Leu Ile Ala Leu Val Gly His Tyr Leu
  1               5                  10                  15

Met Gly Gly Ile Arg Ala Gly Asn Gln Met Thr Gly Gln Lys Ser Phe
             20                  25                  30

Val Ser Arg Gly Ala Arg Thr Gln Leu Ala Val Thr Ala Gly Leu Trp
         35                  40                  45

Met Leu Val Lys Val Ala Gly Tyr Trp Leu Asp Arg Tyr Asp Leu Leu
     50                  55                  60

Thr Lys Glu Asn Ser Thr Phe Thr Gly Ala Ser Tyr Thr Asp Ile Asn
 65                  70                  75                  80

Ala Gln Leu Pro Ala Lys Ile Ile Leu
                 85
```

<210> 423
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXA01455

<400> 423

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agagtggggg agaaacgcat aatcacgtac atataaggat attgtcttgt cgactggtct 60

cacacctcct ccccaaccga tcaagcgacc tcccaaggcg gtg aca tgg atc ttc   115
                                            Val Thr Trp Ile Phe
                                              1               5

gcc att atc gcg ttg gtc att ctc atc gcc cca atg agt gtt ggc ttc   163
Ala Ile Ile Ala Leu Val Ile Leu Ile Ala Pro Met Ser Val Gly Phe
                  10                  15                  20

tat acc gac tgg ctt tgg ttc ggt gaa gtc gat ttc cga ggc gtt ttc   211
Tyr Thr Asp Trp Leu Trp Phe Gly Glu Val Asp Phe Arg Gly Val Phe
              25                  30                  35

agc aag gtt att gtc act cgc att gtt ctc ttt gtg atc ttt gcg cta   259
Ser Lys Val Ile Val Thr Arg Ile Val Leu Phe Val Ile Phe Ala Leu
          40                  45                  50

att gct ggg ttt gtc aca tgg ctt gct ggt tat ttt gtg aca aaa ctt   307
Ile Ala Gly Phe Val Thr Trp Leu Ala Gly Tyr Phe Val Thr Lys Leu
      55                  60                  65

cga cct gat gag atg tcg gcg ttt gat acc cag tcg cct gtg tat cag   355
Arg Pro Asp Glu Met Ser Ala Phe Asp Thr Gln Ser Pro Val Tyr Gln
  70                  75                  80                  85

tac cgt cag atg atc gaa aac agc ctt cgt cgc gtt atg gtg atc att   403
Tyr Arg Gln Met Ile Glu Asn Ser Leu Arg Arg Val Met Val Ile Ile
                  90                  95                 100

cca att ttc gtc gcg ttg ctg gct ggc cta att ggt cag cgt tcg tgg   451
Pro Ile Phe Val Ala Leu Leu Ala Gly Leu Ile Gly Gln Arg Ser Trp
              105                 110                 115

cgc acc gtt caa atg tgg ctg aat ggc cag gac ttt ggc gtt tcg gat   499
Arg Thr Val Gln Met Trp Leu Asn Gly Gln Asp Phe Gly Val Ser Asp
          120                 125                 130

cag cag ttc ggc ttg gat tat gga ttc tac gcg ttt gat ctt ccg atg   547
Gln Gln Phe Gly Leu Asp Tyr Gly Phe Tyr Ala Phe Asp Leu Pro Met
      135                 140                 145

ctt cgc ctc atc gct tgactcactg tcgatgatgt tga                    585
Leu Arg Leu Ile Ala
150
```

<210> 424
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 424

```
Val Thr Trp Ile Phe Ala Ile Ile Ala Leu Val Ile Leu Ile Ala Pro
  1               5                  10                  15

Met Ser Val Gly Phe Tyr Thr Asp Trp Leu Trp Phe Gly Glu Val Asp
              20                  25                  30

Phe Arg Gly Val Phe Ser Lys Val Ile Val Thr Arg Ile Val Leu Phe
          35                  40                  45
```

```
Val Ile Phe Ala Leu Ile Ala Gly Phe Val Thr Trp Leu Ala Gly Tyr
     50                  55                  60

Phe Val Thr Lys Leu Arg Pro Asp Glu Met Ser Ala Phe Asp Thr Gln
 65                  70                  75                  80

Ser Pro Val Tyr Gln Tyr Arg Gln Met Ile Glu Asn Ser Leu Arg Arg
                 85                  90                  95

Val Met Val Ile Ile Pro Ile Phe Val Ala Leu Leu Ala Gly Leu Ile
            100                 105                 110

Gly Gln Arg Ser Trp Arg Thr Val Gln Met Trp Leu Asn Gly Gln Asp
        115                 120                 125

Phe Gly Val Ser Asp Gln Gln Phe Gly Leu Asp Tyr Gly Phe Tyr Ala
    130                 135                 140

Phe Asp Leu Pro Met Leu Arg Leu Ile Ala
145                 150
```

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<210> 425
<211> 987
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(964)
<223> RXA02684

<400> 425

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gcaggttcgt ccacagccgc cggtgattgc aggggatggg gggaggcgtc gaaaagcaat 60

atcttttaag ccccgtggct gcctgggcac gatcgcgggc gtg ctt gct gtg ggc   115
                                            Val Leu Ala Val Gly
                                              1               5

ttg gtg ctt gtg ttt gtg gtg acg ctg tgg gcg gat tcg aag ctg aat   163
Leu Val Leu Val Phe Val Val Thr Leu Trp Ala Asp Ser Lys Leu Asn
                 10                  15                  20

cgc gtg gat gcc acg cct gcg acg cag gtg gcg aac act gcc gga acg   211
Arg Val Asp Ala Thr Pro Ala Thr Gln Val Ala Asn Thr Ala Gly Thr
             25                  30                  35

aac tgg ctg ctg gta ggt tcg gat tcg cgg cag ggt tta agt gat gag   259
Asn Trp Leu Leu Val Gly Ser Asp Ser Arg Gln Gly Leu Ser Asp Glu
         40                  45                  50

gat att gag cgg cta ggt acc ggc ggc gat atc ggt gtg ggc cgt acg   307
Asp Ile Glu Arg Leu Gly Thr Gly Gly Asp Ile Gly Val Gly Arg Thr
     55                  60                  65

gac acg atc atg gtg ttg cat atg ccg cgt act ggc gag ccg acg ctg   355
Asp Thr Ile Met Val Leu His Met Pro Arg Thr Gly Glu Pro Thr Leu
 70                  75                  80                  85

ttg tcg att ccg cgt gat tct tat gtc aat gtc cct ggc tgg ggc atg   403
```

```
Leu Ser Ile Pro Arg Asp Ser Tyr Val Asn Val Pro Gly Trp Gly Met
                 90                  95                 100

gat aag gca aac gcc gca ttt acc gtg ggt ggc ccg gaa ctg ctg acg   451
Asp Lys Ala Asn Ala Ala Phe Thr Val Gly Gly Pro Glu Leu Leu Thr
            105                 110                 115

caa acc gtg gag gag gca act ggc ctg cga att gat cac tat gca gaa   499
Gln Thr Val Glu Glu Ala Thr Gly Leu Arg Ile Asp His Tyr Ala Glu
        120                 125                 130

atc ggc atg ggt ggt ttg gcg aac atg gtt gat gcc gtg ggc ggc gtg   547
Ile Gly Met Gly Gly Leu Ala Asn Met Val Asp Ala Val Gly Gly Val
    135                 140                 145

gaa atg tgt cct gct gag ccg atg tat gat ccg ctc gcg aac ctg gat   595
Glu Met Cys Pro Ala Glu Pro Met Tyr Asp Pro Leu Ala Asn Leu Asp
150                 155                 160                 165

att cag gct ggt tgc cag gaa ttt gat ggg gca gcc gcg ctg ggt tat   643
Ile Gln Ala Gly Cys Gln Glu Phe Asp Gly Ala Ala Ala Leu Gly Tyr
                170                 175                 180

gtg cgc act cgt gcc aca gcc ctg ggt gat ctg gac cgg gtg gtg cgt   691
Val Arg Thr Arg Ala Thr Ala Leu Gly Asp Leu Asp Arg Val Val Arg
            185                 190                 195

cag cgg gaa ttc ttc tcc gct ctg ctg agt aca gct acg tcc ccg ggc   739
Gln Arg Glu Phe Phe Ser Ala Leu Leu Ser Thr Ala Thr Ser Pro Gly
        200                 205                 210

acg ttg ctg aat ccg ttc cgc acc ttc ccg atg atc tcc aac gcg gtg   787
Thr Leu Leu Asn Pro Phe Arg Thr Phe Pro Met Ile Ser Asn Ala Val
    215                 220                 225

gga aca ttc acc gtc ggc gag ggc gat cac gtg tgg cac ctg gcc cga   835
Gly Thr Phe Thr Val Gly Glu Gly Asp His Val Trp His Leu Ala Arg
230                 235                 240                 245

ttg gcg ctg gcg atg cgc gga gga atc gtg acg gag acc gtg ccg att   883
Leu Ala Leu Ala Met Arg Gly Gly Ile Val Thr Glu Thr Val Pro Ile
                250                 255                 260

gcc tca ttc gca gat tac gat gtg gga aat gtt gcg att tgg gac gaa   931
Ala Ser Phe Ala Asp Tyr Asp Val Gly Asn Val Ala Ile Trp Asp Glu
            265                 270                 275

gct gga gcc gaa gca cta ttt agc tcc atg cgc taaaacccca ggtaatcgtt 984
Ala Gly Ala Glu Ala Leu Phe Ser Ser Met Arg
        280                 285

cac                                                               987


<210> 426
<211> 288
<212> PRT
<213> Corynebacterium glutamicum

<400> 426
Val Leu Ala Val Gly Leu Val Leu Val Phe Val Val Thr Leu Trp Ala
```

```
  1               5                  10                  15

Asp Ser Lys Leu Asn Arg Val Asp Ala Thr Pro Ala Thr Gln Val Ala
            20                  25                  30

Asn Thr Ala Gly Thr Asn Trp Leu Leu Val Gly Ser Asp Ser Arg Gln
        35                  40                  45

Gly Leu Ser Asp Glu Asp Ile Glu Arg Leu Gly Thr Gly Gly Asp Ile
    50                  55                  60

Gly Val Gly Arg Thr Asp Thr Ile Met Val Leu His Met Pro Arg Thr
65                  70                  75                  80

Gly Glu Pro Thr Leu Leu Ser Ile Pro Arg Asp Ser Tyr Val Asn Val
                85                  90                  95

Pro Gly Trp Gly Met Asp Lys Ala Asn Ala Ala Phe Thr Val Gly Gly
            100                 105                 110

Pro Glu Leu Leu Thr Gln Thr Val Glu Glu Ala Thr Gly Leu Arg Ile
        115                 120                 125

Asp His Tyr Ala Glu Ile Gly Met Gly Gly Leu Ala Asn Met Val Asp
    130                 135                 140

Ala Val Gly Gly Val Glu Met Cys Pro Ala Glu Pro Met Tyr Asp Pro
145                 150                 155                 160

Leu Ala Asn Leu Asp Ile Gln Ala Gly Cys Gln Glu Phe Asp Gly Ala
                165                 170                 175

Ala Ala Leu Gly Tyr Val Arg Thr Arg Ala Thr Ala Leu Gly Asp Leu
            180                 185                 190

Asp Arg Val Val Arg Gln Arg Glu Phe Phe Ser Ala Leu Leu Ser Thr
        195                 200                 205

Ala Thr Ser Pro Gly Thr Leu Leu Asn Pro Phe Arg Thr Phe Pro Met
    210                 215                 220

Ile Ser Asn Ala Val Gly Thr Phe Thr Val Gly Glu Gly Asp His Val
225                 230                 235                 240

Trp His Leu Ala Arg Leu Ala Leu Ala Met Arg Gly Gly Ile Val Thr
                245                 250                 255

Glu Thr Val Pro Ile Ala Ser Phe Ala Asp Tyr Asp Val Gly Asn Val
            260                 265                 270

Ala Ile Trp Asp Glu Ala Gly Ala Glu Ala Leu Phe Ser Ser Met Arg
        275                 280                 285
```

<210> 427
<211> 522
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> RXN02391

<400> 427
caaagtggcg atcctgaatt tgccatcgaa tctgccgtga gaagagttgc agagctggcg 60

aggcggtaac gctgaacggc ggcgggtaag atatttgagc atg aca caa tca gat 115
Met Thr Gln Ser Asp
1 5

tta ccc gat gat gtt cag gaa ttg gtc act aag atc ttt gga ctg gca 163
Leu Pro Asp Asp Val Gln Glu Leu Val Thr Lys Ile Phe Gly Leu Ala
10 15 20

cgt gat ggg gga gca gaa tcc gca gca acc ctc ggt gca tat gtc gac 211
Arg Asp Gly Gly Ala Glu Ser Ala Ala Thr Leu Gly Ala Tyr Val Asp
25 30 35

aac ggc gtt gac gtt aac ctg tcc aac caa gat ggc aac act ttg ctc 259
Asn Gly Val Asp Val Asn Leu Ser Asn Gln Asp Gly Asn Thr Leu Leu
40 45 50

atg ctc gca gca tat gca gga cat gct gat gtc gtg cag gcg ttg att 307
Met Leu Ala Ala Tyr Ala Gly His Ala Asp Val Val Gln Ala Leu Ile
55 60 65

gag cgt ggc gcc gat gtg gat cgc gtg aac aac cgc aat cag acg ccg 355
Glu Arg Gly Ala Asp Val Asp Arg Val Asn Asn Arg Asn Gln Thr Pro
70 75 80 85

ctg gcg ggc gcg atc ttt aag aag gaa gaa gcc gtc att gag gca ctg 403
Leu Ala Gly Ala Ile Phe Lys Lys Glu Glu Ala Val Ile Glu Ala Leu
90 95 100

ctt gct ggt ggt gct gac cca tac gct gga act cca act gct gtt gat 451
Leu Ala Gly Gly Ala Asp Pro Tyr Ala Gly Thr Pro Thr Ala Val Asp
105 110 115

acc gcc aag atg ttt ggc cgc gag gat ctc gta gct cgc ttc gag tca 499
Thr Ala Lys Met Phe Gly Arg Glu Asp Leu Val Ala Arg Phe Glu Ser
120 125 130

taggccggtg gagtggaccg ctt 522

<210> 428
<211> 133
<212> PRT
<213> Corynebacterium glutamicum

<400> 428
Met Thr Gln Ser Asp Leu Pro Asp Asp Val Gln Glu Leu Val Thr Lys
1 5 10 15

Ile Phe Gly Leu Ala Arg Asp Gly Gly Ala Glu Ser Ala Ala Thr Leu
20 25 30

Gly Ala Tyr Val Asp Asn Gly Val Asp Val Asn Leu Ser Asn Gln Asp

```
          35                  40                  45

Gly Asn Thr Leu Leu Met Leu Ala Ala Tyr Ala Gly His Ala Asp Val
      50                  55                  60

Val Gln Ala Leu Ile Glu Arg Gly Ala Asp Val Asp Arg Val Asn Asn
 65                  70                  75                  80

Arg Asn Gln Thr Pro Leu Ala Gly Ala Ile Phe Lys Lys Glu Glu Ala
                 85                  90                  95

Val Ile Glu Ala Leu Leu Ala Gly Gly Ala Asp Pro Tyr Ala Gly Thr
            100                 105                 110

Pro Thr Ala Val Asp Thr Ala Lys Met Phe Gly Arg Glu Asp Leu Val
        115                 120                 125

Ala Arg Phe Glu Ser
    130
```

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<210> 429
<211> 2826
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2803)
<223> RXN02549

<400> 429
gcagtcgcag tagttggggt ttcaatgatc tcagggcagg acactgttcc cactggtaac 60

gccgtaactg cagacgatgc cctgctcggt ggccctgagt atg gtt cac gcg aag 115
                                        Met Val His Ala Lys
                                          1               5

cag act aag aag cca ctt ccc cgt ttt ctt cac tcg gcg cat ttc tat 163
Gln Thr Lys Lys Pro Leu Pro Arg Phe Leu His Ser Ala His Phe Tyr
                10                  15                  20

gtc tgg att gtg ctg ggt ttt gtg gtg ttt gcg caa cct tat ggt cag 211
Val Trp Ile Val Leu Gly Phe Val Val Phe Ala Gln Pro Tyr Gly Gln
            25                  30                  35

gtt gct gcc gat act aaa cta gat ttg ctg ctc aac ccc gca gga ttt 259
Val Ala Ala Asp Thr Lys Leu Asp Leu Leu Leu Asn Pro Ala Gly Phe
        40                  45                  50

tta acc ggt gcg ctt cat gcg tgg act gac acg ttc acc ttg ggt cag 307
Leu Thr Gly Ala Leu His Ala Trp Thr Asp Thr Phe Thr Leu Gly Gln
    55                  60                  65

ttg caa aac caa gct tat ggc tat ctg ttt ccc caa ggg ttt ttc ttc 355
Leu Gln Asn Gln Ala Tyr Gly Tyr Leu Phe Pro Gln Gly Phe Phe Phe
70                  75                  80                  85

ctc ata act gat ttc ctc cct gac tgg att gcg cag cga ctg tgg tgg 403
Leu Ile Thr Asp Phe Leu Pro Asp Trp Ile Ala Gln Arg Leu Trp Trp
                90                  95                 100
```
```

```
tgg ctt gtt ctt ggc ctg gga ttt tct gga ttc tac gca ctg gta gcc   451
Trp Leu Val Leu Gly Leu Gly Phe Ser Gly Phe Tyr Ala Leu Val Ala
            105                 110                 115

cgg ctg ggg att ggc aat cct gca ttc agg gtg atc gcc gcg ctg ctg   499
Arg Leu Gly Ile Gly Asn Pro Ala Phe Arg Val Ile Ala Ala Leu Leu
        120                 125                 130

ttt gct ctg tcc ccg cgc acg ctc acc acc ctc act gca atc tcc tcc   547
Phe Ala Leu Ser Pro Arg Thr Leu Thr Thr Leu Thr Ala Ile Ser Ser
    135                 140                 145

gaa act tgg cct atc atg ctc gcg cca tgg gta tgt ctg cct ctg ctt   595
Glu Thr Trp Pro Ile Met Leu Ala Pro Trp Val Cys Leu Pro Leu Leu
150                 155                 160                 165

tcg cga aat gtg gat gca cgg gcc atc gcg ttg tcc tta ctt ccc gcg   643
Ser Arg Asn Val Asp Ala Arg Ala Ile Ala Leu Ser Leu Leu Pro Ala
                170                 175                 180

gca tgc atg ggt gca gtt aat gcc acc gcc acg atg gca gca ctc atc   691
Ala Cys Met Gly Ala Val Asn Ala Thr Ala Thr Met Ala Ala Leu Ile
            185                 190                 195

ccg gca gcg ctg atc ttg ctg tat aga ggg ctc ttc tta agg ctg ctt   739
Pro Ala Ala Leu Ile Leu Leu Tyr Arg Gly Leu Phe Leu Arg Leu Leu
        200                 205                 210

ctg tgg gga atg ggc gtt ctc gct gtt aat tca tgg tgg atc gga cct   787
Leu Trp Gly Met Gly Val Leu Ala Val Asn Ser Trp Trp Ile Gly Pro
    215                 220                 225

ttg ttg gtg ctt ggc aaa tac gcc ccg ccc ttc acc gaa ttc atc gaa   835
Leu Leu Val Leu Gly Lys Tyr Ala Pro Pro Phe Thr Glu Phe Ile Glu
230                 235                 240                 245

agt tcc tcc gtc acc act tcc tgg ctc aac cca gta gaa ata ctc cgc   883
Ser Ser Ser Val Thr Thr Ser Trp Leu Asn Pro Val Glu Ile Leu Arg
                250                 255                 260

gga acc acc agt tgg aca ccc ttc gta gac act gaa cga caa gcc gga   931
Gly Thr Thr Ser Trp Thr Pro Phe Val Asp Thr Glu Arg Gln Ala Gly
            265                 270                 275

tat ctc ctg gtc aac gat gct ctc ttt gtc acc ctc agc gtt ctc gtc   979
Tyr Leu Leu Val Asn Asp Ala Leu Phe Val Thr Leu Ser Val Leu Val
        280                 285                 290

gca gcc ctc ggc ttg atc ggc ctc acc ttg atg aaa cac cgt gga ctg   1027
Ala Ala Leu Gly Leu Ile Gly Leu Thr Leu Met Lys His Arg Gly Leu
    295                 300                 305

tgg gca ttc atg ctg gcc atc gga ctc ctc atc ctc ggc agc gcc cac   1075
Trp Ala Phe Met Leu Ala Ile Gly Leu Leu Ile Leu Gly Ser Ala His
310                 315                 320                 325

cta acg gct gtt caa gaa ttc ctc gac ggc cca ggc gca gca ctt cga   1123
Leu Thr Ala Val Gln Glu Phe Leu Asp Gly Pro Gly Ala Ala Leu Arg
                330                 335                 340
```

```
aac atc cac aaa ttt gat cta tta gtc cgc atg ccg ttg atg gtg ggc   1171
Asn Ile His Lys Phe Asp Leu Leu Val Arg Met Pro Leu Met Val Gly
            345                 350                 355

gtt gcc gca ttg ggg tcg cat atc agt ctg ccc ttg ctt ggg acg act   1219
Val Ala Ala Leu Gly Ser His Ile Ser Leu Pro Leu Leu Gly Thr Thr
        360                 365                 370

gca ttg acc agc gga caa ggc aaa cac cac acc atc ccg ctg cct ctc   1267
Ala Leu Thr Ser Gly Gln Gly Lys His His Thr Ile Pro Leu Pro Leu
    375                 380                 385

caa aaa cgc caa gcc gca gga ctc ctc gtg gtg atc atc gct gtc ggt   1315
Gln Lys Arg Gln Ala Ala Gly Leu Leu Val Val Ile Ile Ala Val Gly
390                 395                 400                 405

gct ctt gct ccc gca tgg tcg gca cgg ctg cta cct cag gga acg tgg   1363
Ala Leu Ala Pro Ala Trp Ser Ala Arg Leu Leu Pro Gln Gly Thr Trp
                410                 415                 420

gat gaa gtg cct gac tac tgg tac gaa gcc aca gaa ttc ctc aac caa   1411
Asp Glu Val Pro Asp Tyr Trp Tyr Glu Ala Thr Glu Phe Leu Asn Gln
            425                 430                 435

aac gcc aca ggc acc cgc acg ttg att tgg cct agc tcg ccg ttt gcc   1459
Asn Ala Thr Gly Thr Arg Thr Leu Ile Trp Pro Ser Ser Pro Phe Ala
        440                 445                 450

cgc cag gac tgg gga tgg act cgg gat gaa cca gct caa cca ctt ctt   1507
Arg Gln Asp Trp Gly Trp Thr Arg Asp Glu Pro Ala Gln Pro Leu Leu
    455                 460                 465

gat gtt ccg tgg gct gtc cgc gat gcc att cct ttg gtt ccc ccg gag   1555
Asp Val Pro Trp Ala Val Arg Asp Ala Ile Pro Leu Val Pro Pro Glu
470                 475                 480                 485

gcg att cgc gga tta gat ggt ctc gac gac cta ggc act cta ggc acc   1603
Ala Ile Arg Gly Leu Asp Gly Leu Asp Asp Leu Gly Thr Leu Gly Thr
                490                 495                 500

ggt cta aac gac gag gct tta aaa cgt cta ggc atc ggc gca gta ctg   1651
Gly Leu Asn Asp Glu Ala Leu Lys Arg Leu Gly Ile Gly Ala Val Leu
            505                 510                 515

gtg agg cat gat ctg gaa gcc gac cca gat att gag gtg gat ctg cct   1699
Val Arg His Asp Leu Glu Ala Asp Pro Asp Ile Glu Val Asp Leu Pro
        520                 525                 530

ggg gaa aag cac act ttt ggc tcc caa ggc caa gta gac gtc tac ctc   1747
Gly Glu Lys His Thr Phe Gly Ser Gln Gly Gln Val Asp Val Tyr Leu
    535                 540                 545

acc gac ccc gac cgc aat atg tgg atc act tcc ggc aca tcc aag cag   1795
Thr Asp Pro Asp Arg Asn Met Trp Ile Thr Ser Gly Thr Ser Lys Gln
550                 555                 560                 565

ctg ccc acc gtc gct ggc ggc ggc gaa atc ctc tcg ctc cta gac acc   1843
Leu Pro Thr Val Ala Gly Gly Gly Glu Ile Leu Ser Leu Leu Asp Thr
                570                 575                 580

atc aac ggc tat tcc ccg agg act ttg gtg agt gag aat gcc cag atc   1891
```

```
Ile Asn Gly Tyr Ser Pro Arg Thr Leu Val Ser Glu Asn Ala Gln Ile
            585                 590                 595

gtc acc gat acc cct cag cta gtc ggc aca aat tac ggc gat ggc acc   1939
Val Thr Asp Thr Pro Gln Leu Val Gly Thr Asn Tyr Gly Asp Gly Thr
        600                 605                 610

agt tcc gca gca ttg gcc agc ctt gat gag act gag gtg aaa aac cgc   1987
Ser Ser Ala Ala Leu Ala Ser Leu Asp Glu Thr Glu Val Lys Asn Arg
    615                 620                 625

atc gtg gat tat cct tcc gcg ggg cca atg acg cag gtg gtg cag gaa   2035
Ile Val Asp Tyr Pro Ser Ala Gly Pro Met Thr Gln Val Val Gln Glu
630                 635                 640                 645

ggt tcc atc acg gcg tct tcg tct ggt tcc gat gcc act tct ttc ggc   2083
Gly Ser Ile Thr Ala Ser Ser Ser Gly Ser Asp Ala Thr Ser Phe Gly
                650                 655                 660

ggc gcg gat cct gat cgt tcc ctt aat tca ctt ctt gat cat cgt tac   2131
Gly Ala Asp Pro Asp Arg Ser Leu Asn Ser Leu Leu Asp His Arg Tyr
            665                 670                 675

aac acc gcc tgg tac ccg aca cct ggc gat acg tct ccg tgg ctc gaa   2179
Asn Thr Ala Trp Tyr Pro Thr Pro Gly Asp Thr Ser Pro Trp Leu Glu
        680                 685                 690

gtc tcc ggt acc ggc acc aca tta tcg atc tcc ccc cgc agc acc gtc   2227
Val Ser Gly Thr Gly Thr Thr Leu Ser Ile Ser Pro Arg Ser Thr Val
    695                 700                 705

acc gcc acc atc acc tcc ggc gat tcc gtg atg gtc cgc gag ttc gaa   2275
Thr Ala Thr Ile Thr Ser Gly Asp Ser Val Met Val Arg Glu Phe Glu
710                 715                 720                 725

aaa ggc cgc acc acc aca gtt acg ttg gcg gag cct gaa gct cgc att   2323
Lys Gly Arg Thr Thr Thr Val Thr Leu Ala Glu Pro Glu Ala Arg Ile
                730                 735                 740

gaa ttc gat ggt ttc gta gga att tcc gag ctg tcc cta gag ggt ctc   2371
Glu Phe Asp Gly Phe Val Gly Ile Ser Glu Leu Ser Leu Glu Gly Leu
            745                 750                 755

agc cgc acc atc act gtg ccg gag acc tct cct gac gtg cag caa ttc   2419
Ser Arg Thr Ile Thr Val Pro Glu Thr Ser Pro Asp Val Gln Gln Phe
        760                 765                 770

gtt ttc caa cgc ctc aca gtg ccc acc tcg ttc ctc gac cgc act ttc   2467
Val Phe Gln Arg Leu Thr Val Pro Thr Ser Phe Leu Asp Arg Thr Phe
    775                 780                 785

aca gtc ccc cgc cac atg tcc gtc acc gtg gag gcc caa tcc tgc gtc   2515
Thr Val Pro Arg His Met Ser Val Thr Val Glu Ala Gln Ser Cys Val
790                 795                 800                 805

aca ttg gaa ctc gac ggc gat cgc atc gac tgt ggc ccc tcg aac tca   2563
Thr Leu Glu Leu Asp Gly Asp Arg Ile Asp Cys Gly Pro Ser Asn Ser
                810                 815                 820

ccc ccg gaa ccc aca cgc tgc gca ccc aat cgg aat ggg tca ccc tca   2611
Pro Pro Glu Pro Thr Arg Cys Ala Pro Asn Arg Asn Gly Ser Pro Ser
```

```
            825                 830                 835

ccg aat ccg ctc cgc tcg ccg ctg ttc agc cag caa caa aca tcg agg   2659
Pro Asn Pro Leu Arg Ser Pro Leu Phe Ser Gln Gln Gln Thr Ser Arg
        840                 845                 850

cag cac cca ccg acc gcg tgc tcg tca cca cgc gcg ctt tca att cag   2707
Gln His Pro Pro Thr Ala Cys Ser Ser Pro Arg Ala Leu Ser Ile Gln
    855                 860                 865

gta cca gcg cgc tta tcg acg cca ccc ccc ttt ccc caa tcc aac tcg   2755
Val Pro Ala Arg Leu Ser Thr Pro Pro Pro Phe Pro Gln Ser Asn Ser
870                 875                 880                 885

acg cct cct ccc aag gtt tca tca tcc ccg cga acg cct ccg gcg agt   2803
Thr Pro Pro Pro Lys Val Ser Ser Ser Pro Arg Thr Pro Pro Ala Ser
                890                 895                 900

tgagcttcgc tttcgacggc gaa                                        2826
```

<210> 430
<211> 901
<212> PRT
<213> Corynebacterium glutamicum

<400> 430

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Met Val His Ala Lys Gln Thr Lys Lys Pro Leu Pro Arg Phe Leu His
  1               5                  10                  15

Ser Ala His Phe Tyr Val Trp Ile Val Leu Gly Phe Val Val Phe Ala
            20                  25                  30

Gln Pro Tyr Gly Gln Val Ala Ala Asp Thr Lys Leu Asp Leu Leu Leu
        35                  40                  45

Asn Pro Ala Gly Phe Leu Thr Gly Ala Leu His Ala Trp Thr Asp Thr
    50                  55                  60

Phe Thr Leu Gly Gln Leu Gln Asn Gln Ala Tyr Gly Tyr Leu Phe Pro
65                  70                  75                  80

Gln Gly Phe Phe Phe Leu Ile Thr Asp Phe Leu Pro Asp Trp Ile Ala
                85                  90                  95

Gln Arg Leu Trp Trp Trp Leu Val Leu Gly Leu Gly Phe Ser Gly Phe
            100                 105                 110

Tyr Ala Leu Val Ala Arg Leu Gly Ile Gly Asn Pro Ala Phe Arg Val
        115                 120                 125

Ile Ala Ala Leu Leu Phe Ala Leu Ser Pro Arg Thr Leu Thr Thr Leu
    130                 135                 140

Thr Ala Ile Ser Ser Glu Thr Trp Pro Ile Met Leu Ala Pro Trp Val
145                 150                 155                 160

Cys Leu Pro Leu Leu Ser Arg Asn Val Asp Ala Arg Ala Ile Ala Leu
                165                 170                 175

Ser Leu Leu Pro Ala Ala Cys Met Gly Ala Val Asn Ala Thr Ala Thr
```

```
                180                 185                 190

Met Ala Ala Leu Ile Pro Ala Ala Leu Ile Leu Leu Tyr Arg Gly Leu
        195                 200                 205

Phe Leu Arg Leu Leu Leu Trp Gly Met Gly Val Leu Ala Val Asn Ser
    210                 215                 220

Trp Trp Ile Gly Pro Leu Leu Val Leu Gly Lys Tyr Ala Pro Pro Phe
225                 230                 235                 240

Thr Glu Phe Ile Glu Ser Ser Ser Val Thr Thr Ser Trp Leu Asn Pro
                245                 250                 255

Val Glu Ile Leu Arg Gly Thr Thr Ser Trp Thr Pro Phe Val Asp Thr
            260                 265                 270

Glu Arg Gln Ala Gly Tyr Leu Leu Val Asn Asp Ala Leu Phe Val Thr
        275                 280                 285

Leu Ser Val Leu Val Ala Ala Leu Gly Leu Ile Gly Leu Thr Leu Met
    290                 295                 300

Lys His Arg Gly Leu Trp Ala Phe Met Leu Ala Ile Gly Leu Leu Ile
305                 310                 315                 320

Leu Gly Ser Ala His Leu Thr Ala Val Gln Glu Phe Leu Asp Gly Pro
                325                 330                 335

Gly Ala Ala Leu Arg Asn Ile His Lys Phe Asp Leu Leu Val Arg Met
            340                 345                 350

Pro Leu Met Val Gly Val Ala Ala Leu Gly Ser His Ile Ser Leu Pro
        355                 360                 365

Leu Leu Gly Thr Thr Ala Leu Thr Ser Gly Gln Gly Lys His His Thr
    370                 375                 380

Ile Pro Leu Pro Leu Gln Lys Arg Gln Ala Ala Gly Leu Leu Val Val
385                 390                 395                 400

Ile Ile Ala Val Gly Ala Leu Ala Pro Ala Trp Ser Ala Arg Leu Leu
                405                 410                 415

Pro Gln Gly Thr Trp Asp Glu Val Pro Asp Tyr Trp Tyr Glu Ala Thr
            420                 425                 430

Glu Phe Leu Asn Gln Asn Ala Thr Gly Thr Arg Thr Leu Ile Trp Pro
        435                 440                 445

Ser Ser Pro Phe Ala Arg Gln Asp Trp Gly Trp Thr Arg Asp Glu Pro
    450                 455                 460

Ala Gln Pro Leu Leu Asp Val Pro Trp Ala Val Arg Asp Ala Ile Pro
465                 470                 475                 480

Leu Val Pro Pro Glu Ala Ile Arg Gly Leu Asp Gly Leu Asp Asp Leu
                485                 490                 495

Gly Thr Leu Gly Thr Gly Leu Asn Asp Glu Ala Leu Lys Arg Leu Gly
            500                 505                 510
```

Ile Gly Ala Val Leu Val Arg His Asp Leu Glu Ala Asp Pro Asp Ile
515 520 525

Glu Val Asp Leu Pro Gly Glu Lys His Thr Phe Gly Ser Gln Gly Gln
530 535 540

Val Asp Val Tyr Leu Thr Asp Pro Asp Arg Asn Met Trp Ile Thr Ser
545 550 555 560

Gly Thr Ser Lys Gln Leu Pro Thr Val Ala Gly Gly Gly Glu Ile Leu
565 570 575

Ser Leu Leu Asp Thr Ile Asn Gly Tyr Ser Pro Arg Thr Leu Val Ser
580 585 590

Glu Asn Ala Gln Ile Val Thr Asp Thr Pro Gln Leu Val Gly Thr Asn
595 600 605

Tyr Gly Asp Gly Thr Ser Ser Ala Ala Leu Ala Ser Leu Asp Glu Thr
610 615 620

Glu Val Lys Asn Arg Ile Val Asp Tyr Pro Ser Ala Gly Pro Met Thr
625 630 635 640

Gln Val Val Gln Glu Gly Ser Ile Thr Ala Ser Ser Ser Gly Ser Asp
645 650 655

Ala Thr Ser Phe Gly Gly Ala Asp Pro Asp Arg Ser Leu Asn Ser Leu
660 665 670

Leu Asp His Arg Tyr Asn Thr Ala Trp Tyr Pro Thr Pro Gly Asp Thr
675 680 685

Ser Pro Trp Leu Glu Val Ser Gly Thr Gly Thr Thr Leu Ser Ile Ser
690 695 700

Pro Arg Ser Thr Val Thr Ala Thr Ile Thr Ser Gly Asp Ser Val Met
705 710 715 720

Val Arg Glu Phe Glu Lys Gly Arg Thr Thr Thr Val Thr Leu Ala Glu
725 730 735

Pro Glu Ala Arg Ile Glu Phe Asp Gly Phe Val Gly Ile Ser Glu Leu
740 745 750

Ser Leu Glu Gly Leu Ser Arg Thr Ile Thr Val Pro Glu Thr Ser Pro
755 760 765

Asp Val Gln Gln Phe Val Phe Gln Arg Leu Thr Val Pro Thr Ser Phe
770 775 780

Leu Asp Arg Thr Phe Thr Val Pro Arg His Met Ser Val Thr Val Glu
785 790 795 800

Ala Gln Ser Cys Val Thr Leu Glu Leu Asp Gly Asp Arg Ile Asp Cys
805 810 815

Gly Pro Ser Asn Ser Pro Pro Glu Pro Thr Arg Cys Ala Pro Asn Arg
820 825 830

DC3:1450:1:1:0:0:0:0

```
Asn Gly Ser Pro Ser Pro Asn Pro Leu Arg Ser Pro Leu Phe Ser Gln
        835                 840                 845

Gln Gln Thr Ser Arg Gln His Pro Pro Thr Ala Cys Ser Ser Pro Arg
    850                 855                 860

Ala Leu Ser Ile Gln Val Pro Ala Arg Leu Ser Thr Pro Pro Pro Phe
865                 870                 875                 880

Pro Gln Ser Asn Ser Thr Pro Pro Pro Lys Val Ser Ser Ser Pro Arg
                885                 890                 895

Thr Pro Pro Ala Ser
            900
```

<210> 431
<211> 1581
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1558)
<223> RXN00808

<400> 431

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cgcgatgtcg caccggcacg ttagagtatt gagcatgagt cgattgctta gagcattgaa 60

atggctgtgg ggcacatcgt ggccgctgta tgctgcgacg gtg ctc ggc acg aat   115
                                              Val Leu Gly Thr Asn
                                                1               5

gtg ttt ggt gcg ctc gca gta atg ctg ttt gtg cgc ttc ctc att ccg   163
Val Phe Gly Ala Leu Ala Val Met Leu Phe Val Arg Phe Leu Ile Pro
                  10                  15                  20

cag cca gat gct tca aat ttc aac gct gag atc tcg tat ctg cca gct   211
Gln Pro Asp Ala Ser Asn Phe Asn Ala Glu Ile Ser Tyr Leu Pro Ala
              25                  30                  35

gtt ggt ttc gca tac ctg gcg ttc gcc att gtc gcg ggc atg ctg gtg   259
Val Gly Phe Ala Tyr Leu Ala Phe Ala Ile Val Ala Gly Met Leu Val
          40                  45                  50

aca ttt ttg atg ttc cgc ccg gtg ctt gat tgg cag cga agc cct gaa   307
Thr Phe Leu Met Phe Arg Pro Val Leu Asp Trp Gln Arg Ser Pro Glu
      55                  60                  65

gat cat gac cga aat atg gtg cgc aac ttg gtt atg cgc atc ccc atc   355
Asp His Asp Arg Asn Met Val Arg Asn Leu Val Met Arg Ile Pro Ile
  70                  75                  80                  85

tac cag gca att ctg tgc gca gtg gtg tgg tta atc ggc att gca att   403
Tyr Gln Ala Ile Leu Cys Ala Val Val Trp Leu Ile Gly Ile Ala Ile
                  90                  95                 100

gca acg ttg att tcg gcc agt gtg tct acc agt ttg gcg ctg gtc gtg   451
Ala Thr Leu Ile Ser Ala Ser Val Ser Thr Ser Leu Ala Leu Val Val
              105                 110                 115
```

```
gcg ttt tcc acg ttg atg gct gcc gca atc gtc gtg ctg ctc acc tac   499
Ala Phe Ser Thr Leu Met Ala Ala Ala Ile Val Val Leu Leu Thr Tyr
        120                 125                 130

ctt gag gct gag cgt ttg gtg cgt ccg gtt gct gcg tct gcc ctg gcg   547
Leu Glu Ala Glu Arg Leu Val Arg Pro Val Ala Ala Ser Ala Leu Ala
    135                 140                 145

cgt cga ttt gag gat tcc acg ctg gaa cca cct gtg agc cag cgc ttg   595
Arg Arg Phe Glu Asp Ser Thr Leu Glu Pro Pro Val Ser Gln Arg Leu
150                 155                 160                 165

cgt atg acg tgg ttg ctg acg ttg ggc att cca gtg atg gga att ctg   643
Arg Met Thr Trp Leu Leu Thr Leu Gly Ile Pro Val Met Gly Ile Leu
                170                 175                 180

ctg ctt att tgg ggc tac tcg cag ggc att ttc ggc tct gat gcc tcc   691
Leu Leu Ile Trp Gly Tyr Ser Gln Gly Ile Phe Gly Ser Asp Ala Ser
            185                 190                 195

gga att atg cct gcc atc gca gcg ctc gcg ttt gca tcg ttg gtc acg   739
Gly Ile Met Pro Ala Ile Ala Ala Leu Ala Phe Ala Ser Leu Val Thr
        200                 205                 210

ggt tac ctg ggc aac cgg ctt gtg gtg tcc tct gtg gtg gat ccg att   787
Gly Tyr Leu Gly Asn Arg Leu Val Val Ser Ser Val Val Asp Pro Ile
    215                 220                 225

cgg gaa ctt cag gag gcc atc aac agg gtt cgt cgt ggt gaa aac gat   835
Arg Glu Leu Gln Glu Ala Ile Asn Arg Val Arg Arg Gly Glu Asn Asp
230                 235                 240                 245

gtg cag gtt gat att tat gat ggc tct gag atc ggt gtg ctt cag gct   883
Val Gln Val Asp Ile Tyr Asp Gly Ser Glu Ile Gly Val Leu Gln Ala
                250                 255                 260

ggc ttc aat gag atg atg cgt ggc ctg cgt gaa cgt cag cgc gtc cgt   931
Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu Arg Gln Arg Val Arg
            265                 270                 275

gac ctt ttc ggt cgc tac gtg ggc gct gaa gtg gcc aag cgt gcg ctg   979
Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val Ala Lys Arg Ala Leu
        280                 285                 290

gag gaa cgc ccc act ctg ggt ggc gag gac cgt aag gtt gcc gtg ttg   1027
Glu Glu Arg Pro Thr Leu Gly Gly Glu Asp Arg Lys Val Ala Val Leu
    295                 300                 305

ttt gtc gat gtc atc ggc tcc act acc ttt gcc gtc aac cac act cct   1075
Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala Val Asn His Thr Pro
310                 315                 320                 325

gaa gag gtt gtg gag gcg ctc aat gag ttc ttc gag cac gtc gtg gag   1123
Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe Glu His Val Val Glu
                330                 335                 340

gtt gtg cac cgc aac aag ggt gtt atc aac aag ttc cag ggt gac gcg   1171
Val Val His Arg Asn Lys Gly Val Ile Asn Lys Phe Gln Gly Asp Ala
            345                 350                 355

gcg ttg gcg att ttc ggc gct ccc ctg ccc ctg tct gat gcc acc ggt   1219
```

```
Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu Ser Asp Ala Thr Gly
        360                 365                 370

cat gcg ctt gcg gct gcc cgt gag ctc cgc gca gag ctg aaa gat ctc   1267
His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala Glu Leu Lys Asp Leu
    375                 380                 385

cag ctc aag gcc gga att ggt gtg gct gct ggc cat gtc gtt gct ggt   1315
Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly His Val Val Ala Gly
390                 395                 400                 405

cat atc ggc ggt cac gcg agg ttt gag tac act gtg atc ggc gac gcg   1363
His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr Val Ile Gly Asp Ala
                410                 415                 420

gtg aac cag gct gcg cgc ctg acg gag atc gcg aaa acg acc cca ggc   1411
Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala Lys Thr Thr Pro Gly
            425                 430                 435

cgc acc gtc acc aac gct tcc acg ctg cgt gag gcc aac gag gcg gag   1459
Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu Ala Asn Glu Ala Glu
        440                 445                 450

cag gct cgc tgg acg ctc atg aag tcc gtg gag ctg cgc gga cgt agc   1507
Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu Leu Arg Gly Arg Ser
    455                 460                 465

cag atg acg cag att gcg cgg cct att cgg ccg acg ttg gcg gat agg   1555
Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro Thr Leu Ala Asp Arg
470                 475                 480                 485

tcc taatacgctt ttcgacgcaa aaa                                    1581
Ser
```

<210> 432
<211> 486
<212> PRT
<213> Corynebacterium glutamicum

<400> 432

```
Val Leu Gly Thr Asn Val Phe Gly Ala Leu Ala Val Met Leu Phe Val
  1               5                  10                  15

Arg Phe Leu Ile Pro Gln Pro Asp Ala Ser Asn Phe Asn Ala Glu Ile
            20                  25                  30

Ser Tyr Leu Pro Ala Val Gly Phe Ala Tyr Leu Ala Phe Ala Ile Val
        35                  40                  45

Ala Gly Met Leu Val Thr Phe Leu Met Phe Arg Pro Val Leu Asp Trp
    50                  55                  60

Gln Arg Ser Pro Glu Asp His Asp Arg Asn Met Val Arg Asn Leu Val
65                  70                  75                  80

Met Arg Ile Pro Ile Tyr Gln Ala Ile Leu Cys Ala Val Val Trp Leu
                85                  90                  95

Ile Gly Ile Ala Ile Ala Thr Leu Ile Ser Ala Ser Val Ser Thr Ser
```

```
                100                 105                 110

Leu Ala Leu Val Val Ala Phe Ser Thr Leu Met Ala Ala Ala Ile Val
        115                 120                 125

Val Leu Leu Thr Tyr Leu Glu Ala Glu Arg Leu Val Arg Pro Val Ala
    130                 135                 140

Ala Ser Ala Leu Ala Arg Arg Phe Glu Asp Ser Thr Leu Glu Pro Pro
145                 150                 155                 160

Val Ser Gln Arg Leu Arg Met Thr Trp Leu Leu Thr Leu Gly Ile Pro
                165                 170                 175

Val Met Gly Ile Leu Leu Leu Ile Trp Gly Tyr Ser Gln Gly Ile Phe
            180                 185                 190

Gly Ser Asp Ala Ser Gly Ile Met Pro Ala Ile Ala Ala Leu Ala Phe
        195                 200                 205

Ala Ser Leu Val Thr Gly Tyr Leu Gly Asn Arg Leu Val Val Ser Ser
    210                 215                 220

Val Val Asp Pro Ile Arg Glu Leu Gln Glu Ala Ile Asn Arg Val Arg
225                 230                 235                 240

Arg Gly Glu Asn Asp Val Gln Val Asp Ile Tyr Asp Gly Ser Glu Ile
                245                 250                 255

Gly Val Leu Gln Ala Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu
            260                 265                 270

Arg Gln Arg Val Arg Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val
        275                 280                 285

Ala Lys Arg Ala Leu Glu Glu Arg Pro Thr Leu Gly Gly Glu Asp Arg
    290                 295                 300

Lys Val Ala Val Leu Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala
305                 310                 315                 320

Val Asn His Thr Pro Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe
                325                 330                 335

Glu His Val Val Glu Val Val His Arg Asn Lys Gly Val Ile Asn Lys
            340                 345                 350

Phe Gln Gly Asp Ala Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu
        355                 360                 365

Ser Asp Ala Thr Gly His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala
    370                 375                 380

Glu Leu Lys Asp Leu Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly
385                 390                 395                 400

His Val Val Ala Gly His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr
                405                 410                 415

Val Ile Gly Asp Ala Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala
            420                 425                 430
```

```
Lys Thr Thr Pro Gly Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu
        435                 440                 445

Ala Asn Glu Ala Glu Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu
    450                 455                 460

Leu Arg Gly Arg Ser Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro
465                 470                 475                 480

Thr Leu Ala Asp Arg Ser
                485
```

<210> 433
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXS01425

<400> 433

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agtccctatt aatcccaagg agtttcgact cacagtgctc aatttcattt attggccaat 60

ttcggccatt ctgtggttct ggcataaagc gttcagcttt gtg ctg agc cca gat   115
                                              Val Leu Ser Pro Asp
                                                1               5

tcc gga att acc tgg gcc ttg tcg atc atg ttc ttg acc ttc acc gtg   163
Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe Leu Thr Phe Thr Val
                10                  15                  20

cgt atg gtt ctg gtc aag ccg atg gtc aac acc atg cgt tca cag cgc   211
Arg Met Val Leu Val Lys Pro Met Val Asn Thr Met Arg Ser Gln Arg
            25                  30                  35

aag atg caa gac atg gct cca aag atg cag gcc atc cgc gag aag tac   259
Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala Ile Arg Glu Lys Tyr
        40                  45                  50

aaa aat gac cag cag aag atg atg gag gag acc cgc aaa ctt caa aaa   307
Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr Arg Lys Leu Gln Lys
    55                  60                  65

gaa gtg ggc gtt aac ccc atc gca ggc tgt ttg cca atg ttg gtg cag   355
Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu Pro Met Leu Val Gln
70                  75                  80                  85

atc cca gtg ttc ctg ggt ctg ttc cac gtg ctg cgc tcc ttc aac cgc   403
Ile Pro Val Phe Leu Gly Leu Phe His Val Leu Arg Ser Phe Asn Arg
                90                  95                  100

acc ggt tct ggc gtt ggc cag ctg gaa atg acc gtt gag caa aac gcg   451
Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr Val Glu Gln Asn Ala
            105                 110                 115

aac acc ccg aac tac atc ttc ggt gtc gac gag gtt cag tcc ttc ctg   499
Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu Val Gln Ser Phe Leu
```

```
        120                 125                 130

cgt gca gac ctg ttc ggt gcg cca ctg tcg tcc tac atc acc atg cct   547
Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser Tyr Ile Thr Met Pro
    135                 140                 145

gct gac gcg ttc gac gcg ttc ctt ggc ctg gat gtc tcc cgc ctc aac   595
Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp Val Ser Arg Leu Asn
150                 155                 160                 165

atc gcg ctg gtt gca gct cca atg att ttg atc att gtc gtg gca act   643
Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile Ile Val Val Ala Thr
                170                 175                 180

cac atg aac gcg cgt ctg tcc gtc aac cgc cag gaa gct cgc aag gca   691
His Met Asn Ala Arg Leu Ser Val Asn Arg Gln Glu Ala Arg Lys Ala
            185                 190                 195

gcc ggc aag cag cag gcc gct tcc agc gat cag atg gcc atg cag atg   739
Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln Met Ala Met Gln Met
        200                 205                 210

caa atg atg aac aag atg atg ctc tgg ttc atg cca gcc acc att ttg   787
Gln Met Met Asn Lys Met Met Leu Trp Phe Met Pro Ala Thr Ile Leu
    215                 220                 225

ttc acc ggc ttc atc tgg acc atc ggt ctt ctt gtc tac atg atg tcc   835
Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu Val Tyr Met Met Ser
230                 235                 240                 245

aac aac gtg tgg acc ttc ttc cag cag cgc tac atc ttc gcc aag atg   883
Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr Ile Phe Ala Lys Met
                250                 255                 260

gac gct gag gaa gca gct gag gag gag gaa aag cgc gca gca aag cgc   931
Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys Arg Ala Ala Lys Arg
            265                 270                 275

act acc gct cca aag cct ggc gtg aag cca gaa aac ccc aag aag cgt   979
Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu Asn Pro Lys Lys Arg
        280                 285                 290

aag aag taaaacttca ctaaaaaccg cca                                1008
Lys Lys
    295
```

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<210> 434
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 434

```
Val Leu Ser Pro Asp Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe
  1               5                  10                  15

Leu Thr Phe Thr Val Arg Met Val Leu Val Lys Pro Met Val Asn Thr
             20                  25                  30

Met Arg Ser Gln Arg Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala
         35                  40                  45
```

```
Ile Arg Glu Lys Tyr Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr
     50                  55                  60

Arg Lys Leu Gln Lys Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu
 65                  70                  75                  80

Pro Met Leu Val Gln Ile Pro Val Phe Leu Gly Leu Phe His Val Leu
                85                  90                  95

Arg Ser Phe Asn Arg Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr
            100                 105                 110

Val Glu Gln Asn Ala Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu
        115                 120                 125

Val Gln Ser Phe Leu Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser
    130                 135                 140

Tyr Ile Thr Met Pro Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp
145                 150                 155                 160

Val Ser Arg Leu Asn Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile
                165                 170                 175

Ile Val Val Ala Thr His Met Asn Ala Arg Leu Ser Val Asn Arg Gln
            180                 185                 190

Glu Ala Arg Lys Ala Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln
        195                 200                 205

Met Ala Met Gln Met Gln Met Met Asn Lys Met Met Leu Trp Phe Met
    210                 215                 220

Pro Ala Thr Ile Leu Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu
225                 230                 235                 240

Val Tyr Met Met Ser Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr
                245                 250                 255

Ile Phe Ala Lys Met Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys
            260                 265                 270

Arg Ala Ala Lys Arg Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu
        275                 280                 285

Asn Pro Lys Lys Arg Lys Lys
    290                 295
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<210> 435
<211> 1856
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1833)
<223> RXS01658

<400> 435

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gat cca cag atc ctg tca cca acc ttc acc cag caa cag cag ctg cga   48
Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Leu Arg
  1               5                  10                  15

aac ttc tac ggt ttc cca gac cag ctg gcg atg gac cgc ttt gaa gta   96
Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
            20                  25                  30

gat ggc aaa ctc cgc gac ttt gtt gtg gca gca cgt gag ctc gat cca  144
Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
        35                  40                  45

aac gcc ctg cag caa aac cag cag gac tgg att aac cgt cac act gtt  192
Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
    50                  55                  60

tat acc cac ggc aac ggc ttc att gca gct caa gca aac cag gtg gat  240
Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
65                  70                  75                  80

gag gtc gcc cgc gac gtc gga tcc act cgt ggt ggt tac cct gtc tac  288
Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
                85                  90                  95

acc gtc tct gat ttg cag tcg aat gct cgt gct gca gaa agc gaa gat  336
Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
            100                 105                 110

gct gag gag ctt ggc atc aag gtt gat gag cct cgt gtg tac tac gga  384
Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
        115                 120                 125

cca ctg att gct tct gcg act gat ggt gct gac tac gca att gtc ggt  432
Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
    130                 135                 140

gac acc ggc gat ggc cca gtc gag tac gac act gac acc tcc agc tac  480
Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
145                 150                 155                 160

acc tac gaa ggt gct ggc ggc gtg gac att gga aac atg gtc aac cgt  528
Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
                165                 170                 175

gcg atg ttt gca ttg cgc tac cag gaa atg aac atg ctc ctg tct gat  576
Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
            180                 185                 190

cgt gtt ggt tcc gaa tcc aag atc cta ttt gag cgc gat cct cgt tcc  624
Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
        195                 200                 205

cgt gtg gaa aag gtt gca cct tgg ttg acc act gac tcc aag acc tac  672
Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
    210                 215                 220

cca act gtg att gat ggt cgc atc aag tgg atc gtc gat ggc tac acc  720
Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
225                 230                 235                 240

acc ttg gat agt ctt ccg tac tcc acg cgc acc tca ctg acg gaa gcg  768
```

```
Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
                245                 250                 255

act cag gat gct gtc atg cct gac ggc acc cca cag cca ctg atc aca   816
Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
            260                 265                 270

gat agg gtc ggt tac atc cgc aac tcc gtg aag gct gtt gtt gat gcg   864
Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
        275                 280                 285

tac gac gga act gtt gaa ctc tac gaa ttc gac acc gaa gat cct gtt   912
Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
    290                 295                 300

ctg aag gca tgg cgt ggc gtg ttc cca gac acc gtg aag gac ggg tcg   960
Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
305                 310                 315                 320

gag att tcc gat gag ctt cgc gca cac ctg cgt tac cca gaa gat ttg  1008
Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
                325                 330                 335

ttc aag gtc cag cgt gac atg ctg gcc aag tac aac gtt gat gat tct  1056
Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
            340                 345                 350

gga aca ttc ttc acc aac gat gcg ttc tgg tct gtc cca ggt gac cca  1104
Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
        355                 360                 365

act gca gcg gag ggc cgc cag gaa ctt aag cag cct cct tac tac gtg  1152
Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
    370                 375                 380

gtg gca gca gac cca gag acc ggt gag tcc agc ttc cag ctg atc acc  1200
Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
385                 390                 395                 400

ccg ttc cgt gga ctt cag cgc gag tac ctc tct gca cac atg tct gcg  1248
Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
                405                 410                 415

tcg tct gat cca gtt acc tac ggt gaa atc act gtt cgt gtg ctg cct  1296
Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
            420                 425                 430

acc gat tct gtg acc cag ggt cca aag cag gcc cag gat gcg atg atg  1344
Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
        435                 440                 445

tca tct gac cag gtt gct cag gac caa aca ctg tgg cgt gga tcg aac  1392
Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
    450                 455                 460

gat ctg cac aac gga aac ctg ttg acc ttg cca gtt ggt ggc gga gag  1440
Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
465                 470                 475                 480

atc ctc tac gtt gag ccg att tac tcg cag cgc aag gat cag gca tcg  1488
Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser
```

```
                485                 490                 495

gcc ttc ccg aag ctt ctg cgc gtg ctg gtc ttc tac aag ggt cag gtt   1536
Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val
            500                 505                 510

ggt tac gca cca acg atc gct gaa gcc cta tcg cag gtc ggc att gat   1584
Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp
        515                 520                 525

ccg aag gaa gcg cag gac atc gaa gag gta gat ggc acc gct acg acg   1632
Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr
    530                 535                 540

cca tcg act gat gag act gac act gac act gat cag cct gca acc gaa   1680
Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu
545                 550                 555                 560

acc cca act gca cca gtg agt gag gcg gaa gga atc gcg gcc atc aac   1728
Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn
                565                 570                 575

gat gcg ttg agc aac ctt gaa gct gct cgc gat agc tct ttc gaa gag   1776
Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu
            580                 585                 590

tat ggt cgt gca ctc gat gcg ctt gat cgt gcc gtc gat agc tac cag   1824
Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln
        595                 600                 605

tcc gca cag tagcgtttga gtaaacagcc cga                            1856
Ser Ala Gln
    610
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<210> 436
<211> 611
<212> PRT
<213> Corynebacterium glutamicum

<400> 436

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Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg
  1               5                  10                  15

Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
             20                  25                  30

Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
         35                  40                  45

Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
     50                  55                  60

Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65                  70                  75                  80

Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
                 85                  90                  95

Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
            100                 105                 110
```

Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
115 120 125

Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
130 135 140

Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
145 150 155 160

Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
165 170 175

Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
180 185 190

Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
195 200 205

Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
210 215 220

Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
225 230 235 240

Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
245 250 255

Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
260 265 270

Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
275 280 285

Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
290 295 300

Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
305 310 315 320

Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
325 330 335

Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
340 345 350

Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
355 360 365

Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
370 375 380

Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
385 390 395 400

Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
405 410 415

Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
420 425 430

09614590 the 09614590

```
Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
        435                 440                 445

Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
    450                 455                 460

Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
465                 470                 475                 480

Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser
                485                 490                 495

Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val
            500                 505                 510

Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp
        515                 520                 525

Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr
    530                 535                 540

Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu
545                 550                 555                 560

Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn
                565                 570                 575

Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu
            580                 585                 590

Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln
        595                 600                 605

Ser Ala Gln
    610
```

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<210> 437
<211> 867
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(844)
<223> RXS01677

<400> 437
gtcgccatag ttgagtttta ttcatggctt ttagctaggc gactttagtt gagggctttt 60

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agttgagggc ttcccagcag ggatggttaa ggagaattca gtg aac caa cag agt   115
                                              Val Asn Gln Gln Ser
                                                1               5

aaa aag tgg ctc gta ccg aca ctg gtc gtc atc att gca gtg ctc ctc   163
Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile Ile Ala Val Leu Leu
                  10                  15                  20

atc gca gtt gtt ctg ttg atg tac cga gga aat gcg agt gat acg gcc   211
Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn Ala Ser Asp Thr Ala
              25                  30                  35
```

```
gag ggc gtt tca gcc gct gcg act tcg gac tcg gct gct gct tcg act   259
Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser Ala Ala Ala Ser Thr
          40                  45                  50

gct gct tcg ggt tcc gct tct ggt gct gcg gac tcc gat ctg acc agc   307
Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp Ser Asp Leu Thr Ser
     55                  60                  65

gtg gaa gca cgc gac cct tcc gac cct gtt gcg gtg gga gac gtt gat   355
Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala Val Gly Asp Val Asp
 70                  75                  80                  85

gca cct gtt ggg tta gtg gtg ttt tcc gac tac caa tgc ccg ttc tgt   403
Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr Gln Cys Pro Phe Cys
                 90                  95                 100

gca aag tgg agc gat gaa acc ctg cca cag atg atg aag cat gtg gaa   451
Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met Met Lys His Val Glu
            105                 110                 115

gat gga aac ctc cgc att gaa tgg cgt gaa gtg aac atc ttt gga gaa   499
Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val Asn Ile Phe Gly Glu
        120                 125                 130

cca tct gag cgt gga gct cgc gcg gca tac gct gcg ggt ttg cag gac   547
Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala Ala Gly Leu Gln Asp
    135                 140                 145

gca tac ttg gaa tac cac aac gca ctc ttt gcc aac ggt gaa aaa ccc   595
Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala Asn Gly Glu Lys Pro
150                 155                 160                 165

agc gaa gac ctg ctc agc gaa gag gga ctt att aag ctt gct ggt gac   643
Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile Lys Leu Ala Gly Asp
                170                 175                 180

ctt gga cta gac gaa tcg aaa ttc act gcc gat ttc caa tcc cct gaa   691
Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp Phe Gln Ser Pro Glu
            185                 190                 195

act gca gtc gca att gcg caa cat caa cag ctg gga atc gat ctt ggc   739
Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu Gly Ile Asp Leu Gly
        200                 205                 210

gcc tac tcc acc cca gct ttc ctc cta ggt ggc cag cca atc atg ggc   787
Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly Gln Pro Ile Met Gly
    215                 220                 225

gct cag cct gct tct gta ttt gaa gcc gcc ttc gag caa gca ctg gca   835
Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe Glu Gln Ala Leu Ala
230                 235                 240                 245

gcg aaa gaa taaaccgtgg atgtcggcct agt                            867
Ala Lys Glu
```

<210> 438
<211> 248
<212> PRT

<213> Corynebacterium glutamicum

<400> 438

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Val Asn Gln Gln Ser Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile
  1               5                  10                  15

Ile Ala Val Leu Leu Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn
             20                  25                  30

Ala Ser Asp Thr Ala Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser
         35                  40                  45

Ala Ala Ala Ser Thr Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp
     50                  55                  60

Ser Asp Leu Thr Ser Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala
 65                  70                  75                  80

Val Gly Asp Val Asp Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr
                 85                  90                  95

Gln Cys Pro Phe Cys Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met
            100                 105                 110

Met Lys His Val Glu Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val
        115                 120                 125

Asn Ile Phe Gly Glu Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala
    130                 135                 140

Ala Gly Leu Gln Asp Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala
145                 150                 155                 160

Asn Gly Glu Lys Pro Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile
                165                 170                 175

Lys Leu Ala Gly Asp Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp
            180                 185                 190

Phe Gln Ser Pro Glu Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu
        195                 200                 205

Gly Ile Asp Leu Gly Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly
    210                 215                 220

Gln Pro Ile Met Gly Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe
225                 230                 235                 240

Glu Gln Ala Leu Ala Ala Lys Glu
                245
```

<210> 439
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXS02932

<400> 439

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cactactgcg ttaaggtatg aaagttcgca caccagcgat ttaattctgt gcccaccact 60

agcacgacca tttcagtttt aactttcttg gagttttcta gtg tcc aaa aca gaa   115
                                            Val Ser Lys Thr Glu
                                              1               5

gaa ggc cgt tca gcg gcc ata att att tac gcg ttt cca act ttc att   163
Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala Phe Pro Thr Phe Ile
                  10                  15                  20

ctg ctg ggc gcg atc att gcg ttt atc ttc ccg gaa cca ttc att ccg   211
Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro Glu Pro Phe Ile Pro
              25                  30                  35

ctg aca aac tac att aat atc ttc ctc acg atc atc atg ttc acc atg   259
Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile Ile Met Phe Thr Met
          40                  45                  50

ggt ttg acc ttg acg gtg ccc gat ttt cag atg gtg ctt aaa cgt cca   307
Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met Val Leu Lys Arg Pro
      55                  60                  65

ctg cct atc ttg atc ggt gta gta gcg cag ttt gtc atc atg cca ttc   355
Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe Val Ile Met Pro Phe
  70                  75                  80                  85

ctg gcg atc gtg gtt gcg aaa atg ttc aac ctc aac cca gca ctc gcc   403
Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu Asn Pro Ala Leu Ala
                  90                  95                 100

gtt ggc ctt ctc atg ctg gga tcc gtt ccg ggt ggc acc tcc tcc aat   451
Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly Gly Thr Ser Ser Asn
              105                 110                 115

gtg att gcg ttt ctc gcc cga gga gat gtc gcg cta tcg gtc acc atg   499
Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala Leu Ser Val Thr Met
          120                 125                 130

acc tct gtg tcc acc att gtt tcc cca atc atg acg cct ttc ctc atg   547
Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met Thr Pro Phe Leu Met
      135                 140                 145

ctc atg ctg gca ggt act gaa acc gcc gtc gat ggt gga ggc atg gcg   595
Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp Gly Gly Gly Met Ala
150                 155                 160                 165

tgg act ttg gta caa aca gtg ctg ctg cct gtg atc atc ggc cta gtt   643
Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val Ile Ile Gly Leu Val
                  170                 175                 180

ctg cgt gtc ttc ttg aac aag tgg atc gac aag att ttg ccg atc ctt   691
Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys Ile Leu Pro Ile Leu
              185                 190                 195

cct tat ctc tcc atc ctc ggt atc ggt ggc gtg gtg ttc ggc gca gtc   739
Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val Val Phe Gly Ala Val
          200                 205                 210

gca gcc aac gcg gaa cga ctc gtg tct gtc gga ctc atc gtg ttc gtt   787
```

```
Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly Leu Ile Val Phe Val
    215                 220                 225

gca gtt atc gtg cac aac gta ctt gga tac gtt gtg gga tac ctc acc   835
Ala Val Ile Val His Asn Val Leu Gly Tyr Val Val Gly Tyr Leu Thr
230                 235                 240                 245

ggc cgt gta ttc aaa ttc cca gaa gca gca aac cgc acc atg gcg att   883
Gly Arg Val Phe Lys Phe Pro Glu Ala Ala Asn Arg Thr Met Ala Ile
                250                 255                 260

gaa atc gga acc caa tcc gca ggc ctc gca tcg gga atg gca gga cga   931
Glu Ile Gly Thr Gln Ser Ala Gly Leu Ala Ser Gly Met Ala Gly Arg
            265                 270                 275

ttc ttc acc cca gaa gca gcc ctt cca ggt gct gtc gct gcc ttg gtc   979
Phe Phe Thr Pro Glu Ala Ala Leu Pro Gly Ala Val Ala Ala Leu Val
        280                 285                 290

cac aac atc acc ggc gca gtt tat gtt ggg ctg gta cga aac agg cct  1027
His Asn Ile Thr Gly Ala Val Tyr Val Gly Leu Val Arg Asn Arg Pro
    295                 300                 305

ttg act aag gca tca agg aag aag gaa tcc gtc gcg gtt tcc agc      1072
Leu Thr Lys Ala Ser Arg Lys Lys Glu Ser Val Ala Val Ser Ser
310                 315                 320

taacttattt gctgcccgtt aga                                       1095
```

<210> 440
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 440

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Val Ser Lys Thr Glu Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala
  1               5                  10                  15

Phe Pro Thr Phe Ile Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro
             20                  25                  30

Glu Pro Phe Ile Pro Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile
         35                  40                  45

Ile Met Phe Thr Met Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met
     50                  55                  60

Val Leu Lys Arg Pro Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe
 65                  70                  75                  80

Val Ile Met Pro Phe Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu
                 85                  90                  95

Asn Pro Ala Leu Ala Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly
            100                 105                 110

Gly Thr Ser Ser Asn Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala
        115                 120                 125

Leu Ser Val Thr Met Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met
```

130 135 140

Thr Pro Phe Leu Met Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp
145 150 155 160

Gly Gly Gly Met Ala Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val
165 170 175

Ile Ile Gly Leu Val Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys
180 185 190

Ile Leu Pro Ile Leu Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val
195 200 205

Val Phe Gly Ala Val Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly
210 215 220

Leu Ile Val Phe Val Ala Val Ile Val His Asn Val Leu Gly Tyr Val
225 230 235 240

Val Gly Tyr Leu Thr Gly Arg Val Phe Lys Phe Pro Glu Ala Ala Asn
245 250 255

Arg Thr Met Ala Ile Glu Ile Gly Thr Gln Ser Ala Gly Leu Ala Ser
260 265 270

Gly Met Ala Gly Arg Phe Phe Thr Pro Glu Ala Ala Leu Pro Gly Ala
275 280 285

Val Ala Ala Leu Val His Asn Ile Thr Gly Ala Val Tyr Val Gly Leu
290 295 300

Val Arg Asn Arg Pro Leu Thr Lys Ala Ser Arg Lys Lys Glu Ser Val
305 310 315 320

Ala Val Ser Ser

<210> 441
<211> 844
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(844)
<223> FRXA02402

<400> 441
cactactgcg ttaaggtatg aaagttcgca caccagcgat ttaattctgt gcccaccact 60

agcacgacca tttcagtttt aactttcttg gagttttcta gtg tcc aaa aca gaa 115
Val Ser Lys Thr Glu
1 5

gaa ggc cgt tca gcg gcc ata att att tac gcg ttt cca act ttc att 163
Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala Phe Pro Thr Phe Ile
10 15 20

ctg ctg ggc gcg atc att gcg ttt atc ttc ccg gaa cca ttc att ccg 211

```
Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro Glu Pro Phe Ile Pro
            25                  30                  35

ctg aca aac tac att aat atc ttc ctc acg atc atc atg ttc acc atg   259
Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile Ile Met Phe Thr Met
        40                  45                  50

ggt ttg acc ttg acg gtg ccc gat ttt cag atg gtg ctt aaa cgt cca   307
Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met Val Leu Lys Arg Pro
    55                  60                  65

ctg cct atc ttg atc ggt gta gta gcg cag ttt gtc atc atg cca ttc   355
Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe Val Ile Met Pro Phe
70                  75                  80                  85

ctg gcg atc gtg gtt gcg aaa atg ttc aac ctc aac cca gca ctc gcc   403
Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu Asn Pro Ala Leu Ala
                90                  95                  100

gtt ggc ctt ctc atg ctg gga tcc gtt ccg ggt ggc acc tcc tcc aat   451
Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly Gly Thr Ser Ser Asn
            105                 110                 115

gtg att gcg ttt ctc gcc cga gga gat gtc gcg cta tcg gtc acc atg   499
Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala Leu Ser Val Thr Met
        120                 125                 130

acc tct gtg tcc acc att gtt tcc cca atc atg acg cct ttc ctc atg   547
Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met Thr Pro Phe Leu Met
    135                 140                 145

ctc atg ctg gca ggt act gaa acc gcc gtc gat ggt gga ggc atg gcg   595
Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp Gly Gly Gly Met Ala
150                 155                 160                 165

tgg act ttg gta caa aca gtg ctg ctg cct gtg atc atc ggc cta gtt   643
Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val Ile Ile Gly Leu Val
                170                 175                 180

ctg cgt gtc ttc ttg aac aag tgg atc gac aag att ttg ccg atc ctt   691
Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys Ile Leu Pro Ile Leu
            185                 190                 195

cct tat ctc tcc atc ctc ggt atc ggt ggc gtg gtg ttc ggc gca gtc   739
Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val Val Phe Gly Ala Val
        200                 205                 210

gca gcc aac gcg gaa cga ctc gtg tct gtc gga ctc atc gtg ttc gtt   787
Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly Leu Ile Val Phe Val
    215                 220                 225

gca gtt atc gtg cac aac gta ctt gga tac gtt gtg gga tac ctc acc   835
Ala Val Ile Val His Asn Val Leu Gly Tyr Val Val Gly Tyr Leu Thr
230                 235                 240                 245

ggc cgt gta                                                      844
Gly Arg Val
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<210> 442

<211> 248
<212> PRT
<213> Corynebacterium glutamicum

<400> 442

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Val Ser Lys Thr Glu Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala
  1               5                  10                  15

Phe Pro Thr Phe Ile Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro
             20                  25                  30

Glu Pro Phe Ile Pro Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile
         35                  40                  45

Ile Met Phe Thr Met Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met
     50                  55                  60

Val Leu Lys Arg Pro Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe
 65                  70                  75                  80

Val Ile Met Pro Phe Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu
                 85                  90                  95

Asn Pro Ala Leu Ala Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly
            100                 105                 110

Gly Thr Ser Ser Asn Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala
        115                 120                 125

Leu Ser Val Thr Met Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met
    130                 135                 140

Thr Pro Phe Leu Met Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp
145                 150                 155                 160

Gly Gly Gly Met Ala Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val
                165                 170                 175

Ile Ile Gly Leu Val Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys
            180                 185                 190

Ile Leu Pro Ile Leu Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val
        195                 200                 205

Val Phe Gly Ala Val Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly
    210                 215                 220

Leu Ile Val Phe Val Ala Val Ile Val His Asn Val Leu Gly Tyr Val
225                 230                 235                 240

Val Gly Tyr Leu Thr Gly Arg Val
                245
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<210> 443
<211> 1389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1366)
<223> RXS00654

<400> 443
cagcaatagc gattattgct tgattgtgtg tttttagatc ttcggttctc ttcactcaac 60

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tgctgtgaag tgccacctgt ttggaaaggc gaacacgata gtg ctc gat att ttg   115
                                              Val Leu Asp Ile Leu
                                                1               5

att tac ccg gtg tct gga gtg atg aag ctg tgg cac ctg ctt ctt cac   163
Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp His Leu Leu Leu His
                   10                  15                  20

aac gtt gcg ggt ttg gac gat tca ctg gcg tgg ttc ttt tcc ctt ttc   211
Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp Phe Phe Ser Leu Phe
               25                  30                  35

ggc ctt gtc atc acg atc cgt gca att atc gcg cct ttc acc tgg cag   259
Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala Pro Phe Thr Trp Gln
           40                  45                  50

atg tat aag tcg ggc cgc act gcc gca cat att cgt cct cac cgc gct   307
Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile Arg Pro His Arg Ala
       55                  60                  65

gcg ctc cgg gaa gaa tac aag gga aag tac gat gaa gcg tcc att cgg   355
Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp Glu Ala Ser Ile Arg
   70                  75                  80                  85

gag ttg cag aag cgc cag aat gat ttg aat aag gaa tac ggc att aac   403
Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys Glu Tyr Gly Ile Asn
                   90                  95                 100

ccg ctg gca ggt tgt gtg cct ggg ctg atc cag ata ccg att gtc ctt   451
Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln Ile Pro Ile Val Leu
               105                 110                 115

ggt ctt tac tgg gca ctt ctc cgc atg gct cgc cct gaa ggt ggt ttg   499
Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg Pro Glu Gly Gly Leu
           120                 125                 130

gaa aat ccc gtc ttc cag tcg atc ggc ttc cta act cct gag gaa gtg   547
Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu Thr Pro Glu Glu Val
       135                 140                 145

gaa tct ttc ctc gct ggt cgc gtg agc aat gtg cct ctg ccc gct tat   595
Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val Pro Leu Pro Ala Tyr
   150                 155                 160                 165

gtt tcg atg ccc act gag cag cta aaa tat ttg agc acc acg cag gcg   643
Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu Ser Thr Thr Gln Ala
                   170                 175                 180

gaa gtt ctt agt ttc gtt ttg cca ctg ttc atc aca gcc gca atc ctc   691
Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile Thr Ala Ala Ile Leu
               185                 190                 195

acc gca atc aac atg gcg atg tcc atg tac cgc agc ttc caa acc aac   739
Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg Ser Phe Gln Thr Asn
           200                 205                 210
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gat tac gca tcc gga ttc tct aac ggc atg ctg aag ttc atg atc gtg   787
Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu Lys Phe Met Ile Val
    215                 220                 225

atg tcg atc ctc gcg ccg atc ttc cca ctg tcc ctt ggc ctc aca gga   835
Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser Leu Gly Leu Thr Gly
230                 235                 240                 245

cca ttc ccc aca gca atc gca ctc tat tgg gtc agc aac aac ctg tgg   883
Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val Ser Asn Asn Leu Trp
                250                 255                 260

acg ctc ctc caa aca atc atc atg atg gtc att ttg gaa cgc aaa tac   931
Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile Leu Glu Arg Lys Tyr
            265                 270                 275

cca ctt acc gac gat ttc aaa gtg cac cac cta gag cag cgc gac atc   979
Pro Leu Thr Asp Asp Phe Lys Val His His Leu Glu Gln Arg Asp Ile
        280                 285                 290

tac cgc gca aaa caa aaa gaa aag cgc atc ttc ctg tgg aca cga cgc   1027
Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe Leu Trp Thr Arg Arg
    295                 300                 305

aaa aac cgc gcc ctg atg att ctc acc cca tgg aac gcc tca acg ctt   1075
Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp Asn Ala Ser Thr Leu
310                 315                 320                 325

cac gca aca aac gtg gaa ctc acc aaa acc cgt act gcc gaa atc aac   1123
His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg Thr Ala Glu Ile Asn
                330                 335                 340

gaa gca aaa cag gcc cgc aaa gaa atc gcg aac aag agg cgc gaa acg   1171
Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn Lys Arg Arg Glu Thr
            345                 350                 355

caa cgt gaa atg aac cgc gcc gcc atg cag cgc tta aag cag cgt cgc   1219
Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg Leu Lys Gln Arg Arg
        360                 365                 370

gct gag gtt aaa gct aaa aag aag ggg ctt atc gac gcc tcc ccc aac   1267
Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile Asp Ala Ser Pro Asn
    375                 380                 385

gaa gat acc cct tcg gaa aat gaa gaa act aaa ttg agt agt ccg cag   1315
Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys Leu Ser Ser Pro Gln
390                 395                 400                 405

gtg gag ccg aca aca act gcc gag cca aat cgc gag ccg tct caa gag   1363
Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg Glu Pro Ser Gln Glu
                410                 415                 420

gac tgatgttgtg gaccaatcga gat                                    1389
Asp
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<210> 444
<211> 422
<212> PRT

<213> Corynebacterium glutamicum

<400> 444

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Val Leu Asp Ile Leu Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp
  1               5                  10                  15

His Leu Leu Leu His Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp
             20                  25                  30

Phe Phe Ser Leu Phe Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala
         35                  40                  45

Pro Phe Thr Trp Gln Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile
     50                  55                  60

Arg Pro His Arg Ala Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp
 65                  70                  75                  80

Glu Ala Ser Ile Arg Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys
                 85                  90                  95

Glu Tyr Gly Ile Asn Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln
            100                 105                 110

Ile Pro Ile Val Leu Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg
        115                 120                 125

Pro Glu Gly Gly Leu Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu
    130                 135                 140

Thr Pro Glu Glu Val Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val
145                 150                 155                 160

Pro Leu Pro Ala Tyr Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu
                165                 170                 175

Ser Thr Thr Gln Ala Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile
            180                 185                 190

Thr Ala Ala Ile Leu Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg
        195                 200                 205

Ser Phe Gln Thr Asn Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu
    210                 215                 220

Lys Phe Met Ile Val Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser
225                 230                 235                 240

Leu Gly Leu Thr Gly Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val
                245                 250                 255

Ser Asn Asn Leu Trp Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile
            260                 265                 270

Leu Glu Arg Lys Tyr Pro Leu Thr Asp Asp Phe Lys Val His His Leu
        275                 280                 285

Glu Gln Arg Asp Ile Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe
    290                 295                 300

Leu Trp Thr Arg Arg Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp
```

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305                 310                 315                 320

Asn Ala Ser Thr Leu His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg
                325                 330                 335

Thr Ala Glu Ile Asn Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn
            340                 345                 350

Lys Arg Arg Glu Thr Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg
        355                 360                 365

Leu Lys Gln Arg Arg Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile
    370                 375                 380

Asp Ala Ser Pro Asn Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys
385                 390                 395                 400

Leu Ser Ser Pro Gln Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg
                405                 410                 415

Glu Pro Ser Gln Glu Asp
            420
```